

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: <u>8/15</u>	Search Site	Vendors
Searcher: <u>D. Schaefer 308-4292</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: <u>75</u>	<input checked="" type="checkbox"/> CM-1 <u>GA-03</u>	<input type="checkbox"/> STN
Elapsed time: <u>14</u>	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: _____	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<u>12</u> <input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: <u>5</u>	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>Compugen + GCG</u>

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Schreiber, David

73393

From: Yu, Misook
Sent: Wednesday, August 14, 2002 12:56 PM
To: Schreiber, David
Subject: 09/499,662

Search notes

David,

Is it possible search

1. (X, 18-30 aa)-SEQ ID NO:2-(X, 14 aa)-SEQ ID NO:3-(X, 32 aa)-SEQ ID NO:4-(X, 11 aa) string and
2. (X, 23aa)-SEQ ID NO:5-(X, 15 aa)-SEQ ID NO:6-(X, 32 aa)-SEQ ID NO:7-(X, 10 aa)?

All the SEQ ID NO are small peptides.

Please compare SEQ ID NO:50, 52, 54, 109, 107, 129, 131, 127 against each other. I would like to know what is the differences in the seqs. They are all 218 aa antibody light chain.

Please compare SEQ ID NO:89, 117, 143, 145, 147, 155 against each other.

Please search SEQ ID 129, 131, ~~127~~, 143, 145, 147, 157. They are all amino acid sequences either 218 or 451 aa.

Please search SEQ ID NO:1 (10aa)

Do I have to get approval from someone for these many seq searches?

Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
CM1-8E18 (Room)
CM1-8E12 (Mail Box)

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:12 ; Search time 53.64 Seconds
(without alignments)
7.218 Million cell updates/sec

Title: US-09-499-662-1
Perfect score: 59
Sequence: 1 RFQNTKCRCK 10

Scoring table:
BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	59	100.0	324	1	TNR6_RAT
2	59	100.0	332	1	TNR6_PIG
3	59	100.0	335	1	TNR6_HUMAN
4	55	93.2	323	1	TNR6_BOVIN
5	51	86.4	327	1	TNR6_MOUSE
6	40	67.8	468	1	T10A_HUMAN
7	39	66.1	272	1	TNR4_MOUSE
8	39	66.1	277	1	TNR4_HUMAN
9	37	62.7	360	1	WNT2_MOUSE
10	37	62.7	454	1	TR1A_MOUSE
11	36	61.0	58	1	SCK2_MESMA
12	36	61.0	59	1	SCK3_MESMA
13	36	61.0	219	1	NOLA_BRAEL
14	36	61.0	310	1	YAHB_ECOLI
15	36	61.0	326	1	VEGD_RAT
16	36	61.0	351	1	WN2B_XENLA
17	36	61.0	358	1	VEGD_MOUSE
18	35	59.3	36	1	SCK3_LEIOH
19	35	59.3	350	1	WNT2_BRARE
20	35	59.3	360	1	WNT2_HUMAN
21	35	59.3	413	1	YPRB_BACSU
22	35	59.3	440	1	T10B_HUMAN
23	35	59.3	842	1	ORP7_HUMAN
24	35	59.3	843	1	CO7_HUMAN
25	34	57.6	37	1	SCK2_LEIOH
26	34	57.6	37	1	SCRC_LEIOH
27	34	57.6	86	1	TAT_HVIND
28	34	57.6	99	1	TAT_HVIEL
29	34	57.6	148	1	VEGH_ORFN7
30	34	57.6	259	1	T10C_HUMAN
31	34	57.6	453	1	NRAM_IARWIL
32	34	57.6	454	1	NRAM_IAPUE
33	34	57.6	469	1	NRAM_IAPUR

RESULT 1

ID	TNR6_RAT	STANDARD;	PRT;	324 AA.
AC	Q63199;			
DT	15-JUL-1999 (Rel. 38, Created)			
DT	15-JUL-1999 (Rel. 38, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).			
DE	DE			
GN	TNFRSF6 OR PT1 OR FAS.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RC	STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;			
RA	MEDLINE-94128114; Pubmed-7507668;			
RA	Kimura K., Yamamoto M., Wakatsuki T.;			
RT	"A variant mRNA species encoding a truncated form of Fas antigen in the rat liver."			
RL	Biochem. Biophys. Res. Commun. 198;666-674(1994).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.			
CC	-1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.			
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.			
CC	-----			
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CC	-----			
DR	EMBL; D26112; BAA05108.1; -			
DR	HSP; P25445; IDDF.			
DR	InterPro; IPR000488; Death.			
DR	InterPro; IPR001368; TNFR_c6.			
DR	Pfam; PF00531; death; 1.			
DR	Pfam; PF00020; TNFR_c6; 3.			
DR	SMART; SM00005; DEATH; 1.			
DR	SMART; SM00208; TNFR; 3.			
DR	PROSITE; PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.			

P52172 drosophila
P25509 placobdella
P25510 placobdella
P01499 apis mellif
Q9ni16 mesobuthus
P55950 callinectes
O55038 mus musculu
P12453 human immun
P23252 hordium vul
O62802 canis fami
P22955 red clover
P38565 xenopus lae

ALIGNMENTS

```
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 324
FT
FT DOMAIN 22 171
FT TRANSMEM 172 188
FT DOMAIN 189 324
FT REPEAT 43 79
FT REPEAT 80 123
FT REPEAT 124 163
FT REPEAT 219 303
FT DOMAIN 220 303
FT CARBOHYD 43 43
FT CARBOHYD 114 114
FT CARBOHYD 132 132
FT CARBOHYD 132 132
SQ SEQUENCE 324 AA; 36835 MW; D25D583C909D9D09 CRC64;

Query Match 100.0%; Score 59; DB 1; Length 324;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 117 RTQNTKCRCK 126

RESULT 2
TNR6_PIG STANDARD; PRT; 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC
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CC
CC -----
DR EMBL; AJ001202; CAA04596.1; -.
DR HSP; P25445; 1DDF.
```

```
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 332
FT DOMAIN 17 175
FT TRANSMEM 176 192
FT DOMAIN 193 332
FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 45 81
FT REPEAT 82 125
FT REPEAT 126 164
FT REPEAT 227 311
FT CARBOHYD 38 38
FT CARBOHYD 116 116
FT CARBOHYD 116 116
SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;

Query Match 100.0%; Score 59; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
DB 119 RTQNTKCRCK 128

RESULT 3
TNR6_HUMAN STANDARD; PRT; 335 AA.
ID TNR6_HUMAN
AC P25445;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis.";
RL Cell 66:233-243(1991).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE=92268122; PubMed=1375228;
RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the APO-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the fas antigen.";
RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Urinary bladder;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
```

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RP STRUCTURE BY NMR OF 218-335
RX MEDLINE-97122332; PubMed=8967952;
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";
RL Nature 384:638-641(1996).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".
CC -----
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CC -----
DR EMBL; M67454; AAA63174.1; -.
DR EMBL; X63717; CAA45250.1; -.
DR EMBL; BC012479; AAH12479.1; -.
DR PIR; A40036; A40036.
DR PIR; S24543; S24543.
DR PDB; 1DDF; 12-NOV-97.
DR MIM; 134637; -.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW 3D-structure.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 335 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 17 173 SUPERFAMILY MEMBER 6.
FT TRANSMEM 174 190 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 191 335 POTENTIAL.
FT REPEAT 47 83 CYTOPLASMIC (POTENTIAL).
FT REPEAT 84 127 TNFR-CYS 1.
FT REPEAT 128 166 TNFR-CYS 2.
FT REPEAT 230 314 TNFR-CYS 3.
FT DOMAIN 118 136 DEATH.
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 335 AA; 37732 MW; 0139942535111410 CRC64;
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Query Match 100.0%; Score 59; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 RTQNTKCRCK 10
|
Db 121 RTQNTKCRCK 130
```

RESULT 4

```
TNR6_BOVIN
ID TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen Fas) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96226401; PubMed=86341151;
RA Yoo J., Stone R.F., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234(1996).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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CC -----
DR EMBL; U34794; AAC48546.1; -.
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 17 170 SUPERFAMILY MEMBER 6.
FT TRANSMEM 171 188 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 189 323 POTENTIAL.
FT REPEAT 45 80 CYTOPLASMIC (POTENTIAL).
FT REPEAT 81 124 TNFR-CYS 1.
FT REPEAT 125 163 TNFR-CYS 2.
FT REPEAT 238 306 TNFR-CYS 3.
FT DOMAIN 238 306 DEATH.
SQ SEQUENCE 323 AA; 36445 MW; 4D88A90E9E1F4892 CRC64;
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Query Match 93.2%; Score 55; DB 1; Length 323;
Best Local Similarity 90.0%; Pred. No. 0.0065;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RTQNTKCRCK 10
Db 118 RTNTRKCRCK 127

RESULT 5
TNR6_MOUSE STANDARD; PRT; 327 AA.
AC P25446;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR APT1 OR FAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92148151; PubMed=13711136;
RA Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,
RA Copeland N.G., Jenkins N.A., Nagata S.;
RT "The cDNA structure, expression, and chromosomal assignment of the
RT mouse Fas antigen.";
RL J. Immunol. 148:1274-1279(1992).
RN [2]
RP SEQUENCE OF 1-96 FROM N.A.
RX MEDLINE=93189576; PubMed=7680478;
RA Adachi M., Watanabe-Fukunaga R., Nagata S.;
RT "Aberrant transcription caused by the insertion of an early
RT transposable element in an intron of the Fas antigen gene of lpr
RT mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).
RN [3]
RP VARIANT LPR.
RX MEDLINE=92195401; PubMed=1372994;
RA Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Nagata S.;
RT "Lymphoproliferation disorder in mice explained by defects in Fas
RT antigen that mediates apoptosis.";
RL Nature 356:314-317(1992).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,
CC LIVER, LUNG, HEART, AND ADULT OVARY.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- DISEASE: DEFECTS IN TNFRSF6 ARE THE CAUSE OF A LYMPHOPROLIFERATION
CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY
CC PRODUCTION.
CC -!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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Db EMBL; M83649; AAA37593.1; -
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DR EMBL; S56490; AAB25700.1; -
DR EMBL; S56485; AAB25700.1; JOINED.
DR EMBL; S56486; AAB25700.1; JOINED.
DR PIR; A46484; A46484.
DR HSSP; P25445; LDDF.
DR MGD; MGI:95484; Tnfrsf6.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death_1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR PROSITE; PS00107; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
KW Disease mutation.
FT SIGNAL 1 21 TUMOR NECROSIS FACTOR RECEPTOR
FT CHAIN 22 327 SUPERFAMILY MEMBER 6.
FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 186 POTENTIAL.
FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 79 TNFR-CYS 1.
FT REPEAT 80 123 TNFR-CYS 2.
FT REPEAT 124 162 TNFR-CYS 3.
FT DOMAIN 222 306 DEATH.
FT CARBOHYD 43 43 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 246 246 I -> N (IN LPR).
FT SEQUENCE 327 AA; 37418 MW; F6BFFC5ACE356EEE CRC64;

Query Match 86.4%; Score 51; DB 1; Length 327;
Best Local Similarity 88.9%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQNTKCRCK 10
Db 118 TQNTKCRCK 126

RESULT 6
T10A_HUMAN STANDARD; PRT; 468 AA.
AC O00220;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10A precursor (Death
DE receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL
DE receptor-1) (TRAIL-RL).
GN TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97238921; PubMed=9082980;
RA Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., Ni J.,
RA Dixit V.M.;
RT "The receptor for the cytotoxic ligand TRAIL.";
RL Science 276:111-113(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=98090092; PubMed=9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL Immunity 7:821-830(1997).
CC -!- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates
CC apoptosis in a caspase-dependent manner. Can trigger the nuclear
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CC factor kappaB-pathway and can bind the cytoplasmic adapter
CC molecule FADD/MORF1 which engages initiator caspases such as
CC caspase 8 leading to subsequent activation of effector caspases
CC that execute apoptotic death of the cell.
CC -1- SUBUNIT: Can interact with TRADD and RIP.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed. High levels are found in
CC spleen, peripheral blood leukocytes, small intestine and thymus,
CC but also in K562 erythroleukemia cells, MCF7 breast carcinoma
CC cells and activated T-cells.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U90875; AAC51226.1; -;
CC MIM; 603611; -;
CC HSP; P19438; LEXT.
CC InterPro; IPR000488; Death.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00020; TNFR_c6; 2.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 2. DEATH; 1.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS50050; TNFR_NGFR_2; 2.
CC Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 468
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 10A.
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FT DOMAIN 263 468
FT REPEAT 147 188
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FT REPEAT 24126 24164
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FT REPEAT 24240 24278
FT REPEAT 24278 24316
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FT REPEAT 26938 26976
FT REPEAT 26976 27014
FT REPEAT 27014 27052
FT REPEAT 27052 27090
FT REPEAT 2709

P43489; Q13663;
 01-NOV-1995 (Rel. 32, Created)
 01-NOV-1995 (Rel. 32, Last sequence update)
 16-OCT-2001 (Rel. 40, Last annotation update)
 Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen).
 GN TNFRSF4 OR TKGPI1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94170844; PubMed=7510240;
 RA Latza U., Duerkop H., Schnittger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.;
 RT "The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen.";
 RL Eur. J. Immunol. 24:677-683(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95219871; PubMed=7704935;
 RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
 RT "Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";
 RL Circ. Shock 44:30-34(1994).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD134 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
 CC -----
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 CC -----
 DR EMBL; X75962; CAA53576.1; -;
 DR EMBL; X75962; AAB33944.1; ALT_INIT.
 DR HSP; P25942; 1CDF.
 DR MIM; 600315; -;
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR ProDom; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS50050; TNFR_NGFR_2; 2.
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL
 FT CHAIN 1 28 POTENTIAL.
 FT CHAIN 29 277 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 4.
 FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 235 POTENTIAL.
 FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 30 65 TNFR-CYS 1.
 FT REPEAT 66 107 TNFR-CYS 2.
 FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 127 167 TNFR-CYS 4.
 FT REPEAT 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 277 AA; 29340 MW; 49F15525941550BF CRC64;

Query Match 66.1%; Score 39; DB 1; Length 277;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TQNTKCRCK 10
 II:IIIIII:
 DB 102 TQDTVCRCR 110
 RESULT 9
 WNT2_MOUSE
 ID WNT2_MOUSE STANDARD; PRT; 360 AA.
 AC P21552;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Wnt-2 protein precursor (IRP protein) (INT-1 related protein).
 GN WNT2 OR WNT-2 OR IRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90126394; PubMed=2693041;
 RA McMahon J.A., McMahon A.P.;
 RT "Nucleotide sequence, chromosomal localization and developmental expression of the mouse int-1-related gene.";
 RL Development 107:643-650(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91122634; PubMed=2279700;
 RA Gavin B.J., McMahon J.A., McMahon A.P.;
 RT "Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult mouse development.";
 RL Genes Dev. 4:2319-2332(1990).
 CC -1- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN. MAY BE A SIGNALING MOLECULE WHICH AFFECTS THE DEVELOPMENT OF DISCRETE REGIONS OF TISSUES. IS LIKELY TO SIGNAL OVER ONLY FEW CELL DIAMETERS.
 CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the extracellular matrix.
 CC -1- TISSUE SPECIFICITY: IN EMBRYOS IN THE DEVELOPING ALLANTOIS, IN PERICARDIUM HEART, AND VENTRAL-LATERAL MESODERM; IN ADULTS, IN LUNG, BRAIN, HEART AND PLACENTA.
 CC -1- SIMILARITY: BELONGS TO THE WNT FAMILY.
 DR PIR; B36470; B36470.
 DR PIR; A43558; A43558.
 DR MGI; 98954; Wnt2.
 DR InterPro; IPR000970; Wnt1.
 DR Pfam; PF00110; wnt; 1.
 DR PRINTS; PR01349; WNTPROTEIN.
 DR SMART; SM00097; WNT1; 1.
 DR PROSITE; PS00246; WNT1; 1.
 KW Developmental protein; Glycoprotein; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 360 WNT-2 PROTEIN.
 FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 360 AA; 40496 MW; 5EC265FD3815EF1D CRC64;

Query Match 62.7%; Score 37; DB 1; Length 360;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TQNTKCRCK 10
 I:IIIIII:
 DB 319 TRMTKECK 327
 RESULT 10
 TRIA_MOUSE
 ID TRIA_MOUSE STANDARD; PRT; 454 AA.
 AC P25118;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)
Tumor necrosis factor receptor 1 precursor (p60) (TNF-RI) (TNF-RI) (p55).
TNFRSF1A OR TNFR1 OR TNFR-1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=91187885; PubMed=1849278;
Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.I., Goeddel D.V.;
"Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.";
Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
[2]
SEQUENCE FROM N.A.
MEDLINE=91246168; PubMed=1645445;
Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;
"Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";
Mol. Cell. Biol. 11:3020-3026(1991).
[3]
SEQUENCE FROM N.A.
MEDLINE=91285014; PubMed=1647956;
Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissonerghis A.M., Gray P.W., Feldmann M., Foxwell B.M.J.;
"Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis factor receptor.";
Eur. J. Immunol. 21:1649-1656(1991).
[4]
SEQUENCE FROM N.A.
TISSUE=Splice;
MEDLINE=82039815; PubMed=1657766;
Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;
"Molecular cloning and expression of the mouse Tnf receptor type b.";
Immunogenetics 34:338-340(1991).
[5]
SEQUENCE FROM N.A.
MEDLINE=94245292; PubMed=8188324;
Bebo B.F., Linthicum D.S.;
"Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.";
Immunogenetics 39:450-451(1994).
[6]
SEQUENCE FROM N.A.
MEDLINE=93156721; PubMed=8381516;
Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steinmetz M.;
"Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.";
Mol. Immunol. 30:165-175(1993).
-I- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
-I- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: Type I membrane protein.
-I- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-I- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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CC EMBL; M60468; AAA39751.1; -
DR EMBL; M59377; AAA40464.1; -
DR EMBL; X59238; CAA41922.1; -
DR EMBL; X57796; CAA40936.1; -
DR EMBL; L26349; AAA59361.1; -
DR EMBL; M76656; AAA40465.1; -
DR EMBL; M88067; AAA40465.1; JOINED.
DR EMBL; M76655; AAA40465.1; JOINED.
DR PIR; A38634; GOMST1.
DR PIR; S16677; S16677.
DR PIR; S19021; S19021.
DR HSP; P19438; 1EXT.
DR MGD; MGI:1314884; Tnfrsfla.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
DR PROSITE; PS00117; DEATH_DOMAIN; 1.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR 1.
FT DOMAIN 22 212 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 213 235 POTENTIAL.
FT DOMAIN 236 454 CYTOPLASMIC (POTENTIAL).
FT REPEAT 43 82 TNFR-CYS 1.
FT REPEAT 83 125 TNFR-CYS 2.
FT REPEAT 126 166 TNFR-CYS 3.
FT REPEAT 167 196 TNFR-CYS 4.
FT DOMAIN 339 349 N-SMASE ACTIVATION DOMAIN (NSD).
FT DOMAIN 356 441 DEATH.
FT DISULFID 44 58 BY SIMILARITY.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 81 BY SIMILARITY.
FT DISULFID 84 99 BY SIMILARITY.
FT DISULFID 102 117 BY SIMILARITY.
FT DISULFID 105 125 BY SIMILARITY.
FT DISULFID 127 143 BY SIMILARITY.
FT DISULFID 146 158 BY SIMILARITY.
FT DISULFID 149 166 BY SIMILARITY.
FT DISULFID 168 179 BY SIMILARITY.
FT DISULFID 182 191 BY SIMILARITY.
FT DISULFID 185 195 BY SIMILARITY.
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 394 394 R -> G (IN REF. 6).
SQ SEQUENCE 454 AA; 50129 MW; 0710C2E8C3C2B6D9 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 454;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TQNTKRC 9
| | | | |
Db 161 TQNTVCNC 168

RESULT 11
SCK2_MESMA
ID SCK2_MESMA STANDARD; PRT; 58 AA.

Q9NTI5; P58489;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Toxin BMTX2 precursor (Neurotoxin TX2).
 OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Buthus.
 OX NCBI_TaxID=34649;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20164067; PubMed=10698710;
 RA Dai L., Wu J.-J., Gu Y.H., Lan Z.D., Ling M.-H., Chi C.-W.;
 RT "Genomic organization of three novel toxins from the scorpion Buthus
 martensii Karsch that are active on potassium channels.";
 RL Biochem. J. 346:805-809(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20436245; PubMed=10978761;
 RA Zeng X.-C., Zhu Z.H., Li W.-X., Zhu S.-Y., Peng F., Mao X., Liu H.;
 RT "Molecular cloning and genomic organization of a K(+) channel toxin
 from the Chinese scorpion Buthus martensii Karsch.";
 RL Toxicon 39:407-410(2001).
 RN [3]
 RP SEQUENCE OF 22-58, SYNTHESIS, AND CHARACTERIZATION.
 RX PubMed=9354615;
 RA Romi-Lebrun R., Lebrun B., Martin-Eauclaire M.-F., Ishiguro M.,
 RA Escoubas P., Wu F.O., Hisada M., Pongs O., Nakajima T.;
 RT "Purification, characterization, and synthesis of three novel toxins
 from the Chinese scorpion Buthus martensii, which act on K⁺ channels.";
 RL Biochemistry 36:13473-13482(1997).
 RN [4]
 RP STRUCTURE BY NMR OF 22-58.
 RC TISSUE=Venom;
 RX MEDLINE=98400946; PubMed=9730813;
 RA Blanc E., Romi-Lebrun R., Bornet O., Nakajima T., Darbon H.;
 RT "Solution structure of two new toxins from the venom of the Chinese
 scorpion Buthus martensii Karsch blockers of potassium channels.";
 RL Biochemistry 37:12412-12418(1998).
 CC -!- FUNCTION: Potent blocker of both large-conductance calcium-
 activated potassium channels (BKCa channels) and voltage-gated
 potassium channels (Kv1.3).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
 CHANNEL INHIBITORS SUBFAMILY.
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 CC -----
 DR EMBL; AF208300; AAF63972.1; -;
 DR PDB; 2BMT; 13-JAN-99.
 DR InterPro; IPR001947; Charybdotoxin.
 DR Pfam; PF00451; toxin_2; 1.
 DR ProDom; P003586; Charybdotoxin; 1.
 DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
 KW Neurotoxin; Potassium channel inhibitor; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 58 TOXIN BMTX2.
 FT MOD_RES 22 22 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 28 49
 FT DISULFID 34 54
 FT DISULFID 38 56
 SQ SEQUENCE 58 AA; 6507 MW; F19AA7351B9708B8 CRC64;
 Query Match 61.0%; Score 36; DB 1; Length 58;
 Best Local Similarity 55.6%; Pred. No. 3.2;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RTQNTKRC 9
 Db 48 KCWNSKRC 56
 RESULT 12
 SCK3_MESMA STANDARD; PRT; 59 AA.
 AC Q9NBG9;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Toxin BMTX3 precursor (Neurotoxin TX3).
 OS Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Buthus.
 OX NCBI_TaxID=34649;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ye J., Li Y., Yan Y., Ji Y.;
 RT "Isolation, characterization and cDNA cloning of a novel toxin from
 the Chinese scorpion Buthus martensii Karsch, which acts on potassium
 channel.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Blocks potassium channels.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE SHORT SCORPION TOXIN FAMILY. POTASSIUM
 CHANNEL INHIBITORS SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; AF249746; AAF87224.1; -;
 DR HSP; P24662; 2KTX.
 DR InterPro; IPR001947; Charybdotoxin.
 DR InterPro; IPR003614; Knt1.
 DR Pfam; PF00451; toxin_2; 1.
 DR ProDom; P003586; Charybdotoxin; 1.
 DR SMART; SM00505; Knt1; 1.
 DR PROSITE; PS01138; SCORP_SHORT_TOXIN; 1.
 KW Neurotoxin; Potassium channel inhibitor; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 59 TOXIN BMTX3.
 FT DISULFID 30 51 BY SIMILARITY.
 FT DISULFID 36 56 BY SIMILARITY.
 FT DISULFID 40 58 BY SIMILARITY.
 SQ SEQUENCE 59 AA; 6429 MW; A1A1A2C415D456A7 CRC64;
 Query Match 61.0%; Score 36; DB 1; Length 59;
 Best Local Similarity 55.6%; Pred. No. 3.2;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RTQNTKRC 9
 Db 50 KCQNNQRC 58
 RESULT 13
 NOLA_BRAEL STANDARD; PRT; 219 AA.
 ID NOLA_BRAEL
 AC P50329;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Nodulation protein nola (Fragment).

GN NOLA.
OS Bradyrhizobium elkanii.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group; Bradyrhizobium.
OX NCBI_TaxID=29448;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 94;
RX MEDLINE=95036537; PubMed=7949325;
RA Dobert R.C., Breil B.T., Triplett E.W.;
RT "DNA sequence of the common nodulation genes of Bradyrhizobium
elkanii and their phylogenetic relationship to those of other
nodulating bacteria";
RL Mol. Plant Microbe Interact. 7:564-572(1994).
CC -1- FUNCTION: INVOLVED IN GENOTYPE-SPECIFIC NODULATION OF SOYBEANS.
CC -1- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U04609; AAA63596.1; -;
DR InterPro; IPR000551; HTH_Merr.
DR Pfam; PF00376; merr; 1.
DR SMART; SM00422; HTH_MERR; 1.
DR PROSITE; PS00552; HTH_MERR_FAMILY; 1.
KW Nodulation; Nitrogen fixation; DNA-binding.
FT DNA_BIND 13 32 H-T-H MOTIF (POTENTIAL).
FT NON_TER 219 219
SQ SEQUENCE 219 AA; 24922 MW; 64EA962E8463F029 CRC64;

Query Match 61.0%; Score 36; DB 1; Length 219;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 RTQNTKCRCK 10
I : I : I : I : I :
Db 137 RSQTSRCTCK 146

RESULT 14
YAHB_ECOLI
ID YAHB_ECOLI STANDARD; PRT; 310 AA.
AC P77700;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transcriptional regulator yahb.
GN YAHB OR B0316.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Durcan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis K.,
RA Federspiel N., Hyman R., Kallman S., Komp C., Kurdi O., Lew H., Lin D.,

RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000138; AAC73419.1; -;
DR EMBL; U73857; AAB18042.1; -;
DR EcoGene; EG13586; yahb.
DR InterPro; IPR002197; HTH_Fis.
DR InterPro; IPR000847; HTH_LysR.
DR Pfam; PF00126; HTH_1; 1.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
KW Hypothetical protein; Transcription regulation; DNA-binding;
FT DNA_BIND 22 42 H-T-H MOTIF (POTENTIAL).
FT SEQUENCE 310 AA; 34866 MW; A3EB895E7F69D60C CRC64;

Query Match 61.0%; Score 36; DB 1; Length 310;
Best Local Similarity 71.4%; Pred. No. 14;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 NTKCRCK 10
I : I : I : I : I :
Db 229 NTKCQCQ 235

RESULT 15
VEGD_RAT
ID VEGD_RAT STANDARD; PRT; 326 AA.
AC O35251;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
DE growth factor) (fIGF).
GN FIGF OR VEGFD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Yamada Y., Hirata Y., Nezu J., Shimane M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis
CC and endothelial cell growth, stimulating their proliferation and
CC migration and also has effects on the permeability of blood
CC vessels. May function in the formation of the venous and lymphatic
CC vascular systems during embryogenesis, and also in the maintenance
CC of differentiated lymphatic endothelium in adults. Binds and
CC activates VEGFR-3 (Flt4) receptor (By similarity).
CC -1- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PTM: Undergoes a complex proteolytic maturation which generates a
CC variety of processed secreted forms with increased activity toward
CC VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer
CC linked by disulfide bonds before secretion. The fully processed
CC VEGF-D is composed mostly of two VEGF homology domains (VHDs)
CC bound by non-covalent interactions (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF014827; AAB66557.1; -
DR HSSP; PL5692; LVPP.
DR InterPro; IPR000072; PDGF.
DR Pfam; PF0341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS0278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
KW Cleavage on pair of basic residues; Multigene family.
FT SIGNAL 1 21
FT PROPEP 22 93
FT CHAIN 94 210
FT PROPEP 211 326
FT DOMAIN 227 317
FT REPEAT 227 242
FT REPEAT 263 278
FT REPEAT 282 298
FT REPEAT 306 317
FT DISULFID 116 158
FT DISULFID 147 194
FT DISULFID 151 196
FT DISULFID 141 141
FT DISULFID 150 150
FT CARBOHYD 160 160
FT CARBOHYD 190 190
FT CARBOHYD 292 292
SQ SEQUENCE 326 AA; 37112 MW; 1261AFA373596C00 CRC64;
POTENTIAL.
POTENTIAL.
VASCULAR ENDOTHELIAL GROWTH FACTOR D.
POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-
X(1-3)-C
1 (APPROXIMATE).
2.
3.
4 (INCOMPLETE).
INTRACHAIN (BY SIMILARITY).
INTRACHAIN (BY SIMILARITY).
INTRACHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 61.0%; Score 36; DB 1; Length 326;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 NTKCRC 9

Db 235 NTKCKC 240

Search completed: August 14, 2002, 15:23:12
Job time: 685 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:02 ; Search time 82.88 Seconds
(without alignments)
2.947 Million cell updates/sec

Title: US-09-499-662-1
Perfect score: 59
Sequence: 1 RTQNTKCRCK 10

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	119	2	US-08-219-237B-3
2	59	100.0	119	4	US-08-477-347-14
3	59	100.0	119	4	US-08-476-862-5
4	59	100.0	119	4	US-08-468-560C-3
5	59	100.0	128	4	US-09-180-100-9
6	59	100.0	143	4	US-09-180-100-10
7	59	100.0	144	4	US-09-180-100-21
8	59	100.0	157	4	US-09-180-100-15
9	59	100.0	159	4	US-09-180-100-23
10	59	100.0	219	3	US-08-974-022-45
11	59	100.0	219	4	US-08-795-445A-45
12	59	100.0	219	4	US-08-795-447A-45
13	59	100.0	219	4	US-08-974-186-45
14	59	100.0	219	4	US-08-795-446B-45
15	59	100.0	281	4	US-09-527-236A-3
16	59	100.0	314	1	US-08-444-231-19
17	59	100.0	314	1	US-08-152-443A-19
18	59	100.0	314	5	PCT-US95-17083-4
19	59	100.0	331	4	US-09-086-483A-3
20	59	100.0	335	2	US-08-219-237B-2
21	59	100.0	335	2	US-08-409-338-1
22	59	100.0	335	4	US-08-815-469-6
23	59	100.0	335	4	US-09-290-640-2
24	59	100.0	335	4	US-09-006-353A-7
25	59	100.0	335	4	US-08-468-560C-2
26	59	100.0	335	4	US-09-180-100-20
27	59	100.0	335	5	PCT-US95-17083-2

28	59	100.0	360	4	US-09-180-100-11	Sequence 11, Appl
29	59	100.0	376	4	US-09-180-100-22	Sequence 22, Appl
30	59	100.0	669	4	US-09-013-895A-3	Sequence 3, Appl
31	51	86.4	327	4	US-09-290-640-66	Sequence 66, Appl
32	40	67.8	368	2	US-08-651-579-2	Sequence 2, Appl
33	40	67.8	467	4	US-09-086-483A-6	Sequence 6, Appl
34	40	67.8	468	4	US-09-013-895A-2	Sequence 2, Appl
35	39	66.1	56	4	US-08-866-545-10	Sequence 10, Appl
36	39	66.1	186	1	US-08-089-458B-6	Sequence 6, Appl
37	39	66.1	206	1	US-08-097-827-7	Sequence 7, Appl
38	39	66.1	206	1	US-08-494-574-7	Sequence 7, Appl
39	39	66.1	277	2	US-08-147-784-2	Sequence 2, Appl
40	39	66.1	277	4	US-08-195-967-2	Sequence 2, Appl
41	39	66.1	277	4	US-09-006-353A-12	Sequence 12, Appl
42	39	66.1	277	4	US-08-472-940-2	Sequence 2, Appl
43	39	66.1	416	1	US-08-117-083-61	Sequence 61, Appl
44	39	66.1	438	1	US-08-097-827-11	Sequence 11, Appl
45	39	66.1	438	1	US-08-494-574-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-219-237B-3
; Sequence 3, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-3

Query Match 100.0%; Score 59; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RTQNTKCRCK 10
Db 75 RTQNTKCRCK 84

RESULT 3
US-08-476-862-5
: Sequence 5, Application US/08476862
: Patent No. 6262239
: GENERAL INFORMATION:
: APPLICANT: WALLACH, David
: APPLICANT: BIGDA, Jacek
: APPLICANT: BELETSKY, Igor
: APPLICANT: METT, Igor
: APPLICANT: ENGELMANN, Hartmut
: TITLE OF INVENTION: TNF INHIBITORS

PATENT NO.: 0270390
 GENERAL INFORMATION:
 APPLICANT: NAGATA, Shigekazu
 APPLICANT: ITOH, Naoto
 APPLICANT: YONEHARA, Shin
 TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
 TITLE OF INVENTION: ANTIGEN
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
 STREET: P.O. BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,560C
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR., GERLAD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 20-4393P
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-560C-3

Query Match 100.0%; Score 59; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 75 RTQNTKCRCK 84

RESULT 5
US-09-180-100-9
; Sequence 9, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-9

Query Match 100.0%; Score 59; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 76 RTQNTKCRCK 85

RESULT 6
US-09-180-100-10
; Sequence 10, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu

; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-10

Query Match 100.0%; Score 59; DB 4; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 76 RTQNTKCRCK 85

RESULT 7
US-09-180-100-21
; Sequence 21, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-21

Query Match 100.0%; Score 59; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
Db 92 RTQNTKCRCK 101

RESULT 8
US-09-180-100-15
; Sequence 15, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, No. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 157
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-180-100-15

Query Match 100.0%; Score 59; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 105 RTQNTKCRCK 114
|||||

RESULT 9

US-09-180-100-23
; Sequence 23, Application US/09180100
; Patent No. 6306395
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, NO. 630639510
; APPLICANT: NAGATA, Shigekazu
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE
; FILE REFERENCE: 1110-207P
; CURRENT APPLICATION NUMBER: US/09/180,100
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: PCT/JP97/01502
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-180-100-23

Query Match 100.0%; Score 59; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 92 RTQNTKCRCK 101
|||||

RESULT 10

US-08-974-022-45
; Sequence 45, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-45

Query Match 100.0%; Score 59; DB 3; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130
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RESULT 11

US-08-795-445A-45
; Sequence 45, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-45

Query Match 100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130
|||||

RESULT 12
US-08-795-447A-45
; Sequence 45, Application US/08795447A
; Patent No. 6284728
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-447A-45

Query Match 100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTQTKCRCK 10
Db 121 RTQTKCRCK 130

RESULT 13
US-08-974-186-45
; Sequence 45, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-186-45

Query Match 100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RTQTKCRCK 10
Db 121 RTQTKCRCK 130

RESULT 14
US-08-795-446B-45
; Sequence 45, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-45

Query Match 100.0%; Score 59; DB 4; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130

RESULT 15

US-09-527-236A-3
; Sequence 3, Application US/09527236A
; Patent No. 6358508
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Fan, Ping
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR9
; FILE REFERENCE: PF375P1
; CURRENT APPLICATION NUMBER: US/09/527,236A
; CURRENT FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/052,991
; PRIOR FILING DATE: 1997-06-11
; PRIOR APPLICATION NUMBER: 09/095,094
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/126,019
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/134,220
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-527-236A-3

Query Match 100.0%; Score 59; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130

Search completed: August 14, 2002, 15:17:03
Job time: 686 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:34 ; Search time 230.21 Seconds
(without alignments)
4.825 Million cell updates/sec

Title: us-09-499-662-1
Perfect score: 59
Sequence: 1 RTQNTKCRCK 10

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	AAW83030	Fas epitope recogn
2	59	100.0	10	AAW83030	Human Fas epitope
3	59	100.0	10	AAW83030	Human Fas extracel
4	59	100.0	20	AAW83033	Human Fas peptide
5	59	100.0	20	AAW83033	Human Fas peptide
6	59	100.0	20	AAW83033	Human Fas epitope
7	59	100.0	20	AAW83033	Human Fas extracel
8	59	100.0	144	AAW50286	Human Fas peptide
9	59	100.0	159	AAW50288	Human Fas antigen
10	59	100.0	170	AAW50288	Human Fas receptor
11	59	100.0	173	AAW50288	Human Fas receptor

12	59	100.0	219	22	AAW66978	Fas protein. Unid
13	59	100.0	281	21	AAW66978	Human Fas. Homo s
14	59	100.0	314	16	AAW76238	Fas-delta-TM. Hom
15	59	100.0	314	17	AAW99682	Human Fas soluble
16	59	100.0	314	20	AAW98070	Soluble-Fas recept
17	59	100.0	331	22	AAW50893	Human Fas receptor
18	59	100.0	335	13	AAW80804	Human cell surface
19	59	100.0	335	16	AAW78606	Human Fas protein.
20	59	100.0	335	17	AAW99681	Human Fas antigen.
21	59	100.0	335	17	AAW92528	hFas from plasmid
22	59	100.0	335	18	AAW50289	Human Fas antigen.
23	59	100.0	335	19	AAW49104	Fas protein. Mamm
24	59	100.0	335	21	AAW19341	Amino acid encodin
25	59	100.0	335	21	AAW36267	Human Fas receptor
26	59	100.0	335	21	AAW01335	CD-95 (FAS/APO-1)
27	59	100.0	335	22	AAW50517	Human tumour necro
28	59	100.0	376	18	AAW50287	Human Fas antigen
29	59	100.0	376	19	AAW60037	Antigenic peptide
30	59	100.0	600	16	AAW78610	Expression vector
31	59	100.0	600	17	AAW92526	Fas antigen #1. S
32	59	100.0	669	19	AAW64484	Human TNFRI protei
33	59	100.0	669	16	AAW78612	Plasmid fragment p
34	51	86.4	327	14	AAW41688	Murine Fas. Mus m
35	51	86.4	327	16	AAW78611	Murine Fas antigen
36	51	86.4	327	17	AAW92530	mFas sequence. Sy
37	51	86.4	327	20	AAW86244	Fas ligand (FasL)
38	51	86.4	327	21	AAW19344	Amino acid sequenc
39	51	86.4	576	16	AAW78613	Expression vector
40	51	86.4	592	17	AAW92527	Fas antigen #2. S
41	44	74.6	237	21	AAW53420	Human colon cancer
42	41	69.5	771	21	AAW93336	A human interphoto
43	41	69.5	771	21	AAW57089	Human interphoto
44	40	67.8	368	19	AAW41360	tyb polypeptide.
45	40	67.8	410	20	AAW93577	Human APOBP protei

ALIGNMENTS

RESULT 1
AAW83030
ID AAW83030 standard; Peptide; 10 AA.
XX AC AAW83030;
XX DT 15-MAR-1999 (first entry)
XX DE Fas epitope recognised by MAb HFE7A.
XX KW Fas; epitope; HFE7A; monoclonal antibody; humanised antibody;
XX KW human; apoptosis; autoimmune disease; Hashimoto's disease;
XX KW systemic lupus erythematosus; graft versus host disease;
XX KW Sjogren syndrome; pernicious anaemia; Addison's disease;
XX KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
XX KW rheumatoid arthritis; autoimmune haemolytic anaemia;
XX KW myasthenia gravis; multiple sclerosis; Basedow's disease;
XX KW thrombopenia purpura; insulin-dependent diabetes; allergy;
XX KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
XX KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
XX KW transplant rejection; therapy.
XX OS Homo sapiens.
XX AU9859701-A.
XX PD 08-OCT-1998.
XX PF 30-MAR-1998; 98AU-0059701.
XX PR 08-OCT-1997; 97JP-0276064.
XX PR 01-APR-1997; 97JP-0082953.
XX PR 25-JUN-1997; 97JP-0169088.

PA (SANY) SANKYO CO LTD.
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX Claim 20; Page 184; 292pp; English.
 XX This peptide represents the human Fas epitope recognised by novel
 CC murine anti-human Fas monoclonal antibody HFE7A. It was identified
 CC by ELISA and competitive assays using peptides (see AAW83043-63)
 CC from the extracellular domain of Fas. The epitope is conserved
 CC between mouse and human Fas. The invention provides humanised
 CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
 CC antibodies bind to the Fas epitope. They are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. They are used to evaluate,
 CC in animal models, treatments of diseases that involve Fas/Fas
 CC ligand interactions, and also to treat such diseases, e.g
 CC autoimmune disease (systemic lupus erythematosus, Hashimoto's
 CC disease, graft versus host disease, Sjogren syndrome, pernicious
 CC anaemia, Addison's disease, scleroderma, Goodpasture syndrome,
 CC Crohn's disease, rheumatoid arthritis, autoimmune haemolytic
 CC anaemia, sterility, myasthenia gravis, multiple sclerosis,
 CC Basedow's disease, thrombopenia purpura and insulin-dependent
 CC diabetes), allergies, atopy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerular nephritis, hypoplastic anaemia,
 CC hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 10 AA;
 SQ

Query Match 100.0%; Score 59; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTONTKCRCK 10
 | | | | | | | | | |
 Db 1 rtqntkcrck 10

RESULT 2
 AAB14740
 ID AAB14740 standard; peptide; 10 AA.
 XX AAB14740;
 XX 24-NOV-2000 (first entry)
 DE Human Fas epitope, SEQ ID NO:1.
 KW Human Fas epitope; anti-Fas antibody; murine monoclonal antibody HFE7A;
 KW FERM-BP-5828; humanised antibody; complementarity determining region;
 KW CDR; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancyelophthisis;
 KW hepatitis; AIDS; graft rejection.
 OS Homo sapiens.
 XX JP2000169393-A.
 XX 20-JUN-2000.
 PD 30-SEP-1999; 99JP-0278301.
 PF 30-SEP-1998; 98JP-0276883.
 PR

XX (SANY) SANKYO CO LTD.
 PA WPI; 2000-485645/43.
 DR Preventive or treating agent for the diseases caused by an abnormality
 XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 PT Claim 19; Page 31; 139pp; Japanese.
 XX The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14740 and AAB14751-B14771
 XX represent human Fas epitopes.
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 59; DB 21; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RTONTKCRCK 10
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 Db 1 rtqntkcrck 10

RESULT 3
 AAW90890
 ID AAW90890 standard; peptide; 10 AA.
 XX AAW90890;
 XX 08-AUG-2000 (first entry)
 DE Human Fas extracellular domain peptide fragment.
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Homo sapiens.
 XX EP990663-A2.
 PN 05-APR-2000.
 PD 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI

XX DR WPI; 2000-258930/23.

XX DD New humanized anti-Fas antibody, useful for treating or preventing e.g.

XX PT inflammatory or autoimmune disease, induces apoptosis selectively in

XX PT cells with abnormal Fas-Fas ligand systems

XX PT

XX PS Example reference 6; Page 97; 263pp; English.

XX PS

XX CC This invention describes a novel humanized anti-Fas antibody-like

XX CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

XX CC ligand system, by binding to Fas on the cell surface, and prevents

XX CC apoptosis in cells with a normal system, by inhibiting binding between

XX CC Fas and its ligand. The products of the invention have anti-inflammatory,

XX CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,

XX CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

XX CC antirheumatic, nephrotropic, antinfertility, neuroprotective,

XX CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce

XX CC apoptosis by binding to cell surface Fas or inhibit it by competitive

XX CC inhibition of ligand binding. (I) are used to treat and/or prevent

XX CC diseases associated with the Fas/Fas ligand system, especially systemic

XX CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft

XX CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic

XX CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's

XX CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,

XX CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin

XX CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,

XX CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral

XX CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

XX CC inhibit apoptosis in normal cells but selectively induce it in abnormal

XX CC cells. They bind to both human and murine Fas, so can be evaluated in

XX CC murine disease models. (I) act on the active site of Fas, i.e. they mimic

XX CC the native ligand, do not induce liver disease, and have reduced risk of

XX CC inducing a human anti-murine antibody response. This sequence represents

XX CC a human Fas extracellular domain peptide fragment described in the method

XX CC of the invention.

XX SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 21; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0033;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10

Db | | | | | | | |

1 rtqntkcrck 10

RESULT 4

AAW83053

ID AAW83053 standard; Peptide; 20 AA.

XX AC AAW83053;

XX DT 15-MAR-1999 (first entry)

XX DE Human Fas peptide p11.

XX KW Fas; epitope; HFE7A; monoclonal antibody; humanised antibody;

XX KW human; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;

XX KW systemic lupus erythematosus; graft versus host disease;

XX KW Sjogren syndrome; pernicious anaemia; Addison's disease;

XX KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;

XX KW rheumatoid arthritis; autoimmune haemolytic anaemia;

XX KW myasthenia gravis; multiple sclerosis; Basedow's disease;

XX KW thrombopenia purpura; insulin-dependent diabetes; allergy;

XX KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;

XX KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

XX KW transplant rejection; therapy.

XX OS Synthetic.

OS Homo sapiens.

XX PN AU9859701-A.

XX PD 08-OCT-1998.

XX PF 30-MAR-1998; 98AU-0059701.

XX PR 08-OCT-1997; 97JP-0276064.

XX PR 01-APR-1997; 97JP-0082953.

XX PR 25-JUN-1997; 97JP-0169088.

XX PA (SANY) SANKYO CO LTD.

XX PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX DR WPI; 1998-543440/47.

XX DD New antibodies and proteins bind conserved epitope of Fas antigen -

XX PT used to evaluate drugs in animal models and to treat Fas-associated

XX PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,

XX PT myocarditis, hepatitis and AIDS

XX PS Reference Example 6; Page 87; 292pp; English.

XX CC Synthetic peptides P1-P15 (see AAW83043-57) are partial sequences of

XX CC amino acids 1-157 of the extracellular domain of human Fas, with

XX CC between 9 and 11 amino acid residues overlapping one another. P16

XX CC (see AAW83058) is a negative control having no homology with human

XX CC Fas. P1-P16 were used in an ELISA, which demonstrated that novel

XX CC murine anti-human Fas monoclonal antibody HFE7A specifically binds

XX CC an amino acid sequence contained in P11. The epitope (see AAW83030)

XX CC was subsequently identified. The invention provides humanised

XX CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These

XX CC antibodies are capable of inducing apoptosis in abnormal cells

XX CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal

XX CC cells. They are used to evaluate, in animal models, treatments of

XX CC diseases that involve Fas/Fas ligand interactions, and also to treat

XX CC such diseases.

XX SQ Sequence 20 AA;

Query Match 100.0%; Score 59; DB 19; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0061;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10

Db | | | | | | | |

6 rtqntkcrck 15

RESULT 5

AAB14761

ID AAB14761 standard; peptide; 20 AA.

XX AC AAB14761;

XX DT 24-NOV-2000 (first entry)

XX DE Human Fas epitope, SEQ ID NO:36.

XX KW Human Fas epitope; anti-Fas antibody; murine monoclonal antibody HFE7A;

XX KW FERM-AP-5828; humanised antibody; complementarity determining region;

XX KW CDR; Fas ligand; apoptosis modulator; programmed cell death;

XX KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;

XX KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;

XX KW hepatitis; AIDS; graft rejection.

XX OS Homo sapiens.

XX PN JP2000169393-A.

XX DD

```

PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-0278301.
XX
PR 30-SEP-1998; 98JP-0276883.
XX
PA (SANY ) SANKYO CO LTD.
XX
DR WPI; 2000-485645/43.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
PS Example 6; Page 30; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14740 and AAB14751-B14771
CC represent human Fas epitopes.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 59; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 6 rtqntkerck 15
|||||

RESULT 6
AAW90911
ID AAW90911 standard; peptide; 20 AA.
XX
AC AAW90911;
XX
DT 08-AUG-2000 (first entry)
XX
DE Human Fas extracellular domain antigenic peptide #11.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Homo sapiens.
XX
XX EP990663-A2.
PN
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
XX

```

```

PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY ) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
DR WPI; 2000-258930/23.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
PS Example reference 6; Page 110; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatologic, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a human Fas extracellular domain derived antigenic peptide described in
XX the method of the invention.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 59; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 6 rtqntkerck 15
|||||

RESULT 7
AAW69517
ID AAW69517 standard; peptide; 20 AA.
XX
AC AAW69517;
XX
DT 10-APR-2000 (first entry)
XX
DE Human Fas peptide fragment, Fp11.
XX
XX Fp11; Fas fragment; APO-1; CD95; anti-Fas autoantibody; antibody;
KW modulator; apoptosis; proliferation.
XX
OS Homo sapiens.
XX
XX WO9965935-A2.
PN
XX
XX 23-DEC-1999.
PD
XX

```

PF 15-JUN-1999; 99WO-EP04105.
 XX 18-JUN-1998; 98GB-0013194.
 PR 12-MAR-1999; 99GB-0005793.
 XX (KARO-) KAROLINSKA INNOVATIONS AB.
 XX Chiodi F;
 XX WPI; 2000-106082/09.
 DR Fas peptide fragments useful for the treatment of proliferative
 PT disorders -
 PT
 XX Claim 3; Page 57; 71pp; English.

XX Sequences AAY69514-Y69521 represent peptide fragments of the Fas protein
 CC (also known as APO-1 or CD95). Fas is a type I cellular receptor which
 CC transduces an apoptotic signal on binding of its ligand, Fas ligand
 CC (FasL). Fas antibodies have been isolated from the serum of healthy
 CC blood donors - these may represent an additional mode of regulation of
 CC Fas-mediated signals in vivo. The Fas peptides may be used to modulate
 CC apoptosis via blocking autoantibody binding to Fas, thereby reducing or
 CC increasing FasL binding, which results in inhibition or stimulation of
 CC apoptosis. Fp5 (AAY69514) is thus able to induce apoptosis while Fp11
 CC (AAY69517) and Fp17 (AAY69519) are able to block apoptosis. Fp8
 CC (AAY69515) and Fp9 (AAY69516) comprise amino acids which are important
 CC for binding of Fas to FasL. The Fas peptides can be used to obtain
 CC antibodies containing a Fas binding site. The peptides and antibodies can
 CC be used in assay methods to obtain candidate modulators of Fas-mediated
 CC apoptosis. The candidate modulator may also modulate cellular
 CC proliferation. The peptides, mixtures of peptides, nucleic acids or
 CC antibodies are useful for methods of treating proliferative disorders.
 CC The disorders that may be prevented or treated include tumours, cancer,
 CC psoriasis, type I diabetes, multiple sclerosis, liver cirrhosis and HIV
 CC infection.

XX Sequence 20 AA;

Query Match 100.0%; Score 59; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
 Db 6 rtqntkcrck 15

RESULT 8
 AAW50286
 ID AAW50286 standard; Protein; 144 AA.

XX AC AAW50286;

DT 16-JUL-1998 (first entry)

XX Human Fas antigen derivative.

XX Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
 KW apoptosis modulation.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..16
 FT Peptide /label= sig_peptide
 FT Peptide 17..144
 FT Peptide /label= mat_peptide

XX WO9742319-A1.

XX

PD 13-NOV-1997.
 XX 01-MAY-1997; 97WO-JP01502.
 PR 02-MAY-1996; 96JP-0135760.
 XX (MOCH) MOCHIDA PHARM CO LTD. -
 PA (OSAB-) OSAKA BIOSCIENCE INST.
 XX Nagata S, Nakamura N;
 XX WPI; 1997-558981/51.
 DR N-PSDB; AAV07003.
 XX Fas antigen derivative containing modified extracellular region -
 PT has low antigenicity, promotes apoptosis and is useful in treatment
 PT of viral and other diseases
 XX Disclosure; Fig 3; 102pp; Japanese.
 XX The present sequence is a Fas antigen derivative, which
 CC contain a Fas antigen extracellular region lacking one or more
 CC amino acid residues in the region from the amino-terminal to (but
 CC excluding) the 1st cysteine residue (preferably at least 29
 CC residues are deleted).
 CC The derivative is an effective regulator of apoptosis and can be
 CC used (either by administration of the polypeptide, or by the use
 CC of the coding DNA in gene therapy) to treat a range of diseases,
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases
 CC such as hepatitis, influenza and HIV, by modulating apoptosis of
 CC virus-infected cells.

XX Sequence 144 AA;

Query Match 100.0%; Score 59; DB 18; Length 144;
 Best Local Similarity 100.0%; Pred. No. 0.035;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
 Db 92 rtqntkcrck 101

RESULT 9
 AAW50288
 ID AAW50288 standard; Protein; 159 AA.

XX AC AAW50288;

DT 16-JUL-1998 (first entry)

XX Human Fas antigen derivative/IgG1 hinge fusion.

XX Human; Fas antigen; derivative; apoptosis regulation; gene therapy;
 KW treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV;
 KW apoptosis modulation; immunoglobulin G1 Fc; IgG1 hinge; fusion.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..16
 FT Peptide /label= sig_peptide
 FT Peptide 17..159
 FT Peptide /label= mat_peptide

XX WO9742319-A1.

XX 13-NOV-1997.

XX 01-MAY-1997; 97WO-JP01502.

XX 02-MAY-1996; 96JP-0135760.

XX (MOCH) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N;
XX
XX WPI; 1997-558981/51.
DR N-PSDB; AAV07005.
XX
XX Fas antigen derivative containing modified extracellular region -
PT has low antigenicity, promotes apoptosis and is useful in treatment
PT of viral and other diseases
XX
XX Disclosure; Fig 5; 102pp; Japanese.
XX
XX The present sequence encodes a Fas antigen derivative/IgG1 hinge
CC fusion, which contains a Fas antigen extracellular region lacking
CC one or more amino acid residues in the region from the
CC amino-terminal to (but excluding) the 1st cysteine residue
CC (preferably at least 29 residues are deleted).
CC The derivative is an effective regulator of apoptosis and can be
CC used (either by administration of the polypeptide, or by the use
CC of the coding DNA in gene therapy) to treat a range of diseases,
CC e.g. diabetes, arthritis, lupus and in particular viral diseases
CC such as hepatitis, influenza and HIV, by modulating apoptosis of
CC virus-infected cells.
XX
XX Sequence 159 AA;
SQ

Query Match 100.0%; Score 59; DB 18; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 92 rtqntkcrck 101
|||||

RESULT 10
AAB36228
ID AAB36228 standard; Protein; 170 AA.
XX
XX AAB36228;
XX
XX 19-FEB-2001 (first entry)
XX
XX Rat Fas receptor.
XX
XX Rat; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1;
KW accelerated graft arteriosclerosis; vascular occlusive disease.
XX
XX Rattus sp.
XX
XX WO200063369-A2.
XX
XX 26-OCT-2000.
XX
XX 18-APR-2000; 2000WO-EP03532.
XX
XX 19-APR-1999; 99US-0294176.
PR 10-MAY-1999; 99US-0307690.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Ballermann BJ, Goldschmidt P, Movva RN, Sanfilippo A;
XX
XX WPI; 2000-672735/65.
DR N-PSDB; AAC66557.
XX
XX Genetic modification of target cells for inhibiting excessive

PT proliferation, comprises transferring, to cells or progenitors, the DNA
PT sequence encoding Fas antigen or receptor, or the fibroblast growth
PT factor receptor -
XX
XX Disclosure; Page 33-34; 4lpp; English.
XX
XX The present invention describes a method of gene therapy which involves
CC the use of RasR or FGFR-1 coding sequences to treat vascular diseases.
CC The invention also provides vectors for use in this method. The treatable
CC diseases include vascular occlusive diseases associated with cell
CC proliferation, such as accelerated graft arteriosclerosis and other forms
CC of stenosis.
XX
XX Sequence 170 AA;
SQ

Query Match 100.0%; Score 59; DB 21; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 117 rtqntkcrck 126
|||||

RESULT 11
AAB36229
ID AAB36229 standard; Protein; 173 AA.
XX
XX AAB36229;
XX
XX 19-FEB-2001 (first entry)
XX
XX Human Fas receptor.
XX
XX Human; Fas receptor; gene therapy; vascular cell; stenosis; FGFR-1;
KW accelerated graft arteriosclerosis; vascular occlusive disease.
XX
XX Homo sapiens.
XX
XX WO200063369-A2.
XX
XX 26-OCT-2000.
XX
XX 18-APR-2000; 2000WO-EP03532.
XX
XX 19-APR-1999; 99US-0294176.
PR 10-MAY-1999; 99US-0307690.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Ballermann BJ, Goldschmidt P, Movva RN, Sanfilippo A;
XX
XX WPI; 2000-672735/65.
DR N-PSDB; AAC66558.
XX
XX Genetic modification of target cells for inhibiting excessive
PT proliferation, comprises transferring, to cells or progenitors, the DNA
PT sequence encoding Fas antigen or receptor, or the fibroblast growth
PT factor receptor -
XX
XX Disclosure; Page 35; 4lpp; English.
XX
XX The present invention describes a method of gene therapy which involves
CC the use of RasR or FGFR-1 coding sequences to treat vascular diseases.
CC The invention also provides vectors for use in this method. The treatable
CC diseases include vascular occlusive diseases associated with cell
CC proliferation, such as accelerated graft arteriosclerosis and other forms
CC of stenosis.
XX
XX Sequence 173 AA;

Query Match 100.0%; Score 59; DB 21; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
| | | | | | | | | |
Db 121 rtgntkerck 130

RESULT 12
AAB66978
ID AAB66978 standard; Protein; 219 AA.

XX AC AAB66978;
XX DT 19-APR-2001 (first entry)
XX DE Fas protein.
XX KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
XX KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
XX KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
XX KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
XX KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
XX KW endometrios; fever; glomerulonephritis; inflammatory bowel disease;
XX KW ischaemia; Parkinson's disease.

XX OS Unidentified.

XX PN WO200103719-A2.

XX PD 18-JAN-2001.

XX PF 07-JUL-2000; 2000WO-USI8667.

XX PR 09-JUL-1999; 99US-0350670.

XX PR 09-DEC-1999; 99US-0457647.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX DR WPI; 2001-103031/11.

XX PT Treating conditions leading to bone loss such as rheumatoid arthritis,
XX PT multiple sclerosis and asthma, comprises administering an
XX PT osteoprotegerin protein in conjunction with e.g. inhibitors of
XX PT interleukin and tumor necrosis factor alpha -

XX PS Disclosure; Fig 2; 316pp; English.

XX CC The present invention relates to a method for treating conditions leading
XX CC to bone loss. The method comprises administering a purified and isolated
XX CC osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
XX CC in conjunction with other substances such as tumour necrosis factor-alpha
XX CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
XX CC modulators, fibroblast growth factor (FGF)1-10 modulators and/or platelet
XX CC activating factor (PAF) antagonists. The method is useful for treating
XX CC conditions leading to bone loss such as rheumatoid arthritis, multiple
XX CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
XX CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
XX CC graft-versus-host disease (GVHD). Other diseases that can be treated
XX CC include acute pancreatitis, Alzheimer's disease, anorexia,
XX CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
XX CC cancer, diabetes, endometrios, fever, glomerulonephritis, hyperalgesia,
XX CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
XX CC psoriasis and septic shock. The present sequence was used in a sequence
XX CC homology comparison.

XX SQ Sequence 219 AA;

Query Match 100.0%; Score 59; DB 22; Length 219;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
| | | | | | | | | |
Db 121 rtgntkerck 130

RESULT 13
AAB26982
ID AAB26982 standard; Protein; 281 AA.

XX AC AAB26982;
XX DT 02-FEB-2001 (first entry)
XX DE Human Fas.
XX KW Human; Fas; tumour necrosis factor; TR9 receptor; immunosuppressive;
XX KW antiinflammatory; cardiant; antiasthmatic; antidiabetic; antiallergic;
XX KW antiarthritic; antirheumatic; anti-HIV; anticonvulsant; cytostatic;
XX KW neuroprotective; gene therapy; Death Domain Containing Receptor 6;
XX KW common variable immunodeficiency; X-linked agammaglobulinaemia;
XX KW severe combined immunodeficiency; Wiskott-Aldrich syndrome;
XX KW autoimmune disease; rheumatoid arthritis; allergic encephalomyelitis;
XX KW multiple sclerosis; diabetes mellitus; asthma; epilepsy; cancer;
XX KW cardiovascular disease; neurological disease; protein coordinate data.

XX OS Homo sapiens.

XX PN WO200056862-A1.

XX PD 28-SEP-2000.

XX PF 16-MAR-2000; 2000WO-USO6831.

XX PR 24-MAR-1999; 99US-0126019.

XX PR 14-MAY-1999; 99US-0134220.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Gentz RL, Yu G, Fan P;

XX DR WPI; 2000-594575/56.

XX PT Nucleic acid molecule encoding a human tumor necrosis factor receptor,
XX PT known as TR9, useful for treating, preventing and diagnosing severe
XX PT combined immunodeficiency, autoimmune diseases, HIV infection, epilepsy
XX PT and cancer -

XX PS Disclosure; Fig 2; 220pp; English.

XX CC The present sequence is Fas, a member of the tumour necrosis factor
XX CC receptor family. A novel human tumour necrosis factor receptor,
XX CC designated TR9, has been isolated. The TR9 receptor is also known as
XX CC Death Domain Containing Receptor 6. TR9 polypeptides, polynucleotides or
XX CC agonists are useful for treating, preventing or diagnosing common
XX CC variable immunodeficiency, X-linked agammaglobulinaemia, severe combined
XX CC immunodeficiency and Wiskott-Aldrich syndrome, autoimmune diseases (such
XX CC as rheumatoid arthritis, allergic encephalomyelitis, multiple sclerosis,
XX CC diabetes mellitus and asthma), HIV infection, epilepsy, cancer,
XX CC cardiovascular diseases and other neurological diseases.

XX SQ Sequence 281 AA;

Query Match 100.0%; Score 59; DB 21; Length 281;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10

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Db 121 rtqntkcrck 130
|||||
RESULT 14
AAR76238
ID AAR76238 standard; Protein; 314 AA.
XX
AC AAR76238;
XX
DT 06-NOV-1995 (first entry)
XX
DE Fas-delta-TM.
XX
KW Fas-delta-TM; transmembrane deletion; apoptosis; antibody;
KW adoptive immunotherapy; transgenic animal.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..16
FT Protein /label= Sig_peptide
FT /label= Mat_protein
FT /note= "soluble Fas dell antigen"
FT Domain 17..168
FT /label= Extracellular_domain
FT /note= "the 5 C-terminal residues of the
Fas antigen extracellular domain are
deleted in Fas dell"
FT Domain 169..314
FT /label= cytoplasmic_domain
FT Peptide 164..173
FT /note= "preferred peptide from breakpoint region
(claim 4, page 132)"
FT Peptide 164..174
FT /note= "preferred peptide from breakpoint region"
FT Peptide 161..171
FT /note= "preferred peptide from breakpoint region"
XX
PN WO9513701-A.
PD 26-MAY-1995.
XX
XX 15-NOV-1994; 94WO-US13173.
XX
XX 15-NOV-1993; 93US-0152443.
XX
PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
PI Barr PJ, Kiefer MC, Shapiro JP;
XX
PI WPI; 1995-200120/26.
DR N-PSDB; AAQ93879.
XX
XX New nucleic acid encoding Fas protein without its trans-membrane region
PT - and related vectors, transformed cells, transgenic animals, protein and
PT antibodies, useful for control of Fas mediated apoptosis
XX
XX Claim 9; Fig.3-1 to 3-4; 38pp; English.
XX
XX mRNA was obtd. from human lymphocytes and PCR was used to make
CC cDNA specific for Fas-delta-TM (i.e. Fas lacking the transmembrane
CC region) mRNA. The PCR product was ligated into pBluescript and the
CC recombinant plasmid was used to transfect E. coli DH5-alpha cells. The
CC insert sequence of pBluescript-Fas-delta-TM encoded the protein
CC given in AAR76238.
XX
SQ Sequence 314 AA;

Query Match 100.0%; Score 59; DB 16; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 rtqntkcrck 130
|||||

RESULT 15
AAR99682
ID AAR99682 standard; Protein; 314 AA.
XX
AC AAR99682;
XX
DT 10-OCT-1996 (first entry)
XX
DE Human Fas soluble antigen Fas dell.
XX

```

Fas antigen; autoimmune disease; systemic lupus erythematosus; SLE;
angioimmunoblastic lymphadenopathy; AILD.

Homo sapiens.

Key Location/Qualifiers
Peptide 1..16 /label= Sig_peptide
Protein 17..314 /label= Mat_protein
Domain 17..168 /note= "soluble Fas dell antigen"
Domain 169..314 /label= Extracellular_domain
Peptide 164..173 /note= "the 5 C-terminal residues of the
Fas antigen extracellular domain are
deleted in Fas dell"
Peptide 164..174 /note= "preferred peptide from breakpoint region
(claim 4, page 132)"
Peptide 161..171 /note= "preferred peptide from breakpoint region"
Peptide /note= "preferred peptide from breakpoint region"

WO9620206-A1.
04-JUL-1996.
22-DEC-1995; 95WO-US17083.
23-DEC-1994; 94US-0371263.
(UABR-) UAB RES FOUND.
Cheng J, Liu C, Mountz JD, Zhou T;
WPI; 1996-321796/32.
N-PSDB; AAT34527.
Natural, soluble form of Fas antigen secreted by human cells is
result of alternative mRNA processing - used to diagnose
Fas-associated disease, e.g. systemic lupus erythematosus
Claim 4; Page 114-16; 152pp; English.
A natural, soluble Fas antigen variant (AAR99682), designated Fas
dell, and other Fas variants (AAR99683-85) are derived by alternative
splicing of Fas gene transcripts. A cDNA clone (AAT34527) coding for
the variant was obtd. from human peripheral blood mononuclear cells.
The Fas dell variant lacks the transmembrane domain of insoluble
Fas antigen (AAR99681). Recombinant dell variant, or fragments of
it, can be expressed in prokaryotic or eukaryotic (e.g. COS) cells.
Detection of increased levels of soluble forms of Fas antigen can
be used to diagnose autoimmune diseases, esp. systemic lupus
erythematosus and angioimmunoblastic lymphadenopathy.

Query Match 100.0%; Score 59; DB 17; Length 314;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 rtqntkcrck 130
|||||

Search completed: August 14, 2002, 15:15:34
Job time: 832 sec

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:58 ; Search time 108.64 Seconds
(without alignments)
8.845 Million cell updates/sec

Title: US-09-499-662-1

Perfect score: 59

Sequence: 1 RTONTKCRCK 10

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	59	100.0	314	2 I37383	FAS soluble protei
2	59	100.0	324	2 JC2395	Fas antigen precu
3	59	100.0	335	2 A40036	apoptosis-mediat
4	51	86.4	327	2 A46484	apoptosis-mediat
5	39	66.1	272	2 I48700	gene ox40 protein
6	39	66.1	277	2 I37552	OX40 homolog - hum
7	37	62.7	235	2 I50610	T-cell surface gly
8	37	62.7	360	2 B36470	Wnt-2 protein - mo
9	37	62.7	454	1 GOMST1	tumor necrosis fac
10	37	62.7	761	2 T09052	hypothetical prote
11	36	61.0	86	2 D90874	hypothetical prote
12	36	61.0	86	2 G85524	hypothetical prote
13	36	61.0	163	1 F81938	cytochrome c552 NM
14	36	61.0	310	1 D64758	probable transcrip
15	35	59.3	89	2 T23462	hypothetical prote
16	35	59.3	360	2 S00834	int-1-like protein
17	35	59.3	413	2 C69941	hypothetical prote
18	35	59.3	843	1 A27340	complement C7 prec
19	34	57.6	37	2 A60963	charybdotoxin 1 [v
20	34	57.6	37	2 B60963	charybdotoxin 2 -
21	34	57.6	86	1 TNLJND	trans-activating t
22	34	57.6	139	2 T28303	ORF MSV142 probabl
23	34	57.6	148	2 D49530	lek vascular endot
24	34	57.6	155	2 S51770	grain softness pro
25	34	57.6	164	2 S48186	grain softness pro
26	34	57.6	351	2 T18066	hypothetical prote
27	34	57.6	363	2 C62955	first mannosyl tra
28	34	57.6	447	2 S20711	neuraminidase - in
29	34	57.6	453	1 NWIV3	exo-alpha-sialidas

30 34 57.6 454 1 NWIV
31 34 57.6 596 2 F88188
32 34 57.6 633 2 T23090
33 34 57.6 711 2 T23738
34 34 57.6 779 1 S40382
35 34 57.6 1191 2 B97116
36 34 57.6 2120 2 T30243
37 33 55.9 41 2 S19586
38 33 55.9 41 2 S19621
39 33 55.9 50 1 MDHB
40 33 55.9 57 2 S59073
41 33 55.9 124 2 S08640
42 33 55.9 192 2 P96812
43 33 55.9 200 2 P00245
44 33 55.9 202 2 B45512
45 33 55.9 206 2 T47433

ALIGNMENTS

RESULT 1

I37383

FAS soluble protein - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000

C:Accession: I37383

R:Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.

J. Immunol. 154, 2706-2713, 1995

A:Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule

A:Reference number: I37383; MUID:95181785

A:Accession: I37383

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-314 <RES>

A:Cross-references: EMBL:Z47993; NID:9728578; PIDN:CAA88031.1; PID:9695539

Query Match 100.0%; Score 59; DB 2; Length 314;

Best Local Similarity 100.0%; Pred. No. 0.0073;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RTONTKCRCK 10

|||||

Db 121 RTONTKCRCK 130

RESULT 2

JC2395

Fas antigen precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C:Accession: JC2395; PC2246

R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.

Biochem. Biophys. Res. Commun. 198, 666-674, 1994

A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat 1

A:Reference number: JC2395; MUID:94128114

A:Accession: JC2395

A:Molecule type: mRNA

A:Residues: 1-324 <KIM>

A:Cross-references: DBJ:D26112; NID:9468486; PIDN:BAA05108.1; PID:d1005650; PID:9468

A:Experimental source: thymus

A:Accession: PC2246

A:Molecule type: mRNA

A:Residues: 1-62, 'RFT' <K12>

A:Cross-references: DBJ:D26113; NID:9468488; PIDN:BAA05109.1; PID:d1005651; PID:9468

A:Experimental source: liver

C:Genetics:

C:Superfamily: NGF receptor repeat homology

C:Keywords: transmembrane protein

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-324/Product: Fas antigen #status predicted <MAT>

F:44-79/Domain: NGF receptor repeat homology <NGF>
F:81-124/Domain: NGF receptor repeat homology <NG4>
F:171-188/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 59; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
| | | | | | | | | |

DB 117 RTQNTKCRCK 126

RESULT 3

A40036
apoptosis-mediating surface antigen Fas precursor - human
N:Alternate names: surface antigen APO-1
C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000
C:Accession: A40036; S24543; A38142

R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase, Cell 66, 233-243, 1991
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis

A:Reference number: A40036; MUID:91309137

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <I>O>

A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R:Krammer, P.H.

submitted to the EMBL Data Library, February 1992

A:Reference number: S24543

A:Accession: S24543

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <KRA>

A:Cross-references: EMBL:X63717; NID:g28741; PID:g28742

R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Reich, J. Biol. Chem. 267, 10709-10715, 1992

A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member of the TNF receptor family

A:Reference number: A38142; MUID:92268122

A:Accession: A38142

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-134, 'Q', 136-335 <OE>

A:Experimental source: SKW6.4 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:103810)

A:Note: in NCBI backbone the source is designated as mouse

C:Genetics:

A:Gene: GDB:AP11

A:Cross-references: GDB:132671; OMIM:134637

A:Map position: 10q24.1-10q24.1

C:Superfamily: NGF receptor repeat homology

C:Keywords: apoptosis; surface antigen; transmembrane protein

F:1-16/Domain: signal sequence #status predicted <SIG>

F:85-128/Domain: NGF receptor repeat homology <NG4>

F:174-190/Domain: transmembrane #status predicted <TM>

Query Match 100.0%; Score 59; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
| | | | | | | | | |

DB 121 RTQNTKCRCK 130

RESULT 4

A4684

apoptosis-mediating membrane-associated polypeptide Fas - mouse

C:Species: Mus musculus (house mouse)

C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A46484; A47254
R:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenki J. Immunol. 148, 1274-1279, 1992

A:Title: The cDNA structure, expression, and chromosomal assignment of the mouse Fas gene

A:Reference number: A46484; MUID:92148151

A:Accession: A46484

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-327 <WAY>

A:Cross-references: GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226

A:Experimental source: BAM3 macrophage cell line

A:Note: sequence extracted from NCBI backbone (NCBIN:81544, NCBIP:81545)

R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S. Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993

A:Title: Aberrant transcription caused by the insertion of an early transposable element into the Fas gene

A:Reference number: A47254; MUID:93189576

A:Accession: A47254

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1-96 <ADA>

A:Cross-references: GB:S56490; NID:g298505; PIDN:AAB25700.1; PID:g298506

A:Experimental source: MRL lpr/lpr

A:Note: sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:1268

C:Superfamily: NGF receptor repeat homology

C:Keywords: transmembrane protein

F:44-79/Domain: NGF receptor repeat homology <NGF>

F:81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 86.4%; Score 51; DB 2; Length 327;
Best Local Similarity 88.9%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TQNTKCRCK 10

DB 118 TQNTKCRCK 126

RESULT 5

I48700

gene ox40 protein - mouse

N:Alternate names: OX40 antigen

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000

C:Accession: I48700; I48334; S34377

R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J. J. Immunol. 151, 5261-5271, 1993

A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell

A:Reference number: I48700; MUID:94044750

A:Accession: I48700

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-272 <RES>

A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA9772.1; PID:g312828

R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995

A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40

A:Reference number: I48334; MUID:95255413

A:Accession: I48334

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-14, 'G', 16-272 <RE2>

A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819

C:Genetics:

A:Gene: Ox40

A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1

C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match

Best Local Similarity

Matches

6; Conservative

2; Mismatches

1; Indels

0; Gaps

66.1%; Score 39; DB 2; Length 272;

66.7%; Pred. No. 16;

Qy 2 TQNTKCRCK 10
||| |||
Db 98 TQDTVCRCR 106

RESULT 6
OX40 homolog - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: I37552
R:Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment
A:Reference number: I37552; MUID:94170844
A:Accession: I37552
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:9472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 66.1%; Score 39; DB 2; Length 277;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10
||| |||
Db 102 TQDTVCRCR 110

RESULT 7
I50610
T-cell surface glycoprotein CD8 alpha chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I50610; S33350
R:Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison,
J. Immunol. 154, 4485-4494, 1995
A:Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha
lymphocytes.
A:Reference number: I50609; MUID:95238946
A:Accession: I50610
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-235 <TRE>
A:Cross-references: EMBL:Z22726; NID:9488149; PIDN:CAA80421.1; PID:9297781
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 62.7%; Score 37; DB 2; Length 235;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
||| |||
Db 208 KTRRRRCRCR 217

RESULT 8
B36470
Wnt-2 protein - mouse
N:Alternate names: int-1 related protein
C:Species: Mus musculus (house mouse)
C:Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 15-Jun-1996
C:Accession: B36470; A43558
R:Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A:Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult
A:Reference number: A36470; MUID:91122634

A:Accession: B36470
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-360 <GAV>
R:McMahon, J.A.; McMahon, A.P.
Development 107, 643-650, 1989
A:Title: Nucleotide sequence, chromosomal localization and developmental expression o
A:Reference number: A43558; MUID:90126394
A:Accession: A43558
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-360 <MCM>
C:Superfamily: int-1 transforming protein

Query Match 62.7%; Score 37; DB 2; Length 360;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10
||| |||
Db 319 TRMTRCECK 327

RESULT 9
GQMST1
tumor necrosis factor receptor 1 precursor - mouse
N:Alternate names: tumor necrosis factor receptor, 55K
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 01-Dec-2000
C:Accession: A38634; B40254; S16677; S19021; I54332; I57826
R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
A:Reference number: A38634; MUID:91187885
A:Accession: A38634
A:Molecule type: mRNA
A:Residues: 1-454 <LEW>
A:Cross-references: GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826
R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
Mol. Cell. Biol. 11, 3020-3026, 1991
A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
A:Reference number: A40254; MUID:91246168
A:Accession: B40254
A:Molecule type: mRNA
A:Residues: 1-454 <GO2>
A:Cross-references: GB:M60468; NID:9199825; PIDN:AAA39751.1; PID:9199826
R:Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Fel
Eur. J. Immunol. 21, 1649-1656, 1991
A:Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necro
A:Reference number: S16677; MUID:91285014
A:Accession: S16677
A:Molecule type: mRNA
A:Residues: 1-454 <BAR>
A:Cross-references: EMBL:X59238; NID:953578; PIDN:CAA1922.1; PID:953579
R:Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
Immunogenetics 34, 338-340, 1991
A:Title: Molecular cloning and expression of the mouse Tnf receptor type b.
A:Reference number: S19021; MUID:92039815
A:Accession: S19021
A:Molecule type: mRNA
A:Residues: 1-454 <ROT>
A:Cross-references: EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:954849
R:Bebo, B.F.
Immunogenetics 39, 450-451, 1994
A:Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cel
A:Reference number: I34532; MUID:94245292
A:Accession: I34532
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-454 <RES>
A:Cross-references: GB:L26349; NID:9430732; PIDN:AAA59361.1; PID:9430733
R:Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993
A:Title: Genomic organization and promoter function of the murine tumor necrosis factor
A:Reference number: I57826; MUID:93156721
A:Accession: I57826
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-393, G', 395-454 <R2>
A:Cross-references: GB:W6656; NID:g202100; PIDN:AAA0465.1; PID:g202102
C:Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C:Genetics:
A:Gene: TNFR-2
A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-454/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-212/Domain: extracellular #status predicted <EXT>
F:44-82/Domain: NGF receptor repeat homology <NG1>
F:84-126/Domain: NGF receptor repeat homology <NG2>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:213-235/Domain: transmembrane #status predicted <MEM>
F:236-454/Domain: intracellular #status predicted <INT>
F:54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.7%; Score 37; DB 1; Length 454;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 TQNTKRC 9
| | | | |
Db 161 TQNTVCNC 168

RESULT 10
TQ9052
hypothetical protein DBCCR1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: TQ9052
R:Habuchi, T.; Luscombe, M.; Elder, P.A.; Knowles, M.A.
Genomics 48, 277-288, 1998
A:Title: Structure and methylation-based silencing of a gene (DBCCR1) within a candidate
A:Reference number: Z16537; MUID:98207242
A:Accession: TQ9052
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-761 <HAB>
A:Cross-references: EMBL:AF027734; NID:g3041876; PIDN:AAC39691.1; PID:g3041877
A:Note: IB3089A
C:Genetics:
A:Gene: DBCCR1
A:Map position: 9q32-q33
C:Superfamily: human hypothetical protein DBCCR1

Query Match 62.7%; Score 37; DB 2; Length 761;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 QNTKCRCK 10
| | | | |
Db 261 QNSQCRQC 268

RESULT 11
D90674
hypothetical protein ECs0364 [imported] - Escherichia coli (strain O157:H7, substrain R1
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: D90674

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90674
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA833787.1; PID:g13359821; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs0364

Query Match 61.0%; Score 36; DB 2; Length 86;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 NTKCRCK 10
| | | | |
Db 5 NTKCQCQ 11

RESULT 12
G85524
hypothetical protein Z0404 [imported] - Escherichia coli (strain O157:H7, substrain E
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: G85524
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85524
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-86 <STO>
A:Cross-references: GB:AE005174; NID:g12513132; PIDN:AAG54659.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z0404

Query Match 61.0%; Score 36; DB 2; Length 86;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 NTKCRCK 10
| | | | |
Db 5 NTKCQCQ 11

RESULT 13
F81938
cytochrome c552 NMA0925 precursor [similarity] - Neisseria meningitidis (strain Z2491
C:Species: Neisseria meningitidis
C:Date: 01-Sep-2000 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001
C:Accession: F81938
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556
A:Accession: F81938
A:Molecule type: DNA
A:Residues: 1-163 <PAR>
A:Cross-references: GB:ALI62754; GB:ALI57959; NID:g7379424; PIDN:CAB84197.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA0919; NMA0925
C:Superfamily: T. aquaticus cytochrome c552; cytochrome c6 homology

C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-163/Product: cytochrome c552 #status predicted <MAT>
F:28-109/Domain: cytochrome c6 homology <CY6>
F:38-41/Binding site: heme (Cys) (covalent) #status predicted
F:42-92/Binding site: heme iron (His, Met) (axial ligands) #status predicted

Query Match 61.0%; Score 36; DB 1; Length 163;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RTQNTKCRCK 10
 :|: |||| |
Db 133 KTKOTKRLK 142

RESULT 14

D64758
Probable transcription regulator yahB - Escherichia coli
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: D64758
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: D64758
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <BLAT>
A:Cross-references: GB:AF000138; GB:U00096; MID:gl786501; PIDN:AAAC73419.1; PID:gl786508;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yahB
C:Superfamily: probable transcription regulator ybbs
C:Keywords: DNA binding; transcription regulation
F:22-41/Region: helix-turn-helix motif

Query Match 61.0%; Score 36; DB 1; Length 310;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NTKCRCK 10
 ||||:
Db 229 NTKCQCQ 235

RESULT 15

T23462
hypothetical protein K08E4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23462
R:Percy, C.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19744
A:Accession: T23462
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-89 <WIL>
A:Cross-references: EMBL:Z68316; PIDN:CAA92679.1; GSPDB:GN00022; CESP:K08E4.4
A:Experimental source: clone K08E4
C:Genetics:
A:Gene: CESP:K08E4.4
A:Map position: 4
A:Introns: 45/3

Query Match 59.3%; Score 35; DB 2; Length 89;
Best Local Similarity 55.6%; Pred. No. 32;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 TQNTKCRCK 10
 ||: || |:
Db 21 TQTSKCECQ 29

Search completed: August 14, 2002, 15:18:58
Job time: 686 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:14 ; Search time 187.61 Seconds
(without alignments)
9.221 Million cell updates/sec

Title: US-09-499-662-1
Perfect score: 59
Sequence: 1 RTQNTKCRCK 10

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	150	11	Q9R230 rattus norv
2	59	100.0	310	6	Q9GK28 macaca arc
3	59	100.0	314	4	Q14293 homo sapien
4	59	100.0	327	6	Q97491 ovis aries
5	59	100.0	328	6	Q9BDF0 Q9bdp0 aotus trivi
6	59	100.0	331	6	Q9TSN4 Q9tsn4 macaca fasc
7	59	100.0	331	6	Q9GK36 macaca assa
8	59	100.0	331	6	Q9BDN4 Q9bdn4 cercocobus
9	59	100.0	331	6	Q9BDN0 Q9bdn0 macaca neme
10	59	100.0	333	6	Q9BDF2 Q9bdp2 macaca mula
11	56	94.9	334	6	Q9GL40 Q9gl40 macaca mula
12	51	86.4	327	11	Q9DCQ1 Q9dcq1 mus musculu
13	49	83.1	263	6	Q9XS60 Q9xs60 oryctolagus
14	49	83.1	319	6	Q9TV79 Q9tv79 oryctolagus
15	49	83.1	320	6	Q9XS29 Q9xs29 oryctolagus
16	45	76.3	357	13	Q9DF34 Q9df34 brachydanio

17	44	74.6	385	11	Q9JUL5	Q9jjl5 mus musculu
18	438	71.2	438	13	Q9DFV0	Q9dfv0 brachydanio
19	41	69.5	368	13	Q57408	Q57408 meleagris g
20	41	69.5	381	11	Q9JUL6	Q9jjl6 mus musculu
21	41	69.5	381	11	Q9QZM4	Q9qzm4 mus musculu
22	41	69.5	797	4	Q43686	Q43686 homo sapien
23	40	67.8	368	13	Q9PW79	Q9pw79 gallus gall
24	40	67.8	368	13	Q9IAR7	Q9iar7 gallus gall
25	40	67.8	468	4	Q96E62	Q96e62 homo sapien
26	40	67.8	567	12	Q91TQ7	Q91tg7 tupala herp
27	39	66.1	186	12	Q72735	Q72735 cowpox viru
28	39	66.1	186	12	Q9YB87	Q9yp87 cowpox viru
29	39	66.1	186	12	Q9WJB4	Q9wjb4 vaccinia vi
30	39	66.1	186	12	Q91IR5	Q91lr5 vaccinia vi
31	38	64.4	136	5	Q9XZ89	Q9xz89 plasmodium
32	38	64.4	144	13	Q73822	Q73822 brachydanio
33	38	64.4	188	13	Q73682	Q73682 brachydanio
34	38	64.4	762	10	Q9LE55	Q9le55 oryza sativ
35	38	64.4	843	6	Q9TUQ3	Q9tuq3 sus scrofa
36	38	64.4	2209	5	Q9U0G6	Q9u0g6 plasmodium
37	38	64.4	2277	5	Q9U0G5	Q9u0g5 plasmodium
38	37	62.7	72	15	Q86003	Q86003 human immun
39	37	62.7	72	15	Q75560	Q75560 human immun
40	37	62.7	72	15	F88718	P88718 human immun
41	37	62.7	86	15	Q99BV5	Q99bv5 human immun
42	37	62.7	86	15	Q99BV4	Q99bv4 human immun
43	37	62.7	86	15	Q99BV3	Q99bv3 human immun
44	37	62.7	101	15	Q9Y1Q4	Q9yiq4 human immun
45	37	62.7	101	15	Q90810	Q90810 human immun

ALIGNMENTS

RESULT 1						
Q9R230	ID	Q9R230	PRELIMINARY;	PRT;	150 AA.	
AC	Q9R230;					
DT	01-MAY-2000	(TREMBLrel. 13, Created)				
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)				
DE	FAS RECEPTOR (FRAGMENT).					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=WISTAR; TISSUE=CORPUS LUTEUM;					
RA	Lareu R.R.; Dharmarajan A.;					
RT	"Cloning and expression of Fas and Fas Ligand in the apoptotic rat					
RT	corpus luteum."					
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; AF104034; AAD2021.1; -.					
DR	HSSP; P25942; ICDF.					
DR	InterPro; IPR001368; TNFR_c6.					
DR	Pfam; PF00020; TNFR_c6; 2.					
DR	SMART; SM00208; TNFR; 2.					
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.					
DR	PROSITE; PS50050; TNFR_NGFR_2; 1.					
KW	Receptor.					
FT	NON_TER 1 1					
FT	NON_TER 150 150					
SQ	SEQUENCE 150 AA; 16644 MW; 7DEC76EC40A6BA4F CRC64;					
Query Match 100.0%; Score 59; DB 11; Length 150;						
Best Local Similarity 100.0%; Pred. No. 0.00026;						
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	RTQNTKCRCK 10				
Db	112	RTQNTKCRCK 121				

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RESULT 2
Q9GK28          PRELIMINARY;          PRT;    310 AA.
AC  Q9GK28;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  FAS ANTIGEN APO-1/CD95.
GN  FAS.
OS  Macaca arctoides (Stump-tailed macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC  Cercopithecoidea; Macaca.
OX  NCBI_TaxID=9540;
RN  [1]
SEQUENCE FROM N.A.
RP  Chi L., Shui B., Jiang H., Zhang Y.R., He F.Q., Cai Y.Y.;
RA  "Cloning of fas gene in stump-tailed monkey.";
RL  Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF332357; AAG49394.1; -.
DR  HSSP; P25445; 1DDF.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 2.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 2.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; 1.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ  SEQUENCE 310 AA; 34806 MW; C5C79BF1F804A419 CRC64;

Query Match          100.0%; Score 59; DB 6; Length 310;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RTQNTKCRCK 10
    |||
Db  121 RTQNTKCRCK 130

RESULT 3
Q14293          PRELIMINARY;          PRT;    314 AA.
AC  Q14293;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  FAS SOLUBLE PROTEIN.
GN  FAS/APO 1.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
SEQUENCE FROM N.A.
RP  Cascino I., Fiucci G., Papoff G., Ruberti G.;
RA  "Three functional soluble forms of the human apoptosis-inducing Fas
RT  molecule are produced by alternative splicing.";
RL  J. Immunol. 154:2706-2713(1995).
DR  EMBL; Z47993; CA88031.1; -.
DR  HSSP; P25445; 1DDF.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 2.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 2.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.

RESULT 4
Q97491          PRELIMINARY;          PRT;    327 AA.
AC  Q97491;
DT  01-MAY-1999 (TrEMBLrel. 10, Created)
DT  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  FAS PROTEIN.
GN  FAS.
OS  Ovis aries (Sheep).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovidae; Caprinae; Ovis.
OX  NCBI_TaxID=9940;
RN  [1]
SEQUENCE FROM N.A.
RP  TISSUE-LYMPHOCYTE;
RC  Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RA  "Cloning of sheep fas antigen.";
RL  Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AB011671; BAA37093.1; -.
DR  HSSP; P25445; 1DDF.
DR  InterPro; IPR000488; Death.
DR  InterPro; IPR001368; TNFR_c6.
DR  Pfam; PF00531; death; 1.
DR  Pfam; PF00020; TNFR_c6; 3.
DR  SMART; SM00005; DEATH; 1.
DR  SMART; SM00208; TNFR; 3.
DR  PROSITE; PS50017; DEATH_DOMAIN; 1.
DR  PROSITE; PS00652; TNFR_NGFR_1; 1.
DR  PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ  SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;

Query Match          100.0%; Score 59; DB 6; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RTQNTKCRCK 10
    |||
Db  120 RTQNTKCRCK 129

RESULT 5
Q9BDP0          PRELIMINARY;          PRT;    328 AA.
AC  Q9BDP0;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE  FAS ANTIGEN CD95.
OS  Aotus trivirgatus (Night monkey) (Douroucoul).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.
OX  NCBI_TaxID=9505;
RN  [1]
SEQUENCE FROM N.A.
RP  Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.;
RX  MEDLINE=21383618; PubMed=11491535;
```

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RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344835; AAK37531.1; -.
DR HSSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 157 157 S -> T.
SQ SEQUENCE 328 AA; 37332 MW; B3DED1DAC97D6353 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 120 RTQNTKCRCK 129
|||||

RESULT 6
Q9TSN4 PRELIMINARY; PRT; 331 AA.
ID Q9TSN4
AC Q9TSN4; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DEATH RECEPTOR FAS (APO-1/CD95).
GN FAS.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20237686; PubMed=10773350;
RA Murayama Y., Teruo K., Inoue-Murayama M.;
RT "Molecular cloning and characterization of cynomolgus monkey Fas.";
RL Hum. Immunol. 61:474-485(2000).
DR EMBL; AB031420; BAA83551.1; -.
DR HSSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 331 AA; 37265 MW; OC617508081B05DF CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130
|||||

RESULT 7
Q9GK36 PRELIMINARY; PRT; 331 AA.
ID Q9GK36
AC Q9GK36; 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FAS ANTIGEN APO-1/CD95.
GN FAS.
OS Macaca assamensis (Assam's macaque) (Assam's monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9551;
RN [1]
RP SEQUENCE FROM N.A.
RA Chi L., Shui B., Jiang H., He F.Q., Zhang Y.R., Cai Y.Y.;
RT "Cloning and sequencing of bear monkey Fas antigen cDNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326208; AAG49382.1; -.
DR HSSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 331 AA; 37167 MW; CE58DB046C67834F CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.00051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
Db 121 RTQNTKCRCK 130
|||||

RESULT 8
Q9BDN4 PRELIMINARY; PRT; 331 AA.
ID Q9BDN4
AC Q9BDN4; 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FAS ANTIGEN CD95.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344843; AAK37602.1; -.
DR HSSP; P25445; IDDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT VARIANT 44 44 I -> V.
FT VARIANT 47 47 E -> Q.
FT VARIANT 55 55 R -> D.

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FT VARIANT 60 60 R -> H.
 FT VARIANT 61 61 N -> S.
 FT VARIANT 77 77 E -> G.
 FT VARIANT 95 95 G -> A.
 FT VARIANT 282 282 E -> G.
 FT VARIANT 298 298 G -> D.
 FT VARIANT 300 300 C -> *.
 SQ SEQUENCE 331 AA; 37277 MW; 1D843C4DE1D343F4 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
 |||||
 DB 121 RTQNTKCRCK 130

RESULT 9

ID Q9BDN0 PRELIMINARY; PRT; 331 AA.
 AC Q9BDN0:
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE FAS ANTIGEN CD95.
 OS Macaca nemestrina (Pig-Tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344850; AAK37610.1; -.
 DR HSSP; P25445; 1DDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 331 AA; 37254 MW; A6CFE3DA12C94765 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 331;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
 |||||
 DB 121 RTQNTKCRCK 130

RESULT 10

ID Q9BDP2 PRELIMINARY; PRT; 333 AA.
 AC Q9BDP2:
 DT 01-JUN-2001 (TRENBLrel. 17, Created)
 DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE FAS ANTIGEN CD95.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL; AF344833; AAK37529.1; -.
 DR HSSP; P25445; 1DDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 FT VARIANT 75 75 V -> A.
 FT VARIANT 89 89 E -> K.
 FT VARIANT 196 196 E -> K.
 FT VARIANT 201 201 R -> H.
 SQ SEQUENCE 333 AA; 37468 MW; 98C17F766762F287 CRC64;

Query Match 100.0%; Score 59; DB 6; Length 333;
 Best Local Similarity 100.0%; Pred. No. 0.00051;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
 |||||
 DB 121 RTQNTKCRCK 130

RESULT 11

ID Q9GL40 PRELIMINARY; PRT; 334 AA.
 AC Q9GL40:
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE FAS ANTIGEN.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shui B., Chi L., Zhang Y.R.;
 RT "Cloning and sequencing of Rhesus monkey Fas antigen cDNA.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY007572; AAG16762.1; -.
 DR HSSP; P25445; 1DDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2.
 DR SMART; SM00005; DEATH; 1.
 DR SMART; SM00208; TNFR; 2.
 DR PROSITE; PS00017; DEATH_DOMAIN; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS00050; TNFR_NGFR_2; 2.
 SQ SEQUENCE 334 AA; 37531 MW; 2DC5B1661C3191C6 CRC64;

Query Match 94.9%; Score 56; DB 6; Length 334;
 Best Local Similarity 90.0%; Pred. No. 0.002;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RTQNTKCRCK 10
 |||||

Db 121 RTQNTKCRCK 130

RESULT 12

Q9DCQ1 ID Q9DCQ1 PRELIMINARY; PRT; 327 AA.
AC Q9DCQ1: 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 6.
GN TNFRSF6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RC SEQUENCE FROM N.A.
PC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamaneke I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staehli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Suzuki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK002590; BAB22211.1; -
DR HSSP; P25445; 1DDF.
DR MGD; MGI:95484; Tnfrsf6.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 37437 MW; D8DA95CA525CED56 CRC64;

Query Match 86.4%; Score 51; DB 11; Length 327;

Best Local Similarity 88.9%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TQNTKCRCK 10

Db 118 TQNTKCRCK 126

RESULT 13

Q9XS60 ID Q9XS60 PRELIMINARY; PRT; 263 AA.
AC Q9XS60:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FAS ANTIGEN SPLICED VARIANT.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A.
PC Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021297; BAA78429.1; -
DR HSSP; O14763; 1D4V.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 263 AA; 30374 MW; 6D76782ADED1BFD7 CRC64;

Query Match 83.1%; Score 49; DB 6; Length 263;

Best Local Similarity 100.0%; Pred. No. 0.041; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNTKCRCK 10

Db 108 QNTKCRCK 115

RESULT 14

Q9TV79 ID Q9TV79 PRELIMINARY; PRT; 319 AA.
AC Q9TV79:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE B-TYPE FAS ANTIGEN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RC SEQUENCE FROM N.A.
PC Isono T., Tanbe Y., Nagano Y., Seto A.;
RT "Splicing and allelic variation in the rabbit Fas antigen gene.";
RL submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021298; BAA78430.1; -
DR HSSP; P25445; 1DDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 319 AA; 35961 MW; 06FA0033B1846591 CRC64;

Query Match 83.1%; Score 49; DB 6; Length 319;

Best Local Similarity 100.0%; Pred. No. 0.048; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNTKCRCK 10

Db 108 QNTKCRCK 115

RESULT 15

Q9XS29 ID Q9XS29 PRELIMINARY; PRT; 320 AA.
AC Q9XS29:
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

!!AA_MULTIPLE_ALIGNMENT 1.0
Pileup of: us*

Symbol comparison table: GenRunData:blosum62.comp CompCheck: 1102

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GapLengthWeight: 2

lightchain.msf MSF: 238 Type: P August 15, 2002 08:42 Check: 3138 ..

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Name: us-09-499-662-52 Len: 238 Check: 4096 Weight: 1.00
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Name: us-09-499-662-107 Len: 238 Check: 5008 Weight: 1.00
Name: us-09-499-662-50 Len: 238 Check: 4886 Weight: 1.00

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us-09-499-662-129 METDTILLWV LLLWVPGSTG DIVLTQSPSS LSASVGDVRT ITCKASQSDV
us-09-499-662-109 METDTILLWV LLLWVPGSTG DIVLTQSPSGT LSLSPGERAT LSCCKASQSDV
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51
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us-09-499-662-54 YDGDSYNNWY OQKPGQAPKL LIYAASNLES GIPDRFSGSG SGTDFTLTH
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101
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us-09-499-662-131 SLOPEDFATY YCQSQNEDPR TFGQGTKEI KRTVAAPSVF IFPPSDEQLK
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us-09-499-662-54 PVEEEDAATY YCQSQNEDPR TFGQGTKEI KRTVAAPSVF IFPPSDEQLK
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151
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us-09-499-662-131 SGTASVVCLL NNFYPREKV QMKVDNALQS GNSQESVTEQ DSKDSTYSLS
us-09-499-662-129 SGTASVVCLL NNFYPREKV QMKVDNALQS GNSQESVTEQ DSKDSTYSLS
us-09-499-662-109 SGTASVVCLL NNFYPREKV QMKVDNALQS GNSQESVTEQ DSKDSTYSLS
us-09-499-662-52 SGTASVVCLL NNFYPREKV QMKVDNALQS GNSQESVTEQ DSKDSTYSLS
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us-09-499-662-50 STLTLSKADY EKHVYACEV THOGLSSPVT KSFNRGEC

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09/499,662

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:33 ; Search time 230.21 Seconds
(without alignments)
37.634 Million cell updates/sec

Title: 5_g_6_g_7

Perfect score: 205

Sequence: 1 RASQSVVDGDSYMNXXXXX.....XXXXXXXXXXQSQSDPPT 78

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	205	100.0	238 19	AAW83031 Anti-Fas humanised
2	205	100.0	238 19	AAW83032 Anti-Fas humanised
3	205	100.0	238 19	AAW83033 Anti-Fas humanised
4	205	100.0	238 19	AAW83034 Anti-Fas humanised
5	205	100.0	238 19	AAW83035 Anti-Fas humanised
6	205	100.0	238 19	AAW83042 Anti-Fas MAB HFE7A
7	205	100.0	238 21	AA14748 Mouse anti-Fas ant
8	205	100.0	238 21	AA14772 Humanised anti-Fas
9	205	100.0	238 21	AA14773 Humanised anti-Fas
10	205	100.0	238 21	AA14774 Humanised anti-Fas
11	205	100.0	238 21	AA14777 Humanised anti-Fas

12	205	100.0	238	21	AA14778 Humanised anti-Fas
13	205	100.0	238	21	AAW90898 Murine anti-Fas an
14	205	100.0	238	21	AAW90922 Humanised anti-Fas
15	205	100.0	238	21	AAW90923 Humanised anti-Fas
16	205	100.0	238	21	AAW90924 Humanised anti-Fas
17	205	100.0	238	21	AAW90927 Humanised HFE7A de
18	205	100.0	238	21	AAW90928 Humanised HFE7A de
19	205	100.0	238	21	AAW90930 Humanised anti-Fas
20	205	100.0	238	21	AAW90931 Humanised anti-Fas
21	205	100.0	238	21	AAW90932 Humanised anti-Fas
22	198	96.6	111	20	AAV23781 Light chain variab
23	198	96.6	111	20	AAV18123 Light chain sequen
24	198	96.6	131	16	AAV70202 Humanized antibody
25	198	96.6	131	20	AAV23779 Light chain variab
26	198	96.6	131	20	AAV18126 Light chain sequen
27	198	96.6	132	16	AAW70189 Mouse MAB 3B9 high
28	198	96.6	132	20	AAV23767 Light chain variab
29	198	96.6	132	20	AAV18120 Light chain sequen
30	197	96.1	106	14	AAV33309 MAE15 light chain.
31	197	96.1	106	14	AAV85197 Light chain amino
32	197	96.1	111	10	AAV90541 Immunoglobulin L c
33	197	96.1	111	15	AAV55123 Mouse anti-HIV mu5
34	197	96.1	111	15	AAV55127 Mouse-human chimera
35	197	96.1	111	15	AAV60302 Anti HIV antibody
36	197	96.1	111	15	AAV60306 Chimeric anti HIV
37	197	96.1	112	13	Human x mouse modi
38	197	96.1	112	22	AAV71895 Monoclonal antibod
39	197	96.1	131	10	AAV90543 Amino acids sequen
40	197	96.1	218	18	AAV13563 Humanised anti-L-s
41	197	96.1	222	18	AAV01751 MH1 monoclonal ant
42	195	95.1	131	16	AAV75355 Humanized antibody
43	195	95.1	131	20	AAV23771 Light chain variab
44	195	95.1	131	20	AAV18118 Light chain sequen
45	193	94.1	103	21	AAV59263 Antibody 4H5 L cha

ALIGNMENTS

RESULT 1

AAW83031

ID AAW83031 standard; Protein; 238 AA.

XX AAW83031;

AC AAW83031;

XX 15-MAR-1999 (first entry)

DT Anti-Fas humanised antibody HFE7A light chain HH type.

DE HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;

KW systemic lupus erythematosus; graft versus host disease;

KW Sjogren syndrome; pernicious anaemia; Addison's disease;

KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;

KW rheumatoid arthritis; autoimmune haemolytic anaemia;

KW myasthenia gravis; multiple sclerosis; Basedow's disease;

KW thrombopenia purpura; insulin-dependent diabetes; allergy;

KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

KW transplant rejection; therapy.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein /label= Sig_peptide

FT Region 21..238

FT Region /label= Mat_protein

FT Region 21..131

FT Region /label= Variable

FT Region 132..238

FT Region /label= Constant

FT Region 44..58
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 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 FT XX
 PN AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70074.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 199-199; 292pp; English.
 XX
 CC This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX
 SQ Sequence 238 AA;

 Query Match 100.08; Score 205; DB 19; Length 238;
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

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 DB 44 kasqvdvdygd symwvqkqgqaprllyaaasnlsgipdrfsgsgtdftltisrl 103
 QY 61 XXXXXXXXQSQSNEPRT 78

Db 104 padfavyycqgsnedprt 121
 RESULT 2
 AAW83032
 ID AAW83032 standard; Protein; 238 AA.
 XX
 AC AAW83032;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain HM type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key
 FT Peptide
 FT /label= Sig_peptide
 FT 1..20
 FT Protein
 FT 21..238
 FT /label= Mat_protein
 FT 21..131
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 FT /note= "claim 9"
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 PN 08-OCT-1998.
 PD 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70075.
 XX
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 200; 292pp; English.
 XX

CC This is the amino acid sequence of the HM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AAW83042) entailed making
CC P47A and K49R amino acid substitutions; these residues are
CC conserved in the human light (kappa) chain. Host cell E. coli
CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
CC fragment of the humanised HM type HFE7A light chain and DNA
CC encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6072 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASLNESXXXXXXXXXXXXXXXXX 60
Db 44 kasqsvdydgsymnwyyqkpgqpqpriliyaasnlsgipdrfsgsgtdftihpve 103

Qy 61 XXXXXXXXQOSNEDPRT 78
Db 104 eedaatyccqgsnedprt 121

RESULT 3
AAW83033
ID AAW83033 standard; Protein; 238 AA.
XX AC AAW83033;
XX DT 15-MAR-1999 (first entry)
XX DE Anti-Fas humanised antibody HFE7A light chain MM type.
XX KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FT Peptide 1..20
FT /label= sig_peptide
FT Protein 21..238
FT /label= Mat_protein
FT Region 21..131

FT Region /label= Variable
FT 132..238
FT /label= Constant
FT 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT 74..80
FT /label= CDR_L2
FT /note= "claim 9"
FT 113..121
FT /label= CDR_L3
FT /note= "claim 9"
XX AU9859701-A.
PN 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276084.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX (SANY) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI: 1998-543440/47.
DR N-PSDB; AAV70076.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX Claim 21; Page 202; 292pp; English.
XX This is the amino acid sequence of the MM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
CC SANK 73697 harbors plasmid PHSGMM6 carrying a fusion fragment of the
CC humanised MM type HFE7A light chain and DNA encoding the region of
CC human kappa chain, and is deposited as FERM BP-6071 (claimed). The
CC invention provides methods for producing humanised antibodies by
CC culturing host cells. Humanised versions of HFE7A (see AAW83031-37),
CC like native HFE7A, are capable of inducing apoptosis in abnormal
CC cells expressing Fas, and of inhibiting Fas-induced apoptosis in
CC normal cells. The humanised antibodies are used to evaluate, in
CC animal models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASLNESXXXXXXXXXXXXXXXXX 60
Db 44 kasqsvdydgsymnwyyqkpgqpqpriliyaasnlsgipdrfsgsgtdftihpve 103

Qy 61 XXXXXXXXQOSNEDPRT 78
Db 44 kasqsvdydgsymnwyyqkpgqpqpriliyaasnlsgipdrfsgsgtdftihpve 103

Db 104 eedaatyccgsnedprt 121

RESULT 4
AAW83034
ID AAW83034 standard; Protein; 238 AA.
XX
AC AAW83034;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas humanised antibody HFE7A light chain PDHH type.
XX
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX
OS Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= Sig_peptide 21..238
FT Region /label= Mat_protein 21..131
FT Region /label= Variable 132..238
FT Region /label= Constant 44..58
FT Region /label= CDR_L1 /note= "claim 9"
FT Region 74..80
FT Region /label= CDR_L2 /note= "claim 9"
FT Region 113..121
FT Region /label= CDR_L3 /note= "claim 9"
XX AU9859701-A.
XX
XX 08-OCT-1998.
PD
PF 30-MAR-1998; 98AU-0059701.
XX
PR 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
PA
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 1998-543440/47.
DR N-PSDB; AAV70077.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 218; 292pp; English.
PS
XX This is the amino acid sequence of the PDHH type humanised light

CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AAW83042) entailed making
CC D1E, P47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K
CC amino acid substitutions; these residues are conserved in the
CC human light chain (kappa chain). Host cell Escherichia coli
CC PHSH5 SANK 70398 harbors plasmid PHSH5 carrying a fusion
CC fragment of the humanised PDHH type HFE7A light chain and DNA
CC encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6274 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX
XX Sequence 238 AA:

Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. NO. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KASQSVYDGDGSMYNNKXXXXXXXXXXXXXXXXXASNLXXXXXXXXXXXXXXXXXXXXX 60
Db 44 KASQSVYDGDGSMYNNKXXXXXXXXXXXXXXXXXASNLXXXXXXXXXXXXXXXXXXXXX 103

Oy 61 XXXXXXXXQSQSNEDPRT 78
Db 104 pefavyyccgsnedprt 121

RESULT 5
AAW83035
ID AAW83035 standard; Protein; 238 AA.
XX
AC AAW83035;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas humanised antibody HFE7A light chain PDHH type.
XX
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX
OS Homo sapiens.
OS Synthetic.

FH Key Location/Qualifiers
XX Peptide 1..20
FT Protein /label= Sig_peptide 21..238
FT Protein /label= Mat_protein 21..131
FT Region

FT Region /label= Variable
FT 132..238
FT /label= Constant
FT 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT 74..80
FT /label= CDR_L2
FT /note= "claim 9"
FT 113..121
FT /label= CDR_L3
FT /note= "claim 9"

PN AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

PR 01-APR-1997; 97JP-0082953.

PR 25-JUN-1997; 97JP-0169088.

XX (SANY) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

DR N-PSDB; AAV70078.

XX New antibodies and proteins bind conserved epitope of Fas antigen -

PS Claim 21; Page 220-221; 292pp; English.

XX This is the amino acid sequence of the PDHM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AAW83042) entailed making
CC DIE, P47A, K49R and R107K amino acid substitutions; these
CC residues are conserved in the human light (kappa) chain. Host
CC cell Escherichia coli PHSHM2 SANK 70198 harbors plasmid PHSHM2
CC carrying a fusion of the humanised PDHM type HFE7A light chain and
CC DNA encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6272 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).

XX Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;

Best Local Similarity 39.7%; Pred. No. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Caps 0;

QY 1 KASQSDYDGDGSMNNXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
|||||XXX

Db 44 kasqsvdydgdsgymwyyqgpgqprlliyaaasnlsgipdrfsgsgsgtdftitihpve 103
QY 61 XXXXXXXXQSNEDPRT 78
:XXXXXXXXXXXXXXXXXXXXX
Db 104 eedaatyycqgsnedprt 121

RESULT 6

AAW83042

ID AAW83042 standard; Protein; 238 AA.

XX AC AAW83042;

XX 15-MAR-1999 (first entry)

XX Anti-Fas MAB HFE7A light chain.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy; complementarity determining region;
KW CDR.

XX Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein /label= Sig_peptide

FT Region 21..238

FT Region /label= Mat_protein

FT Region 21..131

FT Region /label= Variable

FT Region 132..238

FT Region /label= Constant

FT Region 44..58

FT Region /label= CDR_L1

FT Region /note= "claim 9"

FT Region /label= CDR_L2

FT Region /note= "claim 9"

FT Region 113..121

FT Region /label= CDR_L3

FT Region /note= "claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

DR N-PSDB; AAV70130.

XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS

```
XX PS Reference Example 4; Page 189-190; 292pp; English.
XX CC This is the amino acid of the light chain of murine anti-human Fas
XX CC monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light
XX CC chain was obtained from HFE7A-secreting hybridoma (FERM-BP-5828)
XX CC RNA by RT-PCR (see AAV70127-28). The invention provides humanised
XX CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
XX CC antibodies are capable of inducing apoptosis in abnormal cells
XX CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX CC cells. They are used to evaluate, in animal models, treatments of
XX CC diseases that involve Fas/Fas ligand interactions, and also to treat
XX CC such diseases, including autoimmune disease (e.g. systemic lupus
XX CC erythematosus, Hashimoto's disease, graft versus host disease,
XX CC Sjogren syndrome, pernicious anaemia, Addison's disease,
XX CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
XX CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
XX CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
XX CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
XX CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
XX CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 19; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMNXNXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 60
DB 44 kasqsvdydgsymnwyyqkpgqpklliyaaaslesgiparfsgsgsgtdftlnhpve 103

QY 61 XXXXXXXXQSQNEPRT 78
DB 104 eedaatyycqgsnedprt 121

RESULT 7
AAB14748
ID AAB14748 standard; Protein; 238 AA.
AC AAB14748;
XX
XX 24-NOV-2000 (first entry)
XX
DE Mouse anti-Fas antibody HFE7A light chain.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; complementarity determining region; CDR; human Fas;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; light chain.
XX
OS Mus musculus.
XX JP2000169393-A.
XX
PN 20-JUN-2000.
XX
PD 30-SEP-1999; 99JP-0278301.
XX
PF 30-SEP-1998; 98JP-0276883.
XX
PR (SANY ) SANKYO CO LTD.
XX
PA WPI; 2000-485645/43.
XX
DR N-PSDB; AAA72109.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
XX PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
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```
XX PS Example 4; Page 70; 139pp; Japanese.
XX CC The invention relates to compositions for the prevention or treatment
XX CC of diseases caused by an abnormality in the Fas/Fas ligand system
XX CC containing an anti-Fas antibody as the active component. The anti-Fas
XX CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX CC or a humanised version of HFE7A containing identical CDRs
XX CC (complementarity determining regions) to antibody HFE7A. Via its
XX CC interaction with Fas, the antibody of the invention acts as a modulator
XX CC of apoptosis. The composition of the invention may therefore be used in
XX CC the treatment or prevention of conditions such as autoimmune diseases,
XX CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX CC and organ graft rejection. The present sequence represents the
XX CC light chain of the murine anti-human Fas monoclonal antibody HFE7A,
XX CC which is produced by hybridoma HFE7A (FERM-BP-5828).
XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDSYMNXNXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 60
DB 44 kasqsvdydgsymnwyyqkpgqpklliyaaaslesgiparfsgsgsgtdftlnhpve 103

QY 61 XXXXXXXXQSQNEPRT 78
DB 104 eedaatyycqgsnedprt 121

RESULT 8
AAB14772
ID AAB14772 standard; Protein; 238 AA.
XX
XX AC AAB14772;
XX
XX 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; light chain.
XX
OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX JP2000169393-A.
XX
PN 20-JUN-2000.
XX
PD 30-SEP-1999; 99JP-0278301.
XX
PF 30-SEP-1998; 98JP-0276883.
XX
PR (SANY ) SANKYO CO LTD.
XX
PA WPI; 2000-485645/43.
XX
DR N-PSDB; AAA72124.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
XX PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX
PS Claim 20; Page 78-79; 139pp; Japanese.
XX
```

CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, hepatitis, AIDS
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis),
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYNNXXXXXXXXXXXXXXXXXAAASLNLEXXXXXXXXXXXXXXXXXXXX 60
 |||||XX
 Db 44 kasqsvdydgdsymnwqkpgqaprllyaaasnlsgipdrfsgsgsgdftltisrl 103

QY 61 XXXXXXXXQOSNEDPRT 78
 :XX
 Db 104 padfavycqgsnedprt 121

RESULT 9
 AAB14773
 ID AAB14773 standard; Protein; 238 AA.
 XX
 AC AAB14773;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.
 DE
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 KW
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AAA72125.
 XX
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 80-81; 139pp; Japanese.
 XX
 PS The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, hepatitis, AIDS
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis),
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX

CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, hepatitis, AIDS
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis),
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYNNXXXXXXXXXXXXXXXXXAAASLNLEXXXXXXXXXXXXXXXXXXXX 60
 |||||XX
 Db 44 kasqsvdydgdsymnwqkpgqaprllyaaasnlsgipdrfsgsgsgdftltihpve 103

QY 61 XXXXXXXXQOSNEDPRT 78
 :XX
 Db 104 eedaatyycqgsnedprt 121

RESULT 10
 AAB14774
 ID AAB14774 standard; Protein; 238 AA.
 XX
 AC AAB14774;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:54.
 DE
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
 KW hepatitis; AIDS; graft rejection; light chain.
 KW
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AAA72125.
 XX
 XX Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 83; 139pp; Japanese.
 XX
 PS The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its

CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;

Best Local Similarity 39.7%; Pred. NO. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSYVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60

Db 44 kasqsvdydgdsymwyyqkpgqpkllyaaasnlsgipdrfsgsgsgtdftltihpve 103

QY 61 XXXXXXXXQSQNEPRT 78

Db 104 eedaatyccgsnedprt 121

RESULT 11

AAB14777

ID AAB14777 standard; Protein; 238 AA.

AC AAB14777;

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CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;

Best Local Similarity 39.7%; Pred. NO. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSYVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60

Db 44 kasqsvdydgdsymwyyqkpgqpkllyaaasnlsgipdrfsgsgsgtdftltihpve 103

QY 61 XXXXXXXXQSQNEPRT 78

Db 104 eedaatyccgsnedprt 121

RESULT 11

AAB14777

ID AAB14777 standard; Protein; 238 AA.

AC AAB14777;

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CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;

Best Local Similarity 39.7%; Pred. NO. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSYVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60

Db 44 kasqsvdydgdsymwyyqkpgqpkllyaaasnlsgipdrfsgsgsgtdftltihpve 103

QY 61 XXXXXXXXQSQNEPRT 78

Db 104 eedaatyccgsnedprt 121

RESULT 11

AAB14777

ID AAB14777 standard; Protein; 238 AA.

AC AAB14777;

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CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;

Best Local Similarity 39.7%; Pred. NO. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSYVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60

Db 44 kasqsvdydgdsymwyyqkpgqpkllyaaasnlsgipdrfsgsgsgtdftltihpve 103

QY 61 XXXXXXXXQSQNEPRT 78

Db 104 eedaatyccgsnedprt 121

RESULT 11

AAB14777

ID AAB14777 standard; Protein; 238 AA.

AC AAB14777;

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CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;

Best Local Similarity 39.7%; Pred. NO. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSYVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60

Db 44 kasqsvdydgdsymwyyqkpgqpkllyaaasnlsgipdrfsgsgsgtdftltihpve 103

QY 61 XXXXXXXXQSQNEPRT 78

Db 104 eedaatyccgsnedprt 121

RESULT 11

AAB14777

ID AAB14777 standard; Protein; 238 AA.

AC AAB14777;

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CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.

XX SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;

Best Local Similarity 39.7%; Pred. NO. 1.2e-05;

Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSYVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60

Db 44 kasqsvdydgdsymwyyqkpgqpkllyaaasnlsgipdrfsgsgsgtdftltihpve 103

QY 61 XXXXXXXXQSQNEPRT 78

Db 104 eedaatyccgsnedprt 121

RESULT 11

AAB14777

ID AAB14777 standard; Protein; 238 AA.

AC AAB14777;

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CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 60
 DB 44 kassvdydgdsymwvqgpgqaprllyaaasnlsgiprfsqsgdftlinhpve 103
 QY 61 XXXXXXXXQSQSNEPRT 78
 DB 104 eedaatyccgsnedprt 121

RESULT 13
 AAW90898
 ID AAW90898 standard; Protein; 238 AA.
 AC AAW90898;
 XX
 XX 08-AUG-2000 (first entry)
 DT
 DE Murine anti-Fas antibody HFE7A light chain protein.
 XX
 XX Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 XX Mus musculus.
 XX
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-0307711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR
 XX 30-SEP-1998; 98JP-0276882.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI
 XX WPI: 2000-258930/23.
 DR
 XX N-PSDB; AAA11547.
 DR
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Example reference 4; Page 104; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,

CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a murine anti-Fas monoclonal antibody HFE7A light chain described in the
 CC method of the invention.
 XX
 SQ Sequence 238 AA;

Query Match 100.0%; Score 205; DB 21; Length 238;
 Best Local Similarity 39.7%; Pred. No. 1.2e-05;
 Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 60
 DB 44 kassvdydgdsymwvqgpgqaprllyaaasnlsgiprfsqsgdftlinhpve 103
 QY 61 XXXXXXXXQSQSNEPRT 78
 DB 104 eedaatyccgsnedprt 121

RESULT 14

AAW90922

ID AAW90922 standard; Protein; 238 AA.

AC AAW90922;

XX 08-AUG-2000 (first entry)

XX Humanised anti-Fas antibody HFE7A light chain HH type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 XX Synthetic.

OS

PN EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX

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DR WPI; 2000-258930/23.
DR N-PSDB; AAA11562.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
PS
PS Example reference 14; Page 114-115; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
XX the method described in the invention.
XX
SQ Sequence 238 AA;
Query Match 100.0%; Score 205; DB 21; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;
QY 1 KASQSVDDGDSYMNKXXXXXXXXXXXXAAASNLKESXXXXXXXXXXXXXXX 60
Db 44 kasqsvdydgsymnwyyqkpgaprllyaaanlesgipdrfsgsgtdftltisrle 103
QY 61 XXXXXXXXXQSNEDPRT 78
Db 104 padfavyvcqgsnedprt 121
RESULT 15
AAW90923
ID AAW90923 standard; Protein; 238 AA.
XX
XX AAW90923;
XX
XX 08-AUG-2000 (first entry)
XX
XX Humanised anti-Fas antibody HFE7A light chain HM type protein.
XX
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
XX dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
XX nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
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KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX Synthetic.
XX EP990663-A2.
XX
PD 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haryuyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI; 2000-258930/23.
XX N-PSDB; AAA11563.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
PS
PS Example reference 14; Page 117-118; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
XX the method described in the invention.
XX
SQ Sequence 238 AA;
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Query Match 100.0%; Score 205; DB 21; Length 238;
Best Local Similarity 39.7%; Pred. No. 1.2e-05;
Matches 31; Conservative 47; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KASQSVDDGDSYMNKXXXXXXXXXXXXAAASNLKESXXXXXXXXXXXXXXX 60
Db 44 kasqsvdydgsymnwyyqkpgaprllyaaanlesgipdrfsgsgtdftltihpve 103
QY 61 XXXXXXXXXQSNEDPRT 78
Db 104 eedaatyvcqgsnedprt 121
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Job time: 832 sec

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09/499, 662

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:02 ; Search time 82.88 Seconds
(without alignments)
22.987 Million cell updates/sec

Title: 5_g_6_g_7
Perfect score: 205
Sequence: 1 KASQSVYDGDSDYNNXXXXX.....XXXXXXXXXXQSQSNDPRT 78

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	198	96.6	111	2	US-08-483-632-73
3	198	96.6	131	2	US-08-483-636-58
4	198	96.6	131	2	US-08-483-632-58
5	198	96.6	132	2	US-08-483-636-2
6	198	96.6	132	2	US-08-483-632-2
7	197	96.1	106	3	US-08-466-151-6
8	197	96.1	106	4	US-08-466-163B-6
9	197	96.1	111	1	US-08-491-845-8
10	197	96.1	111	1	US-08-491-845-16
11	197	96.1	115	3	US-08-513-968-51
12	197	96.1	131	4	US-08-579-378A-14
13	197	96.1	131	4	US-08-579-378A-18
14	197	96.1	218	5	PCT-US96-13152-2
15	195	95.1	131	2	US-08-483-636-14
16	195	95.1	131	2	US-08-483-632-14
17	184	89.8	120	1	US-08-111-080-24
18	184	89.8	120	1	US-08-211-980-24
19	184	89.8	120	5	PCT-US93-07967-24
20	182	88.8	111	2	US-08-887-352B-6
21	182	88.8	111	4	US-09-109-207C-6
22	182	88.8	111	4	US-09-296-005-6
23	182	88.8	114	2	US-08-887-352B-10
24	182	88.8	114	4	US-09-109-207C-10
25	182	88.8	114	4	US-09-296-005-10
26	182	88.8	218	2	US-08-887-352B-13
27	182	88.8	218	3	US-08-466-151-9

28	182	88.8	218	4	US-09-109-207C-13	Sequence 13, Appl
29	182	88.8	218	4	US-09-296-005-13	Sequence 13, Appl
30	182	88.8	218	4	US-08-466-163B-9	Sequence 9, Appl
31	178	86.8	111	2	US-08-887-352B-5	Sequence 5, Appl
32	178	86.8	111	3	US-08-466-151-2	Sequence 2, Appl
33	178	86.8	111	4	US-09-109-207C-5	Sequence 5, Appl
34	178	86.8	111	4	US-09-296-005-5	Sequence 5, Appl
35	178	86.8	111	4	US-08-466-163B-2	Sequence 2, Appl
36	178	86.8	114	2	US-08-887-352B-9	Sequence 9, Appl
37	175	85.4	114	4	US-09-109-207C-9	Sequence 9, Appl
38	175	85.4	114	4	US-09-296-005-9	Sequence 9, Appl
39	165	80.5	239	2	US-08-553-497A-18	Sequence 18, Appl
40	159	77.6	114	2	US-08-887-352B-8	Sequence 8, Appl
41	159	77.6	218	4	US-09-054-255-1	Sequence 1, Appl
42	159	77.6	218	4	US-09-109-207C-8	Sequence 8, Appl
43	156	76.1	114	4	US-09-296-005-8	Sequence 8, Appl
44	156	76.1	114	4	US-08-887-352B-15	Sequence 15, Appl
45	156	76.1	218	2	US-08-887-352B-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-08-483-636-73
; Sequence 73, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown

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; MOLECULE TYPE: protein
US-08-483-636-73

Query Match          96.6%; Score 198; DB 2; Length 111;
Best Local Similarity 38.5%; Pred. No. 3.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLSEGIPSRFSGSGGDTFTLTSSLQ 83
QY 61 XXXXXXXXXQSQSNEDPRT 78
Db 84 PEDIATYVCQSQSNEDPPT 101

RESULT 3
US-08-483-636-58
; Sequence 58, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-636-58

Query Match          96.6%; Score 198; DB 2; Length 131;
Best Local Similarity 38.5%; Pred. No. 5.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60
Db 43 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLSEGVDPDRFSGSGGDTFTLTSSLQ 102
QY 61 XXXXXXXXXQSQSNEDPRT 78

; MOLECULE TYPE: protein
US-08-483-632-73

Query Match          96.6%; Score 198; DB 2; Length 111;
Best Local Similarity 38.5%; Pred. No. 3.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLSEGIPSRFSGSGGDTFTLTSSLQ 83
QY 61 XXXXXXXXXQSQSNEDPRT 78
Db 84 PEDIATYVCQSQSNEDPPT 101

RESULT 2
US-08-483-632-73
; Sequence 73, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-483-632-73

Query Match          96.6%; Score 198; DB 2; Length 111;
Best Local Similarity 38.5%; Pred. No. 3.1e-08;
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; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-2

Query Match 96.6%; Score 198; DB 2; Length 132;
Best Local Similarity 38.5%; Pred. No. 5.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps

QY 1 KASQSDYDGDGSMYNNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60
Db 44 KASQSDYDGDGSMYNNWYQQPQPKLLIYAASNLSEGGIPARFSGSGGDTFTLNIHPVE 103

QY 61 XXXXXXXXXQSQSNEDPPT 78
Db 104 EEDAATYCCQSQSNEDPPT 121

RESULT 6
US-08-483-632-2
; Sequence 2, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,632
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-632-58

Query Match 96.6%; Score 198; DB 2; Length 131;
Best Local Similarity 38.5%; Pred. No. 5.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGSMYNNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 60
Db 43 KASQSDYDGDGSMYNNWYQQPQPKLLIYAASNLSEGGVDPDRFSGSGGDTFTLTISLQ 102

QY 61 XXXXXXXXXQSQSNEDPPT 78
Db 103 AEDVAVYCCQSQSNEDPPT 120

RESULT 5
US-08-483-636-2
; Sequence 2, Application US/08483636

```

NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P.O. Box 1539 / UW2220
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,632
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117366
FILING DATE: 07-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136783
FILING DATE: 14-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US/94/10308
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50186-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 270-5024
TELEFAX: (215) 270-5090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-632-2

Query Match 96.6%; Score 198; DB 2; Length 132;
Best Local Similarity 38.5%; Pred. No. 5.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
|||||XXX
Db 44 KASQSDYDGDSDYMNWYQKQPPLIYAASNLESIGIPARFSGSGTDTLNIHPVE 103
QY 61 XXXXXXXXQSQSDPRT 78
Db 104 EDAATYYCQSQSDPPT 121

RESULT 7
US-08-466-151-6
Sequence 6, Application US/08466151
Patent No. 6037453
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/466163
FILING DATE: 06-Jun-1995
APPLICATION NUMBER: 08/405617
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
FILING DATE: 26-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/879495
FILING DATE: 07-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
FILING DATE: 14-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P07182C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-466-151-6

Query Match 96.1%; Score 197; DB 3; Length 106;
Best Local Similarity 38.5%; Pred. No. 3.3e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
|||||XXX
Db 24 KASQSDYDGDSDYMNWYQKQPPLIYAASNLESIGIPARFSGSGTDTLNIHPVE 83
QY 61 XXXXXXXXQSQSDPRT 78
Db 84 EDAATYYCQSQSDPPT 101

RESULT 8
US-08-466-163B-6
Sequence 6, Application US/08466163B
Patent No. 6329509
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P07182C1D1
CURRENT APPLICATION NUMBER: US/08/466,163B
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 6
LENGTH: 106
TYPE: PRT

db 24 KASOSVDYDGD SYMNYOOPKPGOPKLLIYAASNLESGIPAREFSGSGGTDTLNHPVF 83

Patent No. 6114143
GENERAL INFORMATION:

APPLICANT: EDA, Yasuyuki
APPLICANT: MAEDA, Hiroaki
APPLICANT: MAKIZUMI, Keiichi
APPLICANT: SHIOSAKI, Kouichi
APPLICANT: OSATOMI, Kiyoshi
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: HIGUCHI, Hirofumi
APPLICANT: TOKIYOSHI, Sachio
TITLE OF INVENTION: ANTI-HIV MONOCLONAL ANTIBODY
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,968
FILING DATE: 11-SEP-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 78913/1993
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: EDA=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-737-3528
TELEFAX: 248633
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-513-968-51
Query Match 96.1%; Score 197; DB 3; Length 115;
Best Local Similarity 38.5%; Pred. No. 4.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXASNLESDXXXXXXXXXXXXXXXXXXXX 60
Db 28 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLESGVPSRFGSGSGTDTFTFISSIQ 87
QY 61 XXXXXXXXQSNEDPRT 78
Db 88 PEDIATYCCQSNEDPWT 105
RESULT 12
US-08-579-378A-14
Sequence 14, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California

COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,378A
FILING DATE: 27-DEC-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160,074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/983,946
FILING DATE: 01-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95112895.8
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95114696.8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Liebescheutz, Joe O.
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-579-378A-14
Query Match 96.1%; Score 197; DB 4; Length 131;
Best Local Similarity 38.5%; Pred. No. 6.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASQSDYDGDSDYMNXXXXXXXXXXXXXXXXXASNLESDXXXXXXXXXXXXXXXXXXXX 60
Db 44 KASQSDYDGDSDYMNWYQKPGKAPKLLIYAASNLESGIPARFSGSGTDTFTLNHPVE 103
QY 61 XXXXXXXXQSNEDPRT 78
Db 104 EEDAATYCCQSNEDPWT 121
RESULT 13
US-08-579-378A-18
Sequence 18, Application US/08579378A
Patent No. 6210671
GENERAL INFORMATION:
APPLICANT: Co, Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
TITLE OF INVENTION: L-Selectin
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-18

Query Match          96.1%; Score 197; DB 4; Length 131;
Best Local Similarity 38.5%; Pred. No. 6.2e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGSDYNNXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXX 60
Db 44 KASQSDYDGDGSDYNNWYQKPGKAPKLLIYAASNLSEGPSRFGSGGTDFTLTISLQ 103
QY 61 XXXXXXXXQOSNEDPRT 78
Db 104 PEDFATYQCOSNEDPWT 121

RESULT 14
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
```

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; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match          96.1%; Score 197; DB 5; Length 218;
Best Local Similarity 38.5%; Pred. No. 2.9e-07;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSDYDGDGSDYNNXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSDYDGDGSDYNNWYQKPGKAPKLLIYAASNLSEGPSRFGSGGTDFTLTISLQ 83
QY 61 XXXXXXXXQOSNEDPRT 78
Db 84 PEDFATYQCOSNEDPWT 101

RESULT 15
US-08-483-636-14
; Sequence 14, Application US/08483636
; Patent No. 5914110
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P.O. Box 1539 / UN2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
```

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; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-636-14

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Query Match      95.1%; Score 195; DB 2; Length 131;
Best Local Similarity 38.2%; Pred. No. 9.2e-08;
Matches 29; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 KASQSVYDGDSDYMNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Db 43 KASQSVYDGDSDYMNWYQKPPKLLIYAAASNLESVDPDRFSGSGGTDTLTISLIQ 102
QY 61 XXXXXXXXXQSNEDP 76
Db 103 AEDVAVIYCQSNEDP 118

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Search completed: August 14, 2002, 15:17:02
Job time: 685 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:57 ; Search time 108.64 Seconds
(without alignments)
68.989 Million cell updates/sec

Title: 5_g_6_g_7
Perfect score: 205
Sequence: 1 KASQSDYDGDSDYNNXXXXX.....XXXXXXXXXXQSQSNEEDPRT 78

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	96.6	111	1 KVM583	Ig kappa chain V r
2	197	96.1	111	1 KVM543	Ig kappa chain V r
3	197	96.1	111	1 KVM569	Ig kappa chain V r
4	193	94.1	93	2 A38601	Ig kappa chain V r
5	193	94.1	111	1 KVM508	Ig kappa chain V r
6	191	93.2	81	2 S42193	Ig kappa chain V r
7	190	92.7	112	2 S19971	Ig kappa chain V r
8	190	92.7	131	2 PH1226	Ig kappa chain pre
9	187	91.2	111	1 KVM5C1	Ig kappa chain V r
10	179	87.3	111	2 S09966	Ig kappa chain V-J
11	172.5	84.1	110	1 KVM510	Ig kappa chain V r
12	172	83.9	112	2 S19976	Ig kappa chain V r
13	162	79.0	112	2 S19972	Ig kappa chain V r
14	157	76.6	111	2 D45722	anti-glycoprotein
15	155	75.6	107	2 S26344	Ig kappa chain V r
16	155	75.6	111	1 KVM537	Ig kappa chain V r
17	154	75.1	107	2 S26343	Ig kappa chain V r
18	151	73.7	131	1 KVM5M6	Ig kappa chain pre
19	149	72.7	96	2 B49442	Ig light chain V r
20	147	71.7	115	2 S63596	Ig kappa chain V r
21	137	66.8	111	1 KVM584	Ig kappa chain V r
22	136	66.3	111	2 S09965	Ig kappa chain V-J
23	136	66.3	132	1 KVM532	Ig kappa chain pre
24	135	65.9	109	2 PH0093	Ig kappa chain V r
25	133	64.9	102	2 PH1079	Ig light chain V r
26	133	64.9	111	2 PL0081	Ig kappa chain V r
27	133	64.9	120	2 S06731	Ig kappa chain pre
28	132	64.4	111	1 KVM580	Ig kappa chain V r
29	130	63.4	108	1 KVM554	Ig kappa chain V r

30	130	63.4	111	1 KVM575	Ig kappa chain V r
31	130	63.4	111	2 S09963	Ig kappa chain V-J
32	130	63.4	111	2 E53285	Ig kappa chain V a
33	130	63.4	120	2 S06732	Ig kappa chain pre
34	129	62.9	102	2 PH1076	Ig light chain V r
35	129	62.9	111	2 S09969	Ig kappa chain V-J
36	129	62.9	210	2 A56169	Ig kappa chain V r
37	127	62.0	111	1 KVM540	Ig kappa chain V r
38	127	62.0	111	2 S37202	Ig kappa chain V r
39	127	62.0	112	2 S45715	Ig kappa chain V r
40	127	62.0	123	2 S40331	Ig kappa chain - h
41	125	61.0	111	1 KVM585	Ig kappa chain V r
42	124	60.5	218	2 JC5810	monoclonal antibody
43	123	60.0	111	1 KVM550	Ig kappa chain V r
44	121	59.0	218	2 S68241	Ig kappa chain V r
45	120	58.5	108	2 B49047	Ig kappa chain V r

ALIGNMENTS

RESULT 1
KVM583
Ig kappa chain V region (PC7183) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: B01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: B01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 96.6%; Score 198; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 2.2e-09;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;
QY 1 KASQSDYDGDSDYNNXXXXXAAASNNLESXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSDYDGDSDYNNWYQQKPGQPKLLIYAASNNLESIPARFSGSGGDTFTLNHPVE 83
QY 61 XXXXXXXXQSQSNEEDPRT 78
DB 84 EEDAATYYCQSQSNEEDPLT 101

RESULT 2
KVM543
Ig kappa chain V region (PC7043) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
C:Accession: A01937; S42187; S42194; S42199; S42188; S42191; S42192
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A>Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: A01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A>Title: Variable region gene selection of immunoglobulin G-expressing B cells with s
A:Reference number: S42176; MUID:94009207
A:Accession: S42187

```
A:Molecule type: DNA
A:Residues: 10-99 <MO>
A:Cross-references: EMBL:Z25444; NID:g407832; PIDN:CAA80931.1; PID:g407833
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42194
A:Molecule type: DNA
A:Residues: 12-99 <MO>
A:Cross-references: EMBL:Z25458; NID:g407844; PIDN:CAA80945.1; PID:g407845
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42190
A:Molecule type: DNA
A:Residues: 13-99 <MO>
A:Cross-references: EMBL:Z25450; NID:g407838; PIDN:CAA80937.1; PID:g407839
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42189
A:Molecule type: DNA
A:Residues: 15-99 <MO>
A:Cross-references: EMBL:Z25448; NID:g407836; PIDN:CAA80935.1; PID:g407837
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42188
A:Molecule type: DNA
A:Residues: 12-99 <MO>
A:Cross-references: EMBL:Z25446; NID:g407834; PIDN:CAA80933.1; PID:g407835
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42191
A:Molecule type: DNA
A:Residues: 10-99 <MO>
A:Cross-references: EMBL:Z25452; NID:g407840; PIDN:CAA80939.1; PID:g407841
A:Note: V-kappa-21E; anti-collagen
A:Accession: S42192
A:Molecule type: DNA
A:Residues: 10-99 <MO>
A:Cross-references: EMBL:Z25454; NID:g407842; PIDN:CAA80941.1; PID:g407843
A:Note: V-kappa-21E; anti-collagen
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 2.8e-09;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYMNXKXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVYDGDGYMNYQKQPKPLLIYAASNLESIGIPARFSGSGTDTFLNIHPVE 83

Qy 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPFT 101

RESULT 3
KVMS69
Ig kappa chain V region (PC7769) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: E01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: E01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted
```

```
F:23-92/Disulfide bonds: #status predicted

Query Match          96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 2.8e-09;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYMNXKXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVYDGDGYMNYQKQPKPLLIYAASNLESIGIPARFSGSGTDTFLNIHPVE 83

Qy 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPFT 101

RESULT 4
A38601
Ig kappa chain V region (IG3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C:Accession: A38601
R:Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A:Title: Common structural features among monoclonal antibodies binding the same anti
A:Reference number: A38601; MUID:91115823
A:Accession: A38601
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-93 <GOS>
A:Cross-references: GB:M57978; NID:g196402; PIDN:AAA63359.1; PID:g196403
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match          94.1%; Score 193; DB 2; Length 93;
Best Local Similarity 37.2%; Pred. No. 5.4e-09;
Matches 29; Conservative 47; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQSVYDGDGYMNXKXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60
Db 5 KASQSVYDGDGYMNYQKQPKPLLIYAASNLESIGIPARFSGSGTDTFLNIHPVE 64

Qy 61 XXXXXXXXQSQSNEDPRT 78
Db 65 EEDAATYYCQSQSNEDPFT 82

RESULT 5
KVMS08
Ig kappa chain V region (PC6308) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jan-2000
C:Accession: C01937; A01937
R:Weigert, M.; Gatmaitan, L.; Loh, E.; Schilling, J.; Hood, L.
Nature 276, 785-790, 1978
A:Title: Rearrangement of genetic information may produce immunoglobulin diversity.
A:Reference number: A93204; MUID:79073152
A:Accession: C01937
A:Molecule type: protein
A:Residues: 1-111 <WEI>
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match          94.1%; Score 193; DB 1; Length 111;
Best Local Similarity 37.2%; Pred. No. 7.1e-09;
Matches 29; Conservative 47; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXX 60
|||||
Db 24 KASQSDVDGDSYMNWYQKPGPKLLIYASNLESIGIPARFSGSGTDFTLNIHPVE 83
Qy 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPWT 101

RESULT 6
S42193
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S42193
R:Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A:Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A:Reference number: S42193; MUID:94009207
A:Accession: S42193
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-81 <WQJ>
A:Cross-references: EMBL:225456; NID:g407846; PIDN:CAA80943.1; PID:g407847
A:Note: the authors translated the codon GTT for residue 36 as Ala
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 191; DB 2; Length 81;
Best Local Similarity 36.8%; Pred. No. 7e-09; Mismatches 1; Indels 0; Gaps 0;
Matches 28; Conservative 47;
Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXX 60
|||||
Db 6 KASQSDVDGDSYMNWYQKPGPKLLIYASNLESIGIPARFSGSGTDFTLNIHPVE 65
Qy 61 XXXXXXXXQSQSNEDP 76
Db 66 EEDAATYYCQSQSNEDP 81

RESULT 7
S19971
Ig kappa chain V region (CD4 mAb clone M-T310 and others) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19971; S19973
R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19971
A:Molecule type: mRNA
A:Residues: 1-112 <WEI>
A:Cross-references: EMBL:X65091; NID:g52288; PIDN:CAA46219.1; PID:g52289
A:Experimental source: clone M-T310
A:Accession: S19973
A:Molecule type: mRNA
A:Residues: 1-112 <WEW>
A:Cross-references: EMBL:X65092; NID:g52292; PIDN:CAA46220.1; PID:g52293
A:Experimental source: M-T404
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 190; DB 2; Length 112;
Best Local Similarity 35.9%; Pred. No. 1.5e-08;
Matches 28; Conservative 49; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXX 60
|||||

Db 24 KASQSLDVGDSYMNWYQKPGPKLLIYAASNLESIGIPARFSGSGTDFTLNIHPVE 83
Qy 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EEDAATYYCQSQSNEDPPT 101

RESULT 8
PH1226
Ig kappa chain precursor V region (M-T310) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C:Accession: PH1226
R:Weissenhorn, W.; Scheuer, W.; Kaluza, B.; Schwirzke, M.; Reiter, C.; Flieger, D.; I
Gene 121, 271-278, 1992
A:Title: Combinatorial functions of two chimeric antibodies directed to human CD4 and
A:Reference number: PH1224; MUID:93077041
A:Accession: PH1226
A:Molecule type: mRNA
A:Residues: 1-131 <WEI>
A:Cross-references: GB:S50265; NID:g260765; PIDN:AAB24320.1; PID:g260766
A:Note: this mouse sequence was hybridized and fused with a human constant region gen
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-131/Product: Ig light chain V region #status predicted <MAT>
F:36-114/Domain: immunoglobulin homology <IMM>

Query Match 92.7%; Score 190; DB 2; Length 131;
Best Local Similarity 35.9%; Pred. No. 1.8e-08;
Matches 28; Conservative 49; Mismatches 1; Indels 0; Gaps 0;
Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXX 60
|||||
Db 44 KASQSLDVGDSYMNWYQKPGPKLLIYAASNLESIGIPARFSGSGTDFTLNIHPVE 103
Qy 61 XXXXXXXXQSQSNEDPRT 78
Db 104 EEDAATYYCQSQSNEDPPT 121

RESULT 9
KVMSCL
Ig kappa chain V region (CBFC 101) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 31-Mar-2000
C:Accession: A01936
R:McKean, D.J.; Bell, M.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 3913-3917, 1978
A:Title: Mechanisms of antibody diversity: multiple genes encode structurally related
A:Reference number: A93822; MUID:79012520
A:Accession: A01936
A:Molecule type: protein
A:Residues: 1-111 <MCK>
C:Comment: This chain was isolated from a myeloma protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match 91.2%; Score 187; DB 1; Length 111;
Best Local Similarity 35.9%; Pred. No. 2.9e-08;
Matches 28; Conservative 48; Mismatches 2; Indels 0; Gaps 0;
Qy 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXX 60
|||||
Db 24 KASQSDVDGDSYMNWYQKPGPKLLIYAASNLESIGIPARFSGSGTDFTLNIHPVE 83
Qy 61 XXXXXXXXQSQSNEDPRT 78

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C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19976
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19976
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WE1>
A:Cross-references: EMBL:X65093; NID:g52298; PIDN:CAA46221.1; PID:g52299
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match      83.9%; Score 172; DB 2; Length 112;
Best Local Similarity 32.1%; Pred. No. 9.4e-07;
Matches 25; Conservative 50; Mismatches 3; Indels 0; Gaps

Qy 1 KASQVDYDGDGYMNXXXXXXXXXXXXXXXXXASNLSEXXXXXXXXXXXXXXXXXXXXX 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 24 KASQSLDYDADSYWHYVQKPGRPKLLIYAASNLSEGIPIARFSGSGTDTLNIHPVE 83
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 XXXXXXXXXQOQSNEDPRT 78
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 84 EEDAATYTCQOQSDPVT 101

RESULT 13
S19972
Ig kappa chain V region (M-T321) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19972
R:Weissenhorn, W.; Riethmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19972
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WE1>
A:Cross-references: EMBL:X65094; NID:g52290; PIDN:CAA46222.1; PID:g52291
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match      79.0%; Score 162; DB 2; Length 112;
Best Local Similarity 29.5%; Pred. No. 9.6e-06;
Matches 23; Conservative 52; Mismatches 3; Indels 0; Gaps

Qy 1 KASQVDYDGDGYMNXXXXXXXXXXXXXXXXXASNLSEXXXXXXXXXXXXXXXXXXXXX 60
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 24 RASQVDYNAISYWHYVQKPGPPKLLIYAASNLSEGIPIARFSGSGTDTLNIHPVE 83
    |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 XXXXXXXXXQOQSNEDPRT 78
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 84 EEDAATYTCQOQSDPVT 101

RESULT 14
D45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 10)
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: D45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigen
A:Reference number: A45722; MUID:93100833

```

A:Accession: D45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-111 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120592)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 157; DB 2; Length 111;
Best Local Similarity 28.2%; Pred. No. 3e-05;
Matches 22; Conservative 52; Mismatches 4; Indels 0; Gaps 0;
Qy 1 KASQSDVDGDSYMNXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASESDVSYGKSFHWYQKPGQPKLLIYRASNLESIGIPARFSGSGSRTDFTLTIDPVE 83
Qy 61 XXXXXXXXXQOSNEDPRT 78
Db 84 ADDAATYYCQNNEDPRT 101

RESULT 15
S26344
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26344
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26344
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59209; NID:g52336; PIDN:CAA1919.1; PID:g1334074
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 75.6%; Score 155; DB 2; Length 107;
Best Local Similarity 28.2%; Pred. No. 4.5e-05;
Matches 22; Conservative 52; Mismatches 4; Indels 0; Gaps 0;
Qy 1 KASQSDVDGDSYMNXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Db 23 RASESDVSYGKSFHWYQKPGQPKLLIYRASNLESIGIPARFSGSGSRTDFTLTINPVE 82
Qy 61 XXXXXXXXXQOSNEDPRT 78
Db 83 ADDVATYYCQSNEDPRT 100

Search completed: August 14, 2002, 15:18:58
Job time: 686 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:12 ; Search time 53.64 Seconds
(without alignments)
56.304 Million cell updates/sec

Title: 5_g_6_g_7

Perfect score: 205

Sequence: 1 KASQSVDDGSDYNNXXXXX.....XXXXXXXXXXQSQSNEDPRT 78

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	96.6	111	1	KV3N_MOUSE
2	197	96.1	111	1	KV3M_MOUSE
3	197	96.1	111	1	KV3Q_MOUSE
4	193	94.1	111	1	KV3O_MOUSE
5	187	91.2	111	1	KV3L_MOUSE
6	172.5	84.1	110	1	KV3P_MOUSE
7	155	75.6	111	1	KV3H_MOUSE
8	152	74.1	111	1	KV3J_MOUSE
9	152	74.1	111	1	KV3K_MOUSE
10	151	73.7	131	1	KV3I_MOUSE
11	137	66.8	111	1	KV3R_MOUSE
12	136	66.3	112	1	KV3G_MOUSE
13	136	66.3	132	1	KV3F_MOUSE
14	135	65.9	111	1	KV3C_MOUSE
15	132	64.4	111	1	KV3A_MOUSE
16	130	63.4	108	1	KV3V_MOUSE
17	130	63.4	111	1	KV3S_MOUSE
18	130	63.4	112	1	KV3B_MOUSE
19	127	62.0	111	1	KV3T_MOUSE
20	125	61.0	111	1	KV3U_MOUSE
21	123	60.0	111	1	KV3D_MOUSE
22	113	55.1	108	1	KV1A_HUMAN
23	112	54.6	108	1	KV1E_HUMAN
24	110.5	53.9	113	1	KV2B_HUMAN
25	110	53.7	108	1	KV1K_HUMAN
26	110	53.7	108	1	KV1N_HUMAN
27	110	53.7	129	1	KV1W_HUMAN
28	109	53.2	112	1	KV1U_HUMAN
29	108	52.7	108	1	KV5K_MOUSE
30	108	52.7	108	1	KV5O_MOUSE
31	106	51.7	108	1	KV5L_MOUSE
32	105	51.2	109	1	KV1T_HUMAN
33	104.5	51.0	133	1	KV2F_HUMAN

ALIGNMENTS

```
RESULT_1
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KYMS83.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 96.6%; Score 198; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 6,7e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVDDGSDYNNXXXXXXXXXXXXXXXXXAAASLNLEXXXXXXXXXXXXXXXXXXXXX 60
Db 24 KASQSVDDGSDYNNWYQKPGQPKLLIYAASLNLESGIPARFSGSGGTDTLLNHPVE 83
QY 61 XXXXXXXXXQSQSNEDPRT 78
Db 84 EEDARTTCQSQSNEDPLT 101

RESULT_2
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RA "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM543.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 8.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMNXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSVYDGDGYMNYQKQPPKLLIYAASNLESIPARFSGSGTDTLTNIHPVE 83
QY 61 XXXXXXXXQSQSNEPRT 78
DB 84 EEDAATYYCQSQSNEPRT 101

RESULT 3
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RA "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM569.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 8.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMNXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSVYDGDGYMNYQKQPPKLLIYAASNLESIPARFSGSGTDTLTNIHPVE 83
QY 61 XXXXXXXXQSQSNEPRT 78
DB 84 EEDAATYYCQSQSNEPRT 101

RESULT 3
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RA "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01937; KVM569.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;
```

```
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 96.1%; Score 197; DB 1; Length 111;
Best Local Similarity 38.5%; Pred. No. 8.1e-08;
Matches 30; Conservative 47; Mismatches 1; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMNXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSVYDGDGYMNYQKQPPKLLIYAASNLESIPARFSGSGTDTLTNIHPVE 83
QY 61 XXXXXXXXQSQSNEPRT 78
DB 84 EEDAATYYCQSQSNEPRT 101

RESULT 4
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RA "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 94.1%; Score 193; DB 1; Length 111;
Best Local Similarity 37.2%; Pred. No. 1.8e-07;
Matches 29; Conservative 47; Mismatches 2; Indels 0; Gaps 0;

QY 1 KASQSVYDGDGYMNXKXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 24 KASQSVYDGDGYMNYQKQPPKLLIYAASNLESIPARFSGSGTDTLTNIHPVE 83
QY 61 XXXXXXXXQSQSNEPRT 78
DB 84 EEDAATYYCQSQSNEPRT 101
```

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RESULT 5
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01936; KVMSC1.
DR HSSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;

Query Match 91.2%; Score 187; DB 1; Length 111;
Best Local Similarity 35.9%; Pred. No. 5.8e-07;
Matches 28; Conservative 48; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCQSQSNEPDT 101

RESULT 6
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCQSQSNEPDT 101

RESULT 7
KV3H_MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

Query Match 84.1%; Score 172.5; DB 1; Length 110;
Best Local Similarity 34.6%; Pred. No. 9.7e-06;
Matches 27; Conservative 48; Mismatches 2; Indels 1; Gaps 1;
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Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

RESULT 8
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

Query Match 84.1%; Score 172.5; DB 1; Length 110;
Best Local Similarity 34.6%; Pred. No. 9.7e-06;
Matches 27; Conservative 48; Mismatches 2; Indels 1; Gaps 1;
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```
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

RESULT 9
KV3J_MOUSE
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

Query Match 84.1%; Score 172.5; DB 1; Length 110;
Best Local Similarity 34.6%; Pred. No. 9.7e-06;
Matches 27; Conservative 48; Mismatches 2; Indels 1; Gaps 1;
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```
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

RESULT 10
KV3K_MOUSE
ID KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 3741/TEPC 111.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

Query Match 84.1%; Score 172.5; DB 1; Length 110;
Best Local Similarity 34.6%; Pred. No. 9.7e-06;
Matches 27; Conservative 48; Mismatches 2; Indels 1; Gaps 1;
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```
Qy 1 KASQSDVDGDSYMNXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXX 60
Dy 24 KASQSDVDGDSYMNWYQNPQSPKLLIYAASNLESIGIPARFSGSGTDFTLNHPVE 83
Qy 61 XXXXXXXXQSQSNEPDT 78
Dy 84 EEDAATYYCHQS-EDPWT 100

RESULT 11
KV3L_MOUSE
ID KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.
DR PIR: A01934; KVMSC7.
DR HSSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;
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Qy 61 XXXXXXXXXXQSNEDPRT 78

RT
+ h

Burstein Y., Schechter I.;

Burstein Y., Schechter I.;

Burstein Y., Schechter I.;

RT precursors: implications on the organization and controlled
RL expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400(1978).

RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RL kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RL related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: A01935; KVM56.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

Query Match 73.7%; Score 151; DB 1; Length 131;
Best Local Similarity 26.9%; Pred. No. 0.00092;
Matches 21; Conservative 53; Mismatches 4; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESGVPAFPFSGSGRTDTLTIDPVE 60
DB 44 RASESDVSYGNSFMHWYQKPGPPKLLIYLASNLESGVPAFPFSGSGRTDTLTIDPVE 103
QY 61 XXXXXXXXQSQNEDPRT 78
DB 104 ADDAATYTCQNNEDPWT 121

RESULT 11
KV3R_MOUSE
ID KV3R_MOUSE STANDARD; PRT; 111 AA.
AC P01670;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6684.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Waigert M., Gacmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RL diversity.";
RL Nature 276:785-790(1978).
DR PIR: A01938; KVM54.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 FRAMEWORK-1.
FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 60 FRAMEWORK-2.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 93 101 FRAMEWORK-3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12039 MW; 1E46988341858526 CRC64;

Query Match 66.8%; Score 137; DB 1; Length 111;
Best Local Similarity 25.6%; Pred. No. 0.01;
Matches 20; Conservative 50; Mismatches 8; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESGVPAFPFSGSGRTDTLTIDPVE 60
DB 24 RASKSVSTSGSYSMHWYQKPGPPKLLIYLASNLESGVPAFPFSGSGRTDTLTIDPVE 83
QY 61 XXXXXXXXQSQNEDPRT 78
DB 84 EEDAATYTCQHSRELPT 101

RESULT 12
KV3G_MOUSE
ID KV3G_MOUSE STANDARD; PRT; 112 AA.
AC P01659;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region TEPC 124.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RL kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771(1973).
DR PIR: A01933; KVM52.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 FRAMEWORK-1.
FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 60 FRAMEWORK-2.
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 93 101 FRAMEWORK-3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DBE8E9D71 CRC64;

Query Match 66.3%; Score 136; DB 1; Length 112;
Best Local Similarity 19.2%; Pred. No. 0.013;
Matches 15; Conservative 58; Mismatches 5; Indels 0; Gaps 0;

QY 1 KASQSDVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLESGVPAFPFSGSGRTDTLTIDPVE 60
DB 84 EEDAATYTCQHSRELPT 101

5

Search completed: August. 14, 2002, 15:23:12
Job time: 685 sec

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Db 16 RASESEYTGTSIMQYQKPGPPKLLIYAASNVESGVPAREFSGSGTDFSLNIHPVE 75
QY 61 XXXXXXXXQSQSNEDPRT 78
Db 76 EDDIAMIFCQSKRPVPT 93
RESULT 2
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOPOPE KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT 'Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells.';
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -
FT NON_TER 1 111
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46989AA6858526 CRC64;

Query Match 63.4%; Score 130; DB 11; Length 111;
Best Local Similarity 24.4%; Pred. No. 0.34;
Matches 19; Conservative 50; Mismatches 9; Indels 0; Gaps 0;

QY 1 KASQSYVDYDGDSTYMNXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 24 RASKSVSTSGYSYMHYQKPGPPKLLIYASNLSESGVPAREFSGSGTDFSLNIHPVE 83
QY 61 XXXXXXXXQSQSNEDPRT 78
Db 84 EDAATYICQHSRELPY 101

RESULT 3
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA ADDERSON E.E., SHIKHMAN A.R., WARD K.E., CUNNINGHAM M.W.;
RT "Molecular analysis of polyclonal antibodies from
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
antibody V region genes";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 55.1%; Score 113; DB 4; Length 107;
Matches 15; Conservative 52; Mismatches 1; Indels 4; Gaps 1;
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Best Local Similarity 20.8%; Pred. No. 7.6;
Matches 15; Conservative 52; Mismatches 1; Indels 4; Gaps 1;

QY 1 KASQSYVDYDGDSTYMNXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 24 RASQSI-----SSYLNWYQKPGKAPNLLIYAASLSQSGVPSRFSGSGTDFTLTISLQ 79
QY 61 XXXXXXXXQSQS 72
Db 80 PEDFATYYCQQS 91

RESULT 4
ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetuses";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -
DR HSSP; P01607; IREX.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 55.1%; Score 113; DB 4; Length 108;
Best Local Similarity 20.8%; Pred. No. 7.8;
Matches 15; Conservative 52; Mismatches 1; Indels 4; Gaps 1;

QY 1 KASQSYVDYDGDSTYMNXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXX 60
:||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db 24 RASQSI-----SSYLNWYQKPGKAPNLLIYAASLSQSGVPSRFSGSGTDFTLTISLQ 79
QY 61 XXXXXXXXQSQS 72
Db 80 PEDFATYYCQQS 91

RESULT 5
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
```

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RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 53.7%; Score 110; DB 4; Length 107;
Best Local Similarity 19.4%; Pred. No. 13;
Matches 14; Conservative 53; Mismatches 1; Indels 4; Gaps 1;

Qy 1 KASQSDYDGD SYNNXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASQSI----SNLWVYQKPGKAPNLLIYAASSLQSGVPSRFGSGGDTFTLTISLQ 79

Qy 61 XXXXXXXXXQOS 72
Db 80 AEDFATYCCQS 91

RESULT 6
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR HSP; P80362; IWTLL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 114
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 51.0%; Score 104.5; DB 4; Length 114;
Best Local Similarity 16.9%; Pred. No. 43;
Matches 13; Conservative 53; Mismatches 10; Indels 1; Gaps 1;

Qy 1 KASQSDYDGD SYNNXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXX 59
Db 24 RSSQSPVSDGNTYLNWFQRPQSGPRRLIYKVSNRDGVDPFRFGSGGDTFTLKISRV 83

Qy 60 XXXXXXXXXQOSNEDP 76
Db 84 EAEDVGYYTCMQGTHWP 100

RESULT 8
Q96JM2 PRELIMINARY; PRT; 1299 AA.
AC Q96JM2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIAA1803 PROTEIN (FRAGMENT).
GN KIAA1803.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRAIN;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 8:85-95(2001).
DR EMBL; AB058706; BAB47432.1; -.
FT NON_TER 1 1299
FT NON_TER 1299 1299
SQ SEQUENCE 1299 AA; 148675 MW; 69FFECB5868186DD CRC64;
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RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 53.7%; Score 110; DB 4; Length 107;
Best Local Similarity 19.4%; Pred. No. 13;
Matches 14; Conservative 53; Mismatches 1; Indels 4; Gaps 1;

Qy 1 KASQSDYDGD SYNNXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASQSI----SNLWVYQKPGKAPNLLIYAASSLQSGVPSRFGSGGDTFTLTISLQ 79

Qy 61 XXXXXXXXXQOS 72
Db 80 AEDFATYCCQS 91

RESULT 6
Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3B41FCCA37 CRC64;

Query Match 52.7%; Score 108; DB 4; Length 108;
Best Local Similarity 17.9%; Pred. No. 20;
Matches 14; Conservative 53; Mismatches 7; Indels 4; Gaps 1;

Qy 1 KASQSDYDGD SYNNXXXXXXXXXXAAASLNLESXXXXXXXXXXXXXXXXXXXX 60
Db 24 RASQSI----SNLWVYQKPGKPKSLIYAASTLQSGVPSRFGSGGDTFTLTISLQ 79

Qy 61 XXXXXXXXXQOSNEDP 78
Db 80 PEDVATYCCQKYNAPRT 97
```

Query Match	50.2%;	Score 103;	DB 4;	Length 1299;
Best Local Similarity	17.3%;	Pred. No. 9.7e+03;		
Matches	13;	Conservative	51;	Mismatches 11; Indels 0; Gaps 0;
QY	1	KASQVDYDGDSTYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60		
Db	1169	ESSSDDEKKEENNSKAEDRELMRFSHGGAALNTEKRPCEFCGAFSGQSEWEHVL 1228		
QY	61	XXXXXXXXXXQSNED 75		
Db	1229	HGMALNDTKQVSREE 1243		
RESULT	9			
O09004	PRELIMINARY; PRT; 260 AA.			
ID	O09004			
AC	O09004;			
DT	01-JUL-1997 (TREMBlrel. 04, Created)			
DT	01-JUL-1997 (TREMBlrel. 04, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	F2583.3 KINASE LIKE PROTEIN (FRAGMENT).			
GN	RASGRP2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98001089; PubMed=9341881;			
RA	Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,			
RA	Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;			
RT	"The germline centre kinase gene and a novel CDC25-like gene are			
RT	located in the vicinity of the PYGM gene on 11q13."			
RL	Hum. Genet. 100:611-619(1997).			
CC	-!- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.			
DR	EMBL; Y12339; CAA73008.1; -			
DR	HSSP; P28867; 1PTQ.			
DR	MGI; MGI:1333849; Rasgrp2.			
DR	InterPro; IPR002219; DAG_PE-bind.			
DR	InterPro; IPR002048; EF-hand.			
DR	Pfam; PF00130; DAG_PE-bind; 1.			
DR	Pfam; PF00036; ehand; 2.			
DR	PRINTS; PRO0008; DAGPEDOMAIN.			
DR	SMART; SM00109; Cl; 1.			
DR	PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.			
DR	PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_2.			
KW	Calcium-binding; Kinase.			
FT	NON_TER 1			
SQ	SEQUENCE 260 AA; 29259 MW; 3C0CC2B41F64A12A CRC64;			
Query Match	49.3%;	Score 101;	DB 11;	Length 260;
Best Local Similarity	12.9%;	Pred. No. 4.8e+02;		
Matches	9;	Conservative	55;	Mismatches 6; Indels 0; Gaps 0;
QY	4	QSVVDYDGSYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 63		
Db	88	RNFVDGDGHISQEEFIIRGNFPYLSAFGLDQDQGCISREEMISVFLRSSVILGRM 147		
QY	64	XXXXXXXXXXQSN 73		
Db	148	GFVHNFQESN 157		
RESULT	10			
O9PM23	PRELIMINARY; PRT; 408 AA.			
ID	O9PM23			
AC	O9PM23;			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)			
DE	HYPOTHETICAL PROTEIN CJ1306C.			

GN	CJ1306C.				
OS	Campylobacter jejuni.				
OC	Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;				
OC	Campylobacter.				
OX	NCBI_TaxID=197;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NCIC 11168;				
RA	MEDLINE=20150912; PubMed=10688204;				
RA	Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,				
RA	Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,				
RA	Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,				
RA	Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,				
RA	Whitehead S., Barrell B.G.;				
RT	"The genome sequence of the food-borne pathogen Campylobacter jejuni				
RT	reveals hypervariable sequences.";				
RL	Nature 403:665-668(2000).				
KW	EMBL; AL139078; CAB73733.1; -.				
KW	Hypothetical protein; Complete proteome.				
SQ	SEQUENCE 408 AA; 47256 MW; DD0D034E75EF7C22 CRC64;				
Query Match 49.3%; Score 101; DB 16; Length 408;					
Best Local Similarity 16.0%; Pred. No. 1.2e+03;					
Matches 12; Conservative 49; Mismatches 14; Indels 0; Gaps 0;					
QY	4	QSVYDGDYSNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 63			
Db	239	KSQKTDNGDMYMQGDHFFVSCFLKTHWTRKNSPYFFNNENYFIRTLNKLHLQSQKNK 298			
QY	64	XXXXXXXXXQGSNEDPRT 78			
Db	299	NIIVSYHSKEDPLT 313			
RESULT 11					
Q9FVQ1	ID	Q9FVQ1	PRELIMINARY;	PRT;	557 AA.
AC	Q9FVQ1;				
DT	01-MAR-2001 (TREMBlrel. 16, Created)				
DT	01-MAR-2001 (TREMBlrel. 16, Last sequence update)				
DT	01-JUN-2001 (TREMBlrel. 17, Last annotation update)				
DE	NUM1 PROTEIN, PUTATIVE.				
GN	F27K7.6.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
OX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. COLUMBIA;				
RA	Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,				
RA	Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,				
RA	Barstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;				
RT	"Arabidopsis thaliana chromosome 1 BAC F27K7 genomic sequence.";				
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AC084414; AAG29744.1; -.				
DR	InterPro; IPR000504; RRM.				
DR	Pfam; PF00076; rrm; 2.				
DR	SMART; SM00360; RRM; 2.				
DR	PROSITE; PS01002; RRM; 2.				
DR	PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.				
SQ	SEQUENCE 557 AA; 58773 MW; F6CAA737689B4CBA CRC64;				
Query Match 49.3%; Score 101; DB 10; Length 557;					
Best Local Similarity 17.3%; Pred. No. 2.4e+03;					
Matches 13; Conservative 50; Mismatches 12; Indels 0; Gaps 0;					
QY	1	KASQVDYDGSYNNXXXXXXXXXXXXXXXXXAAASNLESXXXXXXXXXXXXXXXXXXXXX 60			
Db	182	KDSSSSDDSDSEDEKPAKAAAPAAKAAASSSDSDSEDESEDEKPAKADTKA 241			

Query Match	49.3%;	Score 101;	DB 11;
Best Local Similarity	12.9%;	Pred. No. 2.9e+03;	Length 608;
Matches	9;	Conservative	55;
		Mismatches	6;
		Indels	0;
		Gaps	0;

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KW Calcium-binding; Phorbol-ester binding.
SQ SEQUENCE 609 AA; 69248 MW; 8B1321F864D24BC7 CRC64;

Query Match          49.3%; Score 101; DB 4; Length 609;
Best Local Similarity 12.9%; Pred. No. 2.9e+03;
Matches 9; Conservative 55; Mismatches 6; Indels 0; Gaps 0;

QY 4 QSVVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 63
Db 436 RNFVDVGDGHISQEEFQIIRGNFPYLSAFGLDQNDGICISREEMYSYFLRSSVVLGGRM 495
QY 64 XXXXXXQOQN 73
Db 496 GFVHNFQESN 505

RESULT 14
Q9UL65 PRELIMINARY; PRT; 671 AA.
AC Q9UL65;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE GUANINE EXCHANGE FACTOR MCG7 ISOFORM 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20493616; PubMed=10918068;
RA Clyde-Smith J., Sillins G., Gartside M., Grimmond S., Etheridge M.,
RA Apolloni A., Hayward N., Hancock J.F.;
RT "Characterization of RasGRP2, a Plasma Membrane-targeted, Dual
RT Specificity Ras/Rap Exchange Factor.";
RL J. Biol. Chem. 275:32260-32267(2000).
CC -/- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.
DR EMBL; AF043722; AAF07219.1; -.
DR HSP; P28867; 1PTQ.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000651; RasGEFN.
DR InterPro; IPR001895; RasGRF_CDC25.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00036; ehand; 2.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEFN; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_2.
KW Calcium-binding.
SQ SEQUENCE 671 AA; 75547 MW; 67B7BD2B4F4AED4D CRC64;

Query Match          49.3%; Score 101; DB 4; Length 671;
Best Local Similarity 12.9%; Pred. No. 3.5e+03;
Matches 9; Conservative 55; Mismatches 6; Indels 0; Gaps 0;

QY 4 QSVVDGDSYMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXXXXX 63
Db 498 RNFVDVGDGHISQEEFQIIRGNFPYLSAFGLDQNDGICISREEMYSYFLRSSVVLGGRM 557
QY 64 XXXXXXQOQN 73
Db 558 GFVHNFQESN 567

RESULT 15
Q9H1B6 PRELIMINARY; PRT; 827 AA.
ID Q9H1B6
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AC Q9H1B6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE XYLOSYLTRANSFERASE I (EC 2.4.2.26) (FRAGMENT).
GN XT-I.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20553456; PubMed=11099377;
RA Goetting C., Kuhn J., Zahn R., Brinkmann T., Kleesiek K.;
RT "Molecular cloning and expression of human UDP-D-xylose:proteoglycan
RT core protein beta-D-xylosyltransferase and its first isoform XT-II.";
RL J. Mol. Biol. 304:517-528(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Kuhn J., Goetting C., Schnoelzer M., Kempf T., Brinkmann T.,
RA Kleesiek K.;
RT "First isolation of human UDP-D-xylose:proteoglycan core protein
RT beta-D-xylosyltransferase secreted from cultured JAR choriocarcinoma
RT cells.";
RL J. Biol. Chem. 0:0-0(0).
DR EMBL; AJ277441; CAC16787.1; -.
KW Transferase; Glycosyltransferase.
FT NON_TER 1
SQ SEQUENCE 827 AA; 94490 MW; B4A96BE24F094CCF CRC64;

Query Match          49.3%; Score 101; DB 4; Length 827;
Best Local Similarity 17.3%; Pred. No. 5.5e+03;
Matches 13; Conservative 53; Mismatches 7; Indels 2; Gaps 1;

QY 1 KASQSVDDYDGS--YMNXXXXXXXXXXXXXXXXXAAASNLSEXXXXXXXXXXXXXXXXXXXX 58
Db 174 KANKNVQWDEDSVEYMPANPVRIFAFLVYVHGRASRLQRMFKAIYHKHFYIYHVDKRSN 233
QY 59 XXXXXXXXXXXXQOQN 73
Db 234 YLHRQVLQVSQYSN 248

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Job time: 682 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:34 ; Search time 230.21 Seconds
(without alignments)
114.832 Million cell updates/sec

Title: US-09-499-662-127
Perfect score: 1237
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Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1237	100.0	238	21	Humanised anti-Fas
2	1236	99.9	238	21	Humanised anti-Fas
3	1233	99.7	238	21	Humanised anti-Fas
4	1173	94.8	238	19	Anti-Fas humanised
5	1173	94.8	238	21	Humanised anti-Fas
6	1173	94.8	238	21	Humanised anti-Fas
7	1168	94.4	238	19	Humanised anti-Fas
8	1168	94.4	238	21	Humanised anti-Fas
9	1168	94.4	238	21	Humanised anti-Fas
10	1155	93.4	238	19	Anti-Fas humanised
11	1155	93.4	238	21	Humanised anti-Fas

12	1155	93.4	238	21	AAW90923	Humanised anti-Fas
13	1154	93.3	238	19	AAW83035	Anti-Fas humanised
14	1154	93.3	238	21	AAW83035	Humanised anti-Fas
15	1154	93.3	238	21	AAW83035	Humanised anti-Fas
16	1153	93.2	238	19	AAW90928	Humanised anti-Fas
17	1153	93.2	238	21	AAW83033	Humanised anti-Fas
18	1153	93.2	238	21	AAW83033	Humanised anti-Fas
19	1153	93.2	238	21	AAW83033	Humanised anti-Fas
20	1153	93.2	238	21	AAW83033	Humanised anti-Fas
21	1153	93.2	238	21	AAW83033	Humanised anti-Fas
22	1153	93.2	238	21	AAW83033	Humanised anti-Fas
23	1153	93.2	238	21	AAW83033	Humanised anti-Fas
24	1153	93.2	238	21	AAW83033	Humanised anti-Fas
25	1153	93.2	238	21	AAW83033	Humanised anti-Fas
26	1153	93.2	238	21	AAW83033	Humanised anti-Fas
27	1153	93.2	238	21	AAW83033	Humanised anti-Fas
28	1153	93.2	238	21	AAW83033	Humanised anti-Fas
29	1153	93.2	238	21	AAW83033	Humanised anti-Fas
30	1153	93.2	238	21	AAW83033	Humanised anti-Fas
31	1153	93.2	238	21	AAW83033	Humanised anti-Fas
32	1153	93.2	238	21	AAW83033	Humanised anti-Fas
33	1153	93.2	238	21	AAW83033	Humanised anti-Fas
34	1153	93.2	238	21	AAW83033	Humanised anti-Fas
35	1153	93.2	238	21	AAW83033	Humanised anti-Fas
36	1153	93.2	238	21	AAW83033	Humanised anti-Fas
37	1153	93.2	238	21	AAW83033	Humanised anti-Fas
38	1153	93.2	238	21	AAW83033	Humanised anti-Fas
39	1153	93.2	238	21	AAW83033	Humanised anti-Fas
40	1153	93.2	238	21	AAW83033	Humanised anti-Fas
41	1153	93.2	238	21	AAW83033	Humanised anti-Fas
42	1153	93.2	238	21	AAW83033	Humanised anti-Fas
43	1153	93.2	238	21	AAW83033	Humanised anti-Fas
44	1153	93.2	238	21	AAW83033	Humanised anti-Fas
45	1153	93.2	238	21	AAW83033	Humanised anti-Fas

ALIGNMENTS

RESULT 1

AAW90930
ID AAW90930 standard; Protein; 238 AA.

AC AAW90930;

DT 08-AUG-2000 (first entry)

DE Humanised anti-Fas designed light chain Leu 1 protein.

AAW90930
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

PN EP990663-A2.

PD 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AAL1631.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX Claim 3; Page 156-157; 263pp; English.
 PS This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 1
 CC which is described in the method of the invention.
 XX Sequence 238 AA;

Query Match 100.0%; Score 1237; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 6.7e-62;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYNNWY 60
 Db 1 metdtilwvllwvpgstgdivltqspsslsasvgdrtvitckasqsdvdygdsymwy 60
 QY 61 QOKPKGKAPLLIYAASNLSEGVPSRFGSGSGTDFLTITSLQPEDFATYQCQSNEDPR 120
 Db 61 qkpkgakplliyaasnlesgvpsrfgsgsgtdftltitsslqpedfatycqsgnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYFREAKVQMKVDNALQS 180
 Db 121 tfgggtkveikrtvaapsvfifppsdeqlksgtasvvcllnnfyfreakvqmkvdnalqs 180
 QY 181 GNSQSVTEQDSDSTYSLSSTLTLSKADYKHKYACEVTHOGLSSPTKSFNRGEC 238
 Db 181 gnsqsveqgdskdstyslsstltlskadyekhykkyacevthoglspsptksfnrgec 238

RESULT 2
 AAW90932
 ID AAW90932 standard; Protein: 238 AA.
 XX AAW90932;
 XX AAW90932;
 DT 08-AUG-2000 (first entry)
 XX Humanised anti-Fas designed light chain Leu 3 protein.

XX Fas: antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW hepatotropic; antiinfertility; neuroprotective; antirheumatic; antidiabetic;
 KW Hashimoto disease; apoptosis; systemic lupus erythematosus;
 KW Sjorgen's syndrome; rheumatoid arthritis; graft versus host disease;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 DR WPI: 2000-258930/23.
 DR N-PSDB; AAL1633.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX Claim 3; Page 161-162; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 3
 CC which is described in the method of the invention.
 XX Sequence 238 AA;

Query Match 99.9%; Score 1236; DB 21; Length 238;
 Best Local Similarity 99.6%; Pred. No. 7.6e-62;
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYNNWY 60

Db 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtltckasqsvdygdsgymwv 60
 Qy 61 QOKPGKAPKLLIYAASNLSESGVPSRFSGSGCTDFTLTISLQPDQDFATYYCOQSNEDPR 120
 Db 61 qkpgkpklliyaasnlsegsiprfsqsgsgtdftltisslqpedfatyycqsgnedpr 120
 Qy 121 TFGQGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180
 Db 121 tfgggtkeikrtvaapsvfippsdeqlksgtasvcllnffypreakvqwkvdnalqs 180
 Qy 181 GNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqdsksdystlsstltlskadyekhkyvacevthqglsspvtksfnrgec 238

RESULT 3
 ID AAW90931 standard; Protein: 238 AA.
 XX
 AC AAW90931;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed light chain Leu 2 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 FN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 XX
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI: 2000-258930/23.
 DR N-PSDB: AAA11632.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 PS Claim 2; Page 159; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 2
 CC which is described in the method of the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.7%; Score 1233; DB 21; Length 238;
 Best Local Similarity 99.6%; Pred. No. 1.1e-61;
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDTILLWLLWVPGSTGDIVLTQSPSSLSASVSGDRVTITCKASQSVDYDQDSIMNMY 60
 Db 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtitckasqsvdydgsymwv 60
 Qy 61 QOKPGKAPKLLIYAASNLSESGVPSRFSGSGCTDFTLTISLQPDQDFATYYCOQSNEDPR 120
 Db 61 qkpgkpklliyaasnlsegsiprfsqsgsgtdftltisslqpedfatyycqsgnedpr 120
 Qy 121 TFGQGTKEIKRTVAAPSVFIPPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180
 Db 121 tfgggtkeikrtvaapsvfippsdeqlksgtasvcllnffypreakvqwkvdnalqs 180
 Qy 181 GNSQSVTEQDSKDYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqdsksdystlsstltlskadyekhkyvacevthqglsspvtksfnrgec 238

RESULT 4
 AAW83034
 ID AAW83034 standard; Protein: 238 AA.
 XX
 AC AAW83034;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain PDHH type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease; sterility;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20 /label= Sig_peptide
 FT Protein 21..238 /label= Mat_protein
 FT Region 21..131 /label= Variable

Best Local Similarity 92.9%; Pred. No. 2.4e-58;
Matches 221; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYMMWY 60
Db 1 metdtillwvllwvpgstgeivltqspgtislsppgeratiscasqsdvdygdsymw 60

Qy 61 QOKPGKAPKLIYAAASNLSEGVPRFSGSGGTDTFTLTISLQPEDFATYYCQSQSNEPDR 120
Db 61 qkpgqapqlliyaaasnlsgipdrfsgsggtftltisrlepedfavyycqsgnedpr 120

Qy 121 TFGOGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
Db 121 tfgogtkleikrtvaapsvfippsdeqlksgtasvvcllnnfypreakvqkvdnalqs 180

Qy 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqsvteqdsksdstylstltlskadyekhkvyacevthqglsspvtksfngrec 238

RESULT 6
AAW90927
ID AAW90927 standard; Protein: 238 AA.

XX
AC AAW90927;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed light chain protein.

XX Kw Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX Kw anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
XX Kw dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX Kw nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
XX Kw hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Kw Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Kw Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Kw Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX Kw multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX Kw insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX Kw cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX OS Synthetic.

XX FN EP990663-A2.
XX PD 05-APR-2000.
XX PF 29-SEP-1999; 99EP-0307711.
XX PR 30-SEP-1998; 98JP-0276881.
XX PR 30-SEP-1998; 98JP-0276882.
XX PA (SANY) SANKYO CO LTD.
XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX DR WPI; 2000-258930/23.
XX DR N-PSDB; AAA11614.

XX PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX PT inflammatory or autoimmune disease, induces apoptosis selectively in
XX PT cells with abnormal Fas-Fas ligand systems -
XX PS Claim 3; Page 141-142; 263pp; English.

XX CC This invention describes a novel humanized anti-Fas antibody-like
XX CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX CC ligand system, by binding to Fas on the cell surface, and prevents
XX CC apoptosis in cells with a normal system, by inhibiting binding between
XX CC Fas and its ligand. The products of the invention have anti-inflammatory,
XX CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
XX CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
CC the method described in the invention.

XX SQ Sequence 238 AA;

Query Match 94.8%; Score 1173; DB 21; Length 238;
Best Local Similarity 92.9%; Pred. No. 2.4e-58;
Matches 221; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYMMWY 60
Db 1 metdtillwvllwvpgstgeivltqspgtislsppgeratiscasqsdvdygdsymw 60

Qy 61 QOKPGKAPKLIYAAASNLSEGVPRFSGSGGTDTFTLTISLQPEDFATYYCQSQSNEPDR 120
Db 61 qkpgqapqlliyaaasnlsgipdrfsgsggtftltisrlepedfavyycqsgnedpr 120

Qy 121 TFGOGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
Db 121 tfgogtkleikrtvaapsvfippsdeqlksgtasvvcllnnfypreakvqkvdnalqs 180

Qy 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqsvteqdsksdstylstltlskadyekhkvyacevthqglsspvtksfngrec 238

RESULT 7
AAW83031
ID AAW83031 standard; Protein: 238 AA.

XX
AC AAW83031;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas humanised antibody HFE7A light chain HH type.

XX Kw HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
XX Kw apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
XX Kw systemic lupus erythematosus; graft versus host disease;
XX Kw Sjogren syndrome; pernicious anaemia; Addison's disease;
XX Kw scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
XX Kw rheumatoid arthritis; autoimmune haemolytic anaemia;
XX Kw myasthenia gravis; multiple sclerosis; Basedow's disease;
XX Kw thrombopenia purpura; insulin-dependent diabetes; allergy;
XX Kw atopy; arteriosclerosis; myocarditis; cardiomyopathy;
XX Kw glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
XX Kw transplant rejection; therapy.

XX OS Homo sapiens.
XX OS Synthetic.

XX FH Key Location/Qualifiers
XX FT Peptide 1..20 /label= Sig_peptide
XX FT

FT	Protein	21..238	
FT	/label=	Mat_protein	
FT	Region	21..131	
FT	/label=	Variable	
FT	Region	132..238	
FT	/label=	Constant	
FT	Region	44..58	
FT	/label=	CDR_L1	
FT	/note=	"claim 9"	
FT	Region	74..80	
FT	/label=	CDR_L2	
FT	/note=	"claim 9"	
FT	Region	113..121	
FT	/label=	CDR_L3	
FT	/note=	"claim 9"	
PW	AU9859701-A.		
XX	08-OCT-1998.		
XX	30-MAR-1998;	98AU-0059701.	
XX	08-OCT-1997;	97JP-0276064.	
PR	01-APR-1997;	97JP-0082953.	
PR	25-JUN-1997;	97JP-0169088.	
XX	(SANY) SANKYO CO LTD.		
XX	Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;		
PI	Masahiko O, Nobufusa S, Shin Y, Tohru T;		
XX	WPI; 1998-543440/47.		
DR	N-PSDB; RAV7007A.		
XX	New antibodies and proteins bind conserved epitope of Fas antigen -		
PT	used to evaluate drugs in animal models and to treat Fas-associated		
PT	diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,		
PT	myocarditis, hepatitis and AIDS		
XX	Claim 21; Page 199-199; 292pp; English.		
XX	This is the amino acid sequence of the HH type humanised light		
CC	chain of murine anti-human Fas monoclonal antibody HFE7A.		
CC	Humanisation of the murine sequence (see AAW83042) entailed making		
CC	P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid		
CC	substitutions; these residues are conserved in the human light		
CC	chain (kappa chain). Host cell Escherichia coli PHSGHH7 SANK 73497		
CC	harbors plasmid PHSGHH7 carrying a fusion fragment of the humanised		
CC	HH type HFE7A light chain and DNA encoding the region of human		
CC	immunoglobulin kappa chain, and is deposited as FERM BP-6073		
CC	(claimed). The invention provides methods for producing humanised		
CC	antibodies by culturing host cells. Humanised versions of HFE7A		
CC	(see AAW83031-37), like native HFE7A, are capable of inducing		
CC	apoptosis in abnormal cells expressing Fas, and of inhibiting		
CC	Fas-induced apoptosis in normal cells. The humanised antibodies		
CC	are used to evaluate, in animal models, treatments of diseases that		
CC	involve Fas/Fas ligand interactions, and also to treat such		
CC	diseases, including autoimmune disease (e.g. systemic lupus		
CC	erythematosus, Hashimoto's disease, graft versus host disease,		
CC	Sjogren syndrome, pernicious anaemia, Addison's disease,		
CC	scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid		
CC	arthritis, autoimmune haemolytic anaemia, sterility, myasthenia		
CC	gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura		
CC	and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,		
CC	myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic		
CC	anaemia, hepatitis, AIDS and transplant rejection (all claimed).		
XX	Sequence 238 AA;		
SQ	Query Match 94.4%; Score 1168; DB 19; Length 238;		
	Best Local Similarity 92.4%; Pred. No. 4.6e-56;		
	Matches 220; Conservative 10; Mismatches 8; Indels 0; Gaps 0;		

Query Match 94.4%; Score 1168; DB 21; Length 238;
 Best Local Similarity 92.4%; Pred. No. 4.6e-58;
 Matches 220; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDVRTTTCRASQSVVDGDSYMNWY 60
 Db 1 metdtillwvllwvpgstgdivltqspsslsasvgdvrttcrasqsvvddgdsymnw 60

QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDFTLTISLQPEDFATYTCQSQSNEPR 120
 Db 61 qkpgqaprllyiaasnlsgvpsrfsgsgsgtdftltisllqpddfatytcqssnedpr 120

QY 121 TFGGCTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVWCLLNFPYPRKAVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfifpssdeqlksgtasvsvcllnfpypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSTLILSKADYKHKVYACEVTHQGLSSPVTXSFNRGEC 238
 Db 181 gnsqesvteqdsksstyslsstlilskadyekhkvayacevthqglsspvtksfnrgec 238

RESULT 9
 ID AAW90922 standard; Protein: 238 AA.
 XX AAW90922;
 AC AAW90922;
 DT 08-AUG-2000 (first entry)
 XX Humanised anti-Fas antibody HFE7A light chain HH type protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS EP990663-A2.
 XX EP990663-A2.
 PN 05-APR-2000.
 XX 05-APR-2000.
 PD 29-SEP-1999; 99EP-0307711.
 XX 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX 30-SEP-1998; 98JP-0276882.
 FA (SANY) SANKYO CO LTD.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 XX WPI: 2000-258930/23.
 DR N-PSDB: AAA11562.
 XX N-PSDB: AAA11562.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX cells with abnormal Fas-Fas ligand systems -
 PS Example reference 14; Page 114-115; 263pp; English.
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 CC the method described in the invention.

XX
 SQ Sequence 238 AA;

Query Match 94.4%; Score 1168; DB 21; Length 238;
 Best Local Similarity 92.4%; Pred. No. 4.6e-58;
 Matches 220; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDVRTTTCRASQSVVDGDSYMNWY 60
 Db 1 metdtillwvllwvpgstgdivltqspsslsasvgdvrttcrasqsvvddgdsymnw 60

QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDFTLTISLQPEDFATYTCQSQSNEPR 120
 Db 61 qkpgqaprllyiaasnlsgvpsrfsgsgsgtdftltisllqpddfatytcqssnedpr 120

QY 121 TFGGCTKVEIKRTVAAPSVFIFFPSDEQLKSGTASVWCLLNFPYPRKAVQKVDNALQS 180
 Db 121 tfggtrleikrtvaapsvfifpssdeqlksgtasvsvcllnfpypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSTLILSKADYKHKVYACEVTHQGLSSPVTXSFNRGEC 238
 Db 181 gnsqesvteqdsksstyslsstlilskadyekhkvayacevthqglsspvtksfnrgec 238

RESULT 10
 AAW83032 standard; Protein: 238 AA.
 ID AAW83032 standard; Protein: 238 AA.
 XX AAW83032;
 AC AAW83032;
 DT 15-MAR-1999 (first entry)
 XX 15-MAR-1999 (first entry)

XX Anti-Fas humanised antibody HFE7A light chain HM type.
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX Homo sapiens.
 OS Synthetic.
 OS Synthetic.

FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= Sig_peptide
FT 21..238
FT /label= Mat_protein
FT Region 21..131
FT /label= Variable
FT Region 132..238
FT /label= Constant
FT Region 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT Region 74..80
FT /label= CDR_L2
FT /note= "claim 9"
FT Region 113..121
FT /label= CDR_L3
FT /note= "claim 9"
PN AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI: 1998-543440/47.
DR N-PSDB; AA70075.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 200; 292pp; English.
XX
XX This is the amino acid sequence of the HM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AA83042) entailed making
CC P47A and K49R amino acid substitutions; these residues are
CC conserved in the human light (kappa) chain. Host cell E. coli
CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
CC fragment of the humanised HM type HFE7A light chain and DNA
CC encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6072 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AA83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX
XX Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 19; Length 238;
Best Local Similarity 91.6%; Pred. No. 2.4e-57;
Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTITCKASQSDYDGDSTNNWY 60
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 metdtillwvllwpgstgdivltqspgtlsipgderatlsckasgsdydgdssymwy 60
QY 61 QQPKGKAPKLLIYAASNLSESGVPSRFSGSGTGDTFTLTISLQPEDFANTYCCQSNEDPR 120
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 qqkpgqaprlllyaaasnlsegiipdrfsgsgsgtdfclthpveedaatyccqcsnedpr 120
QY 121 TFGQGTKEIKRTVAAPSFIFFPPSDEQLKSGTASVVCILNNFYPREAKYQWQVDNALQS 180
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
121 tfgggrtrieikrtvaapsvfifppsdeqiksgtasvvcilnnfnfpreakvqwkvdnalqs 180
QY 181 GNSQESVTEQDSKDSYSLSSLTLSKADYEHKHVYACEVTHQGLSSPYTKSFNRSEC 238
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
181 gnsqesvteqdkdstyslsstltlskadyekhkvacevthqglsspytksfnrsec 238
RESULT 11
AAB14773
ID AAB14773 standard; Protein; 238 AA.
XX
XX AAB14773;
XX
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody light chain, SEQ ID NO:52.
DE
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; light chain.
XX
XX Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI: 2000-485645/43.
DR N-PSDB; AAA72125.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
XX Claim 20; Page 80-81; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
CC of diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.
 XX Sequence 238 AA;
 SQ

Query Match 93.4%; Score 1155; DB 21; Length 238;
 Best Local Similarity 91.6%; Pred. No. 2.4e-57;
 Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVTTITCKASQSDVDGDSYMNWY 60
 Db 1 metdtillwllvpgstgdivltqspgtlslpgeratlsckasqsdvdgdsymnw 60

Qy 61 QQKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTFTLTISSLOPEDFATYTCQSNEDPR 120
 Db 61 qqkpgqaprllyiaasnlsgvpsrfgsgsgtdftltihpveeadaatyycqsgnedpr 120

Qy 121 TFGGCTKVEIKRTVAAPSVFFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 Db 121 tfgggtleikrtvaapsvffppsdqksgtasvvcllnnfypreakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 238
 Db 181 gnsqesvteqskdstyslsstltlskadyekhkvyacevthqglsspvtksfnregc 238

RESULT 12
 AAW90923
 ID AAW90923 standard; Protein: 238 AA.
 AC AAW90923;
 XX
 XX 08-AUG-2000 (first entry)
 XX Humanised anti-Fas antibody HFE7A light chain HM type protein.
 XX
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 XX Synthetic.
 OS
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-0307711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR
 XX 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 XX N-PSDB: AAA11563.
 DR
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 XX Example reference 14; Page 117-118; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiartherosclerotic, cardiac and hepatotropic activity. (I) induce
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 21; Length 238;
 Best Local Similarity 91.6%; Pred. No. 2.4e-57;
 Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVTTITCKASQSDVDGDSYMNWY 60
 Db 1 metdtillwllvpgstgdivltqspgtlslpgeratlsckasqsdvdgdsymnw 60

Qy 61 QQKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTFTLTISSLOPEDFATYTCQSNEDPR 120
 Db 61 qqkpgqaprllyiaasnlsgvpsrfgsgsgtdftltihpveeadaatyycqsgnedpr 120

Qy 121 TFGGCTKVEIKRTVAAPSVFFPPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180
 Db 121 tfgggtleikrtvaapsvffppsdqksgtasvvcllnnfypreakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNREGC 238
 Db 181 gnsqesvteqskdstyslsstltlskadyekhkvyacevthqglsspvtksfnregc 238

RESULT 13
 AAW83035
 ID AAW83035 standard; Protein: 238 AA.
 XX
 XX AAW83035;
 XX
 XX 15-MAR-1999 (first entry)
 DT
 XX Anti-Fas humanised antibody HFE7A light chain PDHM type.
 DE
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX

OS Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..20 /label= Sig_peptide
FT Protein 21..238 /label= Mat_protein
FT Region 21..131 /label= Variable
FT Region 132..238 /label= Constant
FT Region 44..58 /label= CDR_L1
FT FT /note= "claim 9"
FT Region 74..80 /label= CDR_L2
FT FT /note= "claim 9"
FT Region 113..121 /label= CDR_L3
FT FT /note= "claim 9"
XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI: 1998-543440/47.
XX N-PSDB; AAV70078.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 220-221; 292pp; English.
XX
XX This is the amino acid sequence of the PDHM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A.
XX Humanisation of the murine sequence (see AAW83042) entailed making
XX DIE, P47A, K49R and R107K amino acid substitutions; these
XX residues are conserved in the human light (kappa) chain. Host
XX cell Escherichia coli PHSM2 SANK 70198 harbors plasmid PHSM2
XX carrying a fusion of the humanised PDHM type HFE7A light chain and
XX DNA encoding the region of human immunoglobulin kappa chain, and is
XX deposited as FERM BP-6272 (claimed). The invention provides
XX methods for producing humanised antibodies by culturing host
XX cells. Humanised versions of HFE7A (see AAW83031-37), like native
XX HFE7A, are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. The humanised antibodies are used to evaluate, in animal
XX models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).

SQ Sequence 238 AA;
Query Match 93.3%; Score 1154; DB 19; Length 238;
Best Local Similarity 91.6%; Pred. No. 2.7e-57;
Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWLLIWPVGSTGDIVLTQSPSSLSASVGDRTVITTCASQSDYDGDGSDYNNWY 60
|||||
DB 1 metdtillwlllwpvgstgeivltqspgtlspsgeratlsckaasgvdgdsgymwy 60
|||||
QY 61 QQKPGKAPKLLIYAASNLESGVPSRFGSGSGTDFLTITSSLOPEDFATYYCQSQSNEDEPR 120
|||||
DB 61 gqkpggaprlliyaaenlesgipdrfsgsgsgtdfltihpveeadaatyycqsgsnepr 120
|||||
QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
|||||
DB 121 tfgggtkleikrtvaapsvfifppsdeqiksgtasvvcllnnfyfreakvqwkvdnalqs 180
|||||
QY 181 GNSQESVTEQDSKDSSTYSLSSTLTLSKADYERHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||||
DB 181 gnsqesvteqdsksdstyslsstltliskadyekkhvyacevthqglsspvtksfnrgec 238
|||||
RESULT 14
AAAB14778
ID AAB14778 standard; Protein; 238 AA.
XX
XX AAB14778;
XX
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody light chain, SEQ ID NO:109.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX hepatitis; AIDS; graft rejection; light chain.
XX
XX Chimeric - Mus musculus.
XX Chimeric - Homo sapiens.
XX
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI: 2000-485645/43.
XX N-PSDB; AAA72177.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX
XX Claim 20; Page 103; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
XX antibodies.
SQ Sequence 238 AA;

Query Match 93.3%; Score 1154; DB 21; Length 238;
Best Local Similarity 91.6%; Pred. No. 2.7e-57;
Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwllwpgstgeivltqspgtlslspgeratlsckasqsdvdygdsymnw 60
QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSNEDPR 120
Db 61 qqkpgqprlliyaasnlsgipdrfsgsgtdftltihpveedaatyycqgsnedpr 120
QY 121 TFGOGTKVEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFNFPREAKYQWKVDNALQS 180
Db 121 tfgggtkleikrtvaapsvfiffpsdeqlksgtasvcllnfnfpreakvqkvkvdnalqs 180
QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdstyslslstltlskadyekkhkvyacevthqglsspvtksfnrgec 238

RESULT 15
AAW90928
ID AAW90928 standard; Protein; 238 AA.
AC AAW90928;
XX XX
DT 08-AUG-2000 (first entry)
XX XX
DE Humanised HFE7A designed light chain protein #2.
XX XX

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; sterility;
KW Goodpasture syndrome; Crohn's disease; scleroderma; sterility;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX Synthetic.

XX EP990663-A2.
XX XX
XX 05-APR-2000.
XX XX
XX 29-SEP-1999; 99EP-0307711.
XX XX
XX 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX XX
XX (SANY) SANKYO CO LTD.
XX XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX N-PSDB; AAA11615.
XX XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems

PS

XX

CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, Goodpasture syndrome, Crohn's
CC anemia, Addison's disease, scleroderma, thrombopenia purpura, allergy,
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
XX the method described in the invention.

SQ Sequence 238 AA;

Query Match 93.3%; Score 1154; DB 21; Length 238;
Best Local Similarity 91.6%; Pred. No. 2.7e-57;
Matches 218; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 METDTILLWLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwllwpgstgeivltqspgtlslspgeratlsckasqsdvdygdsymnw 60
QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSNEDPR 120
Db 61 qqkpgqprlliyaasnlsgipdrfsgsgtdftltihpveedaatyycqgsnedpr 120
QY 121 TFGOGTKVEIKRTVAAPSVFIFFPSDQLKSGTASVCLLNFNFPREAKYQWKVDNALQS 180
Db 121 tfgggtkleikrtvaapsvfiffpsdeqlksgtasvcllnfnfpreakvqkvkvdnalqs 180
QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdstyslslstltlskadyekkhkvyacevthqglsspvtksfnrgec 238

Search completed: August 14, 2002, 15:15:34
Job time: 832 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:03 ; Search time 82.88 Seconds
(without alignments)
70.141 Million cell updates/sec

Title: US-09-499-662-127
Perfect score: 1237
Sequence: 1 MTDRIILLWLLVWPGSTG.....EVTHOGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1112	89.9	218	5	PCT-US96-13152-2
2	1100	88.9	218	2	US-08-887-352B-13
3	1100	88.9	218	3	US-08-466-151-9
4	1100	88.9	218	4	US-09-109-207C-13
5	1100	88.9	218	4	US-09-296-005-13
6	1100	88.9	218	4	US-08-466-163B-9
7	1077	87.1	218	4	US-09-282-505-1
8	1077	87.1	218	4	US-09-054-255-1
9	1074	86.8	218	2	US-08-887-352B-15
10	1074	86.8	218	2	US-08-887-352B-17
11	1074	86.8	218	2	US-08-887-352B-19
12	1074	86.8	218	2	US-08-887-352B-24
13	1074	86.8	218	4	US-09-109-207C-15
14	1074	86.8	218	4	US-09-109-207C-17
15	1074	86.8	218	4	US-09-109-207C-19
16	1074	86.8	218	4	US-09-109-207C-24
17	1074	86.8	218	4	US-09-296-005-15
18	1074	86.8	218	4	US-09-296-005-17
19	1074	86.8	218	4	US-09-296-005-19
20	1074	86.8	218	4	US-09-296-005-24
21	1022.5	82.7	233	2	US-07-934-373C-25
22	1022.5	82.7	233	3	US-08-437-642B-25
23	1022.5	82.7	233	5	PCT-US93-07832-25
24	1019	82.4	214	2	US-07-934-373C-39
25	1019	82.4	214	3	US-08-437-642B-39
26	1019	82.4	214	5	PCT-US93-07832-39
27	1014	82.0	214	2	US-07-934-373C-40

Sequence 11, Appl
Sequence 40, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 40, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 2, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 97, Appl
Sequence 51, Appl
Sequence 51, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 56, Appl

28 1014 82.0 214 2 US-08-788-800-11
29 1014 82.0 214 3 US-08-437-642B-40
30 1014 82.0 214 3 US-09-097-309-2
31 1014 82.0 214 4 US-09-097-171A-2
32 1014 82.0 214 5 PCT-US93-07832-40
33 1014 82.0 237 3 US-09-097-309-6
34 1014 82.0 237 4 US-09-097-171A-10
35 1014 82.0 237 4 US-09-422-712B-2
36 1014 82.0 237 4 US-09-607-756-2
37 1010.5 81.7 242 3 US-09-027-449-62
38 1010.5 81.7 242 4 US-09-026-985-62
39 1009.5 81.6 235 4 US-09-171-945-97
40 1009.5 81.6 242 3 US-09-027-449-51
41 1009.5 81.6 242 3 US-08-804-444A-51
42 1009.5 81.6 242 4 US-09-026-985-51
43 1006.5 81.4 219 3 US-09-027-449-72
44 1006.5 81.4 219 4 US-09-026-985-72
45 1006.5 81.4 242 3 US-09-027-449-56

ALIGNMENTS

RESULT 1
PCT-US96-13152-2
; Sequence 2, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 638-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 89.9%; Score 1112; DB 5; Length 218;
Best Local Similarity 98.2%; Pred. No. 1.6e-87;

Qy 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4

US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 88.9%; Score 1100; DB 4; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.7e-86;
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASYLE 60
Qy 81 GVPFRFSGSGSGTDFTLTISSLQPEDFAFYTCQQSHEDPYTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFAFYTCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 88.9%; Score 1100; DB 4; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.7e-86;
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASYLE 60
Qy 81 GVPFRFSGSGSGTDFTLTISSLQPEDFAFYTCQQSHEDPYTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFAFYTCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-08-466-163B-9
; Sequence 9, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1d1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1, light chain
US-08-466-163B-9

Query Match 88.9%; Score 1100; DB 4; Length 218;
Best Local Similarity 97.7%; Pred. No. 1.7e-86;
Matches 213; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSDYDGDSDYMMWYQKPGKAPKLLIYAASYLE 60
Qy 81 GVPFRFSGSGSGTDFTLTISSLQPEDFAFYTCQQSHEDPYTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSGTDFTLTISSLQPEDFAFYTCQQSHEDPYTFGQGTKEIKRTVAAPSVF 120
Qy 141 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
Qy 201 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLKADYKHKYKYYACEVTHQGLSSPVTKSFNRGEC 218

Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 7
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Eschoe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match 87.1%; Score 1077; DB 4; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.6e-84;
Matches 209; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYNNWYQKPGKAPKLLIYAASVLS 80
|||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYNNWYQKPGKAPKLLIYAASVLS 60
QY 81 GVPFRSGSGSGDTFTLTISLQPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 140
|||
Db 61 GVPFRSGSGSGDTFTLTISLQPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 8
US-09-054-255-1
; Sequence 1, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Eschoe Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match 87.1%; Score 1077; DB 4; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.6e-84;
Matches 209; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYNNWYQKPGKAPKLLIYAASVLS 80
|||

Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYNNWYQKPGKAPKLLIYAASVLS 60
QY 81 GVPFRSGSGSGDTFTLTISLQPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 140
|||
Db 61 GVPFRSGSGSGDTFTLTISLQPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||
Db 181 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 9
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match 86.8%; Score 1074; DB 2; Length 218;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYNNWYQKPGKAPKLLIYAASVLS 80
|||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYNNWYQKPGKAPKLLIYAASVLS 60
QY 81 GVPFRSGSGSGDTFTLTISLQPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 140
|||
Db 61 GVPFRSGSGSGDTFTLTISLQPEDFATYCCQSNEDPRTFGQGTVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNFPYQKQVQKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTSLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match 86.8%; Score 1074; DB 2; Length 218;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSNEDPRFTGQGTKEIKRTVAAPSVF 140
DB 61 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180

QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 13
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15

Query Match 86.8%; Score 1074; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSNEDPRFTGQGTKEIKRTVAAPSVF 140

DB 61 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 14
US-09-109-207C-17
; Sequence 17, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17

Query Match 86.8%; Score 1074; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80
DB 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSNEDPRFTGQGTKEIKRTVAAPSVF 140
DB 61 GVPFRFSGSGSGTDFTLTITSSLPQEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
DB 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
QY 201 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 238
DB 181 STLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 15
US-09-109-207C-19
; Sequence 19, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

Query Match      86.8%; Score 1074; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 2.8e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVTITCKASQSVYDGDSDYNNWYQKPKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGRVTITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60

Qy 81 GVPFRFGSGSGTDFTLTISSLQPEDFATYYCQGSNEDPRFTGGGTKEIKRTVAAPSVF 140
Db 61 GVPFRFGSGSGTDFTLTISSLQPEDFATYYCQGSNEDPRFTGGGTKEIKRTVAAPSVF 120

Qy 141 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180

Qy 201 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
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(without alignments)
210.505 Million cell updates/sec

Title: US-09-499-662-127
Perfect score: 1237
Sequence: 1 METDRIILLWVLLLMVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945.5	76.4	215	2 JE0242	Ig kappa chain NIG
2	926.5	74.9	215	2 JE0244	Ig kappa chain NIG
3	903.5	73.0	215	2 JE0243	Ig kappa chain NIG
4	885.5	71.6	215	2 A23746	Ig kappa chain V-I
5	877	70.9	216	2 JE0241	Ig kappa chain Am3
6	809	65.4	240	2 S06084	Ig kappa chain pre
7	756	61.1	234	2 S14237	Ig kappa chain pre
8	749	60.5	218	2 S68241	Ig kappa chain V r
9	748.5	60.5	230	2 S33161	Ig kappa chain - s
10	747	60.4	218	2 JC5810	monoclonal antibod
11	729	58.9	234	2 S01320	Ig kappa chain pre
12	726	58.7	220	2 A31790	Ig kappa chain V r
13	718	58.0	210	2 A56169	Ig kappa chain V r
14	716.5	57.9	225	2 S37484	Ig kappa chain - m
15	709.5	57.4	219	2 PC4203	Ig kappa chain (mo
16	706.5	57.1	219	2 S38865	Ig kappa chain - m
17	706.5	57.1	235	2 S25058	Ig kappa chain - m
18	703.5	56.9	219	2 S52028	Ig kappa chain - m
19	697	56.3	214	2 S68212	Ig kappa chain (Ma
20	693.5	56.1	217	2 S42772	Ig kappa chain V r
21	687.5	55.6	219	2 S16112	Ig kappa chain V r
22	676.5	54.7	225	2 JL0029	Ig kappa chain pre
23	613.5	49.6	229	2 A20969	Ig kappa chain pre
24	608.5	49.2	135	2 S52059	JC-kappa protein -
25	608	49.2	178	2 PT0219	Ig kappa chain V-C
26	582.5	47.1	197	2 S29593	Ig kappa chain (WM
27	579	46.8	131	2 PH1226	Ig kappa chain pre
28	568.5	46.0	238	2 A49633	Ig lambda-like cha
29	548	44.3	106	1 K3HU	Ig kappa chain C r

30	547	44.2	144	2 PL0106	Ig kappa chain pre
31	532	43.0	131	1 KVMSM6	Ig kappa chain pre
32	522	42.2	123	2 S40331	Ig kappa chain - h
33	521	42.1	127	2 S40367	Ig kappa chain V-J
34	520	42.0	233	2 S29577	Ig light chain - r
35	519	42.0	132	1 KVMS32	Ig kappa chain pre
36	518	41.9	141	2 A49134	Ig kappa chain V-I
37	513	41.5	99	2 A37927	Ig kappa chain C r
38	511	41.3	139	2 S40365	Ig kappa chain - h
39	507	41.0	99	2 S26653	Ig kappa chain C r
40	505.5	40.9	145	2 S20631	Ig kappa chain - h
41	504	40.7	122	2 S40370	Ig kappa chain - h
42	504	40.7	140	2 PN0446	Ig kappa chain pre
43	503	40.7	132	2 S40334	Ig kappa chain - h
44	499	40.3	131	2 S55027	Ig light chain pre
45	499	40.3	131	2 S40352	Ig kappa chain V-J

ALIGNMENTS

RESULT 1
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region: immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 76.4% ; Score 945.5 ; DB 2 ; Length 215 ;
Best Local Similarity 83.5% ; Pred. No. 1.2e-54 ;
Matches 182 ; Conservative 15 ; Mismatches 18 ; Indels 3 ; Gaps 1 ;

Qy	21	DIVLTQSPSSLSASVGDRVTITCRASQSDYDGDSDYMMWYQKPKGKAPKLLIYASNL	80
Db	1	EIVLTQSPGTLISLSPGERATLSCRASQSV---SNNLAWYQKPKGAPSLIYDASSRAT	57
Qy	81	GVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF	140
Db	58	GIPDRFSGSGSGTDFTLTISSLQPEDFAVYCCQYDRPPTFGQGTKEIKRTVAAPSVF	117
Qy	141	IFPPSDEQLKSGTASVGVCLLNNFYPRKAVQWKNVDNALQSGNSQESVTEQDSKDSYSL	200
Db	118	IFPPSDEQLKSGTASVGVCLLNNFYPRKAVQWKNVDNALQSGNSQESVTEQDSKDSYSL	177
Qy	201	STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC	238
Db	178	STLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC	215

RESULT 2
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H. submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

R;Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA

A;Reference number: S06084; MUID:90016888

A;Accession: S06084

A;Molecule type: mRNA

A;Residues: 1-240 <CRO>

A;Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-240/Product: Ig kappa chain #status predicted <MAT>

F;153-222/Domain: immunoglobulin homology <IMM>

Query Match 65.4%; Score 809; DB 2; Length 240;
Best Local Similarity 64.6%; Pred. No. 9.8e-46;
Matches 155; Conservative 31; Mismatches 52; Indels 2; Gaps 1;

Qy 1 METDTILLVLLVPGSTGDIVLTQSPSSLSASVGRVTTTCRASQSDVDYGD--SYMN 58

Db 1 MESQTQVMSLLISGTCGDFVMTQSPSSSLAVSAGETVTTNCKSSOSLFYSGNKNVLA 60

Qy 59 WYQKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTFTLTISLQPEDFATYYCQSNED 118

Db 61 WYQKPGSPKLLIYWASTRGSGVDPDRFISGSGTDTFTLTISVQAEALAIYICLQYVET 120

Qy 119 PRTEGQGTKEIKRTVAAPSFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNAL 178

Db 121 PYTFGAGTKLEKLRADAAPTIVSIFPPSTEQLATGASVVCMLNNFYPRDISVKKKIDGTE 180

Qy 179 QSGNSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 RDGVLDSVTDDQSKSTYSMSSTLSLSKADYSHNLYTCEVHKTSSTSSPVVKSFNRNEC 240

RESULT 7

S14237

Ig kappa chain precursor (15C5) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

A;Accession: S14237

R;Vandamme, A.M.; Bultens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.

Eur. J. Biochem. 192, 767-775, 1990

A;Title: Construction and characterization of a recombinant murine monoclonal antibody c

A;Reference number: S14236; MUID:91006173

A;Accession: S14237

A;Molecule type: mRNA

A;Residues: 1-234 <VNA>

A;Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

Query Match 61.1%; Score 756; DB 2; Length 234;
Best Local Similarity 60.5%; Pred. No. 2.6e-42;
Matches 144; Conservative 34; Mismatches 56; Indels 4; Gaps 1;

Qy 1 METDTILLVLLVPGSTGDIVLTQSPSSLSASVGRVTTTCRASQSDVDYGDSDYNNWY 60

Db 1 MRTPAQFLGILLVPPGKIDKRTQSPSSMYASLGERVTVTCRASQDI----NSYLSWI 56

Qy 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDTFTLTISLQPEDFATYYCQSNEDPR 120

Db 57 QOKPGKSPKLLIYKGNRLVAGVPSRFGSGSGGQDYSLTISLSEVEDGVYICLRIDFPP 116

Qy 121 TFGQGTKEIKRTVAAPSFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQS 180

Db 117 TFGSGTKLEIKRADAAPTIVSIFPPSSQLATSGGASVVCFLNNFYPKDINVKWKIDGSE 176

Qy 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 177 NGVLNSWTDQDSKSTYSMSSTLTLTDKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234

RESULT 8

S68241

Ig kappa chain V region (Mab13-1) - mouse (fragment)

N;Alternate names: immunoglobulin light chain

C;Species: Mus musculus (house mouse)

C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C;Accession: S68241; S68214

R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,

submitted to the EMBL Data Library, March 1994

A;Description: Specific peroxidase activity by formation of an antibody L-chain-porpha

A;Reference number: S68241

A;Accession: S68241

A;Molecule type: mRNA

A;Residues: 1-218 <TAK>

A;Cross-references: EMBL:D29670; NID:g473962; PIDN:BA06141.1; PID:g473963

R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka,

FEBS Lett. 375, 273-276, 1995

A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphy

A;Reference number: S68211; MUID:96085223

A;Accession: S68214

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 'N1',3-212 <TAM>

A;Cross-references: EMBL:D29670

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: immunoglobulin

Query Match 60.5%; Score 749; DB 2; Length 218;

Best Local Similarity 64.2%; Pred. No. 6.9e-42;

Matches 140; Conservative 31; Mismatches 47; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVTTTCRASQSDVDYGDSDYNNWYQOKPGKAPKLLIYAASNL 80

Db 1 ELVLTQSPASLAVSLGORATISCRASKSVASGYIYHMYQOKPGQPKLLISLATNL 60

Qy 81 GVPFRFGSGSGTDTFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPS 140

Db 61 GVPARFGSGSGTDTFTLTINHPVEEDVATYYCQHSRELPLTFGAGTKLELRADAAPT 120

Qy 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSNQSVTEQDSKSTYSLS 200

Db 121 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSENGVLNSWTDQDSKSTYSMS 180

Qy 201 STLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 STLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 218

RESULT 9

S33161

Ig kappa chain - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C;Accession: S33161

R;Foley, R.C.; Beh, K.J.

submitted to the EMBL Data Library, July 1990

A;Description: Isolation and characterisation of sheep kappa light chain cDNA.

A;Reference number: S33161

A;Accession: S33161

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-230 <FOL>

A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CAA38046.1; PID:g1364221

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;143-212/Domain: immunoglobulin homology <IMM>

Query Match

60.5%; Score 748.5; DB 2; Length 230;

Best Local Similarity 62.2%; Pred. No. 7.9e-42;
Matches 145; Conservative 36; Mismatches 47; Indels 5; Gaps 2;

QY 7 LLVLLVLL-VPGSTGDIVLTQSPSSLSASVGRVITTCASQSYVDYDGSYMNWYQKQPG 65
Db 2 LIGLLLLVLPAGARCDIQVTSQPSLSASLTERVSTCTRTSOSV-----SNLYNWYQKQPG 57

QY 66 KAPKLLIYAASNLSEGVSRFSGSGSGTDTLTITISLQPEDFATYYCQSQNSDPRTFGGG 125
Db 58 QAPKLLIYATRLHTDVPFRFSGSGSGTDYTLTISNLEANDATYYCLOYESTPLAFGGG 117

QY 126 TVTEIKRTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQE 185
Db 118 TNVEIKRSDAQPVSFLKPESEQLRTGTVVVCLVNDVFPKDVNVKVGDTQNSNFQN 177

QY 186 SVTEQDSKDSYSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238
Db 178 SFTQDSKRSKSYSLSTLTLSSEYQSHNAYACEVSHKSLPTALVKSFNRNEC 230

RESULT 10
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 60.4%; Score 747; DB 2; Length 218;
Best Local Similarity 64.7%; Pred. No. 9.3e-42;
Matches 141; Conservative 29; Mismatches 48; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITTCASQSYVDYDGSYMNWYQKQPGKAPKLLIYAASNLSE 80
Db 1 NIVLTQSPASLASVLSQGRATISCRASKSVASGYIYMHYQKQPGPPKLLISLASNLSE 60

QY 81 GYPSRFSGSGGTDTFTLTISLQPEDFATYYCQSQNSDPRTFGGGTVKVEIKRTVAAPSVF 140
Db 61 GVPARFSGSGGTDTFTLTHPVEEDVATYYCQHSRELPLTFGAGTKLEKLRADRAPTVS 120

QY 141 IFPPDDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTPQDSKDSYSL 200
Db 121 IFPPSSEQLTSGGASVVCFLNNFYPRKDVNKKIDGSRQNGVLSWTQDSKDSYSL 180

QY 201 STLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTTLTKDEYERHNSYTCETHKTSTSPIVKSFNRNEC 218

RESULT 11
S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
A:Reference number: S01320; MUID:88329081
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234
A:Cross-References: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785

A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 729; DB 2; Length 234;
Best Local Similarity 58.3%; Pred. No. 1.5e-40;
Matches 140; Conservative 37; Mismatches 55; Indels 8; Gaps 2;

QY 1 METDTILLVLLVLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSYVDYDGSYMN-- 58
Db 1 MSVPTQVLGLLLLTARCDIQMTQSPASLSVSGESVITTCRASENI-----YSNLA 54

QY 59 WYQKRPKAPKLLIYAASNLSEGVSRFSGSGSGTDTLTITISLQPEDFATYYCQSQNSD 118
Db 55 WYQKQKQKSPQLLVYVATKLVDPVSRFSGSGSGTGYSLKINSLOQSEDFGYYCQHFWD 114

QY 119 PRTEGGTQKVEIKRTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQKVDNAL 178
Db 115 PTFGSGTKLEMKRADAPTIVFIFFPSSEQLTSGGASVVCFLNNFYPRKDVNKKIDGSE 174

QY 179 QSGNSQESVTEQDSKDSYSLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 175 RQGVLSNWTQDSKDSYSLSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 234

RESULT 12
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-References: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.7%; Score 726; DB 2; Length 220;
Best Local Similarity 61.8%; Pred. No. 2.2e-40;
Matches 136; Conservative 33; Mismatches 49; Indels 2; Gaps 1;

QY 21 DIVLTQSPSSLSASVGRVITTCASQSYVDYDGC--DSYMNWYQKQKAPKLLIYAASNL 78
Db 1 DIVMTQSPSSLVITAGEKVTMSCTSSQSLFNSGKQKNLYLTWYQKQPGPKVLIYASIR 60

QY 79 ESGVPSRFSGSGSGTDTLTITISLQPEDFATYYCQSQNSDPRTFGGGTVKVEIKRTVAAP 138
Db 61 ESGVDPDRFTGSGSGTDTLTITISSVQAEADLVAVYCYNDYNSPLTFGGGTLEKLRADAAPT 120

QY 139 VFIFPPDDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 198
Db 121 VSIFPPSSEQLTSGGASVVCFLNNFYPRKDVNKKIDGSRQNGVLSWTQDSKDSYSL 180

QY 199 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 MSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNRNEC 220

RESULT 13
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)

Db 178 DSKDSTYSMSSTLTTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 225

Job time: 686 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:12 ; Search time 53.64 Seconds
(without alignments)
171.798 Million cell updates/sec

Title: US-09-499-662-127

Perfect score: 1237

Sequence: 1 METDTILLWLLWVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:

BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	548	44.3	106	1 KAC_HUMAN
2	532	43.0	131	1 KV3I_MOUSE
3	519	42.0	132	1 KV3F_MOUSE
4	483	39.0	111	1 KV3M_MOUSE
5	481	38.9	111	1 KV3N_MOUSE
6	480	38.8	129	1 KV1W_HUMAN
7	479	38.7	111	1 KV3O_MOUSE
8	478.5	38.7	129	1 KV3L_HUMAN
9	476	38.5	111	1 KV3Q_MOUSE
10	468	37.8	111	1 KV3L_MOUSE
11	461	37.3	108	1 KV1H_HUMAN
12	458.5	37.1	110	1 KV3P_MOUSE
13	456.5	36.9	129	1 KV3M_HUMAN
14	452	36.5	108	1 KV1G_HUMAN
15	449	36.3	108	1 KV1M_HUMAN
16	448	36.2	108	1 KV1K_HUMAN
17	448	36.2	134	1 KV4C_HUMAN
18	446	36.1	108	1 KV1B_HUMAN
19	445	36.0	108	1 KV1E_HUMAN
20	445	36.0	108	1 KV1F_HUMAN
21	445	36.0	108	1 KV1N_HUMAN
22	442	35.7	108	1 KV1V_HUMAN
23	441	35.7	108	1 KV1A_HUMAN
24	441	35.7	117	1 KV1J_HUMAN
25	436	35.2	111	1 KV3H_MOUSE
26	435	35.2	108	1 KV1O_HUMAN
27	434	35.1	108	1 KV1P_HUMAN
28	432.5	35.0	133	1 KV4B_HUMAN
29	431.5	34.9	129	1 KV3H_HUMAN
30	430	34.8	108	1 KV1Y_HUMAN
31	429	34.7	108	1 KV1R_HUMAN
32	429	34.7	108	1 KV1S_HUMAN
33	429	34.7	129	1 KV1X_HUMAN

34	427	34.5	111	1	KV3J_MOUSE	P01662	mus musculus
35	426	34.4	111	1	KV3K_MOUSE	P01663	mus musculus
36	425.5	34.4	109	1	KV1T_HUMAN	P01612	homo sapien
37	425	34.4	128	1	KV3K_HUMAN	P06311	homo sapien
38	422	34.1	108	1	KV1L_HUMAN	P01604	homo sapien
39	422	34.1	111	1	KV3R_MOUSE	P01670	mus musculus
40	420	34.0	108	1	KV1Q_HUMAN	P01609	homo sapien
41	419.5	33.9	107	1	KV1D_HUMAN	P01596	homo sapien
42	419	33.9	117	1	KV1I_HUMAN	P01601	homo sapien
43	416.5	33.7	133	1	KV2F_HUMAN	P06310	homo sapien
44	416	33.6	115	1	KV3I_HUMAN	P04433	homo sapien
45	415	33.5	128	1	KV5E_MOUSE	P01637	mus musculus

ALIGNMENTS

RESULT	1
KAC_HUMAN	
ID	KAC_HUMAN
AC	P01834;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Ig kappa chain C region.
GN	IGKC.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE (MYELOMA PROTEIN EU).
RX	MEDLINE=71064023; PubMed=5489770;
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
RL	Biochemistry 9:3155-3161(1970).
RN	[2]
RP	DISULFIDE BONDS.
RX	MEDLINE=71064027; PubMed=4923144;
RA	Gall W.E., Edelman G.M.;
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";
RL	Biochemistry 9:3188-3196(1970).
RN	[3]
RP	SEQUENCE (BENCE-JONES PROTEIN TI).
RX	MEDLINE=72188439; PubMed=5027703;
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=81042304; PubMed=6775818;
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";
RL	Cell 22:197-207(1980).
RN	[5]
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;
RL	(In) Franek F., Shugar D. (eds.);
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).
RN	[6]
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).
RX	MEDLINE=68242259; PubMed=5586923;
RA	Hilschmann N.;
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

```
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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CC -----
DR EMBL: J00241; AAA58989.1; -.
DR EMBL: V00557; CAA23823.1; -.
DR PIR: A02116; K3HU.
DR HSP: P01842; 7FAB.
DR MIM: 147200; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_C1.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 26 86
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTID-VAR_003897.
FT CONFLICT 14 14
FT CONFLICT D -> N (IN REF. 7 AND 8).
FT CONFLICT E -> O (IN REF. 5 AND 6).
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 44.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 133 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRAKWKQVDNALQSGNSQESVTEQDS 192
DB 1 TVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPRAKWKQVDNALQSGNSQESVTEQDS 60
QY 193 KDSYLSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
DB 61 KDSYLSLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106
RESULT 2
KV3I_MOUSE
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
```

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RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: Implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79019520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: A01935; KVM5M6.
DR HSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 73 FRAMEWORK-2.
FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 81 112 FRAMEWORK-3.
FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 131 FRAMEWORK-4.
FT DISULFID 43 112 BY SIMILARITY.
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 43.0%; Score 532; DB 1; Length 131;
Best Local Similarity 75.6%; Pred. No. 4.6e-36;
Matches 99; Conservative 18; Mismatches 14; Indels 0; Gaps 0;
QY 1 METDTLLWVLLWVPGSTGDIVLITQSPSSLSASVGDRTVITCKASQSYDYDGDSTMMNY 60
DB 1 METDTLLWVLLWVPGSTGDIVLITQSPSSLSASVGDRTVITCKASQSYDYDGDSTMMNY 60
QY 61 QOKPKAKPLLIYKASNLSESGSGSGTDFLTITSLQPEDFATYYCQSNEDPR 120
DB 61 QOKPKAKPLLIYKASNLSESGSGSGTDFLTITSLQPEDFATYYCQSNEDPR 120
QY 121 TFGQGTKEIK 131
DB 121 TFGQGTKEIK 131
RESULT 3
KV3F_MOUSE
ID KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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Query Match 38.9%; Score 481; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 4.5e-32;
Matches 89; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 60

QY 81 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTKEIK 131
DB 61 GIPARFSGSGSGTDFLTINHPVEEDATYYCQSNEDPRTFGAGTKLEIK 111

RESULT 6
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 38.8%; Score 480; DB 1; Length 129;
Best Local Similarity 74.0%; Pred. No. 6.5e-32;
Matches 97; Conservative 12; Mismatches 18; Indels 4; Gaps 1;

QY 1 METDTILLVLLIWPVSGTDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWY 60
DB 3 MRVPAQLGLLLWLRGARDIQMTQSPSSLSASVGDRTVITCKASQSI----SNVLN 58

QY 61 QOKPGKAPKLLIYAASNL 120
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Db 59 QOKPGKAPKLLIYAASLSQSGVTSRFSGSGTDFLTITSSLOPEDATYYCQSYSTLI 118
QY 121 TFGQGTKEIK 131
DB 119 TFGQGTKEIK 129

RESULT 7
KV3O_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gamaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; C01937; KVM508.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 38.7%; Score 479; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 6.4e-32;
Matches 89; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 60

QY 81 GVPFRSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTKEIK 131
DB 61 GIPARFSGSGSGTDFLTINHPVEEDATYYCQSNEDPRTFGSGTKLEIK 111

RESULT 8
KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

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RX MEDLINE=98171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
RT mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
CC LEUKEMIA.
CC PIR; PLO022; K3HUHA.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 38.7%; Score 478.5; DB 1; Length 129;
Best Local Similarity 68.9%; Pred. No. 8.5e-32;
Matches 91; Conservative 17; Mismatches 21; Indels 3; Gaps 1;

Qy 1 METDTILWLLVWPGSTGDIVLTQSPSSLSASVGRVITITCRASQSDVDYDGSYMNWY 60
Db 1 METPAQLLFLLLLWLPDPTGEIVLTQSPGTLISLSPGERATISCRASQSV---SSYLAWY 57

Qy 61 QOKPGKAPKLIYASNLSESGVPSRFGSGSGTDTFTLTISLQPEDFATYTCQSQSNEDPR 120
Db 58 QOKPGQAPRLIYGAASSRATGIPDRFGSGSGTDTFTLTISRLEPDFAVYTCQVGTSPR 117

Qy 121 TFGQGTKEIKR 132
Db 118 TFGQGTKEIKR 129

RESULT 9
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.

Query Match 37.8%; Score 468; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 4.9e-31;
Matches 87; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVITITCRASQSDVDYDGSYMNWYQOKPGKAPKLIYASNLSE 80
Db 1 DIVLTQSPASLAVSLGQRATISCRASQSDVDYDGSYMNWYQOKPGQPKVLIFASNLSE 60

Qy 81 GVPFRFGSGSGTDTFTLTISLQPEDFATYTCQSQSNEDPRTFGQGTKEIK 131
Db 61 GIPARFGSGSGTDTFTLTNIHFVEEDAAATYTCQSQSNEDPWTFGSGTKLEIK 111

RESULT 10
KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2B1AD98AD965962 CRC64;
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Db 61 GIPARFSGSGGDTFTLNHPVEEDAATYCCQSNEDPTFGGKLEIK 111
      ||:|||||
RESULT 11
KV3P_HUMAN
ID KV3P_MOUSE STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
chain of subgroup I (Bence-Jones Protein Hau): subdivision within
subgroups.";
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -|- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868; K1HUHU.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 37.3%; Score 461; DB 1; Length 108;
Best Local Similarity 80.4%; Pred. No. 1.7e-30;
Matches 90; Conservative 11; Mismatches 7; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRVTITCKASQSYVDYDGDSDYMNWYQKPGKAPKLLIYAASNL 80
      ||:|||||
Db 1 DIQMTQSPSSLSASVGDRVTITCKASQSI----SSYLSWYQKPGKAPQVLIYAASSLPS 56

QY 81 GVPSRFSGSGGTDFLTITSLQPEDFATYCCQSNEDPTFGGKLEIKR 132
      ||:|||||
Db 57 GVPSRFSGSGGTDFLTITSLQPEDFATYCCQNYITPTFGGKTRVEIKR 108

RESULT 12
KV3P_MOUSE
ID KV3P_MOUSE STANDARD; PRT; 110 AA.
AC P01668;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
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RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR; D01937; KVM510.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 100 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 101 110 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 110 110
SQ SEQUENCE 110 AA; 11950 MW; 69F1A5CE886B1249 CRC64;

Query Match 37.1%; Score 458.5; DB 1; Length 110;
Best Local Similarity 78.4%; Pred. No. 2.8e-30;
Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRVTITCKASQSYVDYDGDSDYMNWYQKPGKAPKLLIYAASNL 80
      ||:|||||
Db 1 DIVLTQSPASLAVSLQGRATISCKASQSYVDYDGDSDYMNWYQKPGKAPKLLIYAASNL 60

QY 81 GVPSRFSGSGGTDFLTITSLQPEDFATYCCQSNEDPTFGGKLEIK 131
      ||:|||||
Db 61 GIPARFSGSGGTDFLTINHPVEEDAATYCCQSNEDPTFGGKLEIK 110

RESULT 13
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -|- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
DR PIR; P00021; K3HUH1.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
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QY      81  GVPFRFSGSGSGDFTLTISSQLQPEDFATYYCQSQNEDPRTFGQGTKEIKR 132
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      57  GVPFRFSGSGAGTEFTLTIISSQLQPEDFATYYCQQNSYPSRFGQGTKEIKR 108

RESULT 15
KVIM_HUMAN          STANDARD;          PRT;          108 AA.
ID      KVIM_HUMAN          108 AA.
AC      P01605;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Ig kappa chain V-I region Lay.
DE      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RZ      SEQUENCE.
RX      MEDLINE=77038198; PubMed=824717;
RA      Capra J.D., Klappper D.G.;
RT      "Complete amino acid sequence of the variable domains of two human
RT      IgM anti-gamma globulins (Lay/Pom) with shared idiotypic
RT      specificities.";
RL      Scand. J. Immunol. 5:677-684(1976).
CC      -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC      CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN.
CC      WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC      -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA-
CC      GLOBULIN ACTIVITY.
CC      PIR; A01871; K1HULY.
DR      HSP; P01607; 1REI.
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003596; Ig_v.
DR      Pfam; PF00047; Ig_1.
DR      SMART; SM00406; Igv; 1.
KW      Immunoglobulin V region.
FT      DOMAIN 1 23
FT      DOMAIN 24 34
FT      DOMAIN 35 49
FT      DOMAIN 50 56
FT      DOMAIN 57 88
FT      DOMAIN 89 97
FT      DOMAIN 98 107
FT      DISULFID 23 88
FT      NON_TER 108 108
SQ      SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match          36.3%; Score 449; DB 1; Length 108;
Best Local Similarity 78.6%; Pred No. 1.6e-29;
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 0

QY      21  DIVLTQSPSSLSASVGRVTITCKASQSYDYGDSYMMWYQQKPGKAPKLLIYAASNL 80
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  DIQMTQSPSSLSVSGDRVITTCQASQNV---NAYLNWYQQKPGKAPKLLIYGASTREA 56

QY      81  GVPFRFSGSGSGTDFTLTISSQLQPEDFATYYCQSQNEDPRTFGQGTKEIKR 132
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      57  GVPFRFSGSGSGTDFTLTISSQLQPEDATYYCQYNWNPPTFGQGTKEIKR 108

Search completed: August 14, 2002, 15:23:13
Job time: 686 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:14 ; Search time 187.61 Seconds
(without alignments)
219.459 Million cell updates/sec

Title: US-09-499-662-127
Perfect score: 1237
Sequence: 1 METDRIILWVLLWVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62GX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL19:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_organelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**
- 15: sp_rvirus:**
- 16: sp_bacteriap:**
- 17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	746.5	60.3	238	11 Q99M37	Q99M37 mus musculus
2	739	59.7	234	11 Q91WF8	Q91WF8 mus musculus
3	738	59.7	233	11 Q91WS9	Q91WS9 mus musculus
4	725	58.6	214	11 Q91IA5	Q91IA5 mus musculus
5	705.5	57.0	235	11 Q91W12	Q91W12 mus musculus
6	704	56.9	211	11 Q91XLO	Q91XLO mus musculus
7	471	38.1	108	4 Q9UL77	Q9UL77 homo sapien
8	463.5	37.5	107	4 Q96SA9	Q96SA9 homo sapien
9	450	36.4	108	4 Q9UL70	Q9UL70 homo sapien
10	438.5	35.4	107	4 Q9UL81	Q9UL81 homo sapien
11	437	35.3	108	4 Q9UL79	Q9UL79 homo sapien
12	433	35.0	116	4 Q96EF6	Q96EF6 homo sapien
13	431.5	34.9	235	11 Q99M11	Q99M11 mus musculus
14	429	34.7	236	4 Q96E61	Q96E61 homo sapien
15	415	33.5	111	11 Q920E9	Q920E9 mus musculus
16	394.5	31.9	109	4 Q9UL78	Q9UL78 homo sapien

17	382.5	30.9	233	4	Q96I69	Q96I69 homo sapien
18	380	30.7	108	4	Q9UL83	Q9UL83 homo sapien
19	379	30.6	298	11	Q9QYF0	Q9QYF0 mus musculus
20	377	30.5	233	11	Q91V32	Q91V32 m adult mal
21	371.5	30.0	109	4	Q9UL86	Q9UL86 homo sapien
22	371.5	30.0	109	4	Q9UL85	Q9UL85 homo sapien
23	366	29.6	103	11	Q9JL80	Q9JL80 mus musculus
24	365	29.5	109	11	Q920E6	Q920E6 mus musculus
25	351	28.4	127	11	Q925S9	Q925S9 mus musculus
26	350	28.3	114	4	Q9UL80	Q9UL80 homo sapien
27	346.5	28.0	106	5	Q9U410	Q9U410 schistosoma
28	346	28.0	107	11	Q9ERZ9	Q9ERZ9 mus musculus
29	345	27.9	99	11	Q9JL74	Q9JL74 mus musculus
30	335	27.1	101	11	Q9JL78	Q9JL78 mus musculus
31	328.5	26.6	241	11	Q921A6	Q921A6 mus musculus
32	328	26.5	97	11	Q9JL76	Q9JL76 mus musculus
33	321.5	26.0	104	11	Q9JL82	Q9JL82 mus musculus
34	306	24.7	109	6	Q9N0W5	Q9N0W5 oryctolagus
35	297	24.0	107	11	Q9JL84	Q9JL84 mus musculus
36	275.5	22.3	218	11	Q925S1	Q925S1 mus musculus
37	243	19.6	107	4	Q9UL82	Q9UL82 homo sapien
38	238.5	19.3	107	4	Q9NSD6	Q9NSD6 mus musculus
39	236.5	19.1	108	4	Q96SB0	Q96SB0 mus musculus
40	232	18.8	130	4	Q9NP29	Q9NP29 mus musculus
41	225	18.2	130	11	Q9D8W4	Q9D8W4 mus musculus
42	215	17.4	112	4	Q96JD1	Q96JD1 mus musculus
43	212	17.1	267	13	Q90529	Q90529 ginglymosto
44	208.5	16.9	112	4	Q96JD2	Q96JD2 mus musculus
45	207.5	16.8	116	4	Q96JD0	Q96JD0 mus musculus

ALIGNMENTS

RESULT 1						
Q99M37	Q99M37	PRELIMINARY;	PRT;	238 AA.		
AC	Q99M37;					
DT	01-JUN-2001 (Tremblrel. 17, Created)					
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)					
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)					
DE	HYPOTHETICAL 26.3 KDA PROTEIN.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS					
RC	TISSUE.;					
RA	Strausberg R.;					
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.					
DR	EMBL; BC002035; AAH02035.1; -					
DR	HSSP; P01679; 2FBJ					
DR	InterPro; IPR003599; Ig.					
DR	InterPro; IPR003597; Ig-cl.					
DR	InterPro; IPR003600; Ig-like.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	InterPro; IPR003596; Ig_v.					
DR	SMART; SM00409; Ig; 2.					
DR	SMART; SM00407; IGC1; 1.					
DR	SMART; SM00406; IGV; 1.					
DR	SMART; SM00410; IG_Like; 1.					
DR	PROSITE; PS00290; IG_MHC; UNKNOWN1.					
KW	Hypothetical protein					
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;					

Query Match 60.3%; Score 746.5; DB 11; Length 238;
Best Local Similarity 58.5%; Pred. No. 1.5e-57;
Matches 137; Conservative 40; Mismatches 56; Indels 1; Gaps 1;

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QY 6 ILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYMNYQQRP 64
DB 5 VRLVLMFWIPASSDWMVTPSLPSVLGDAQSICRSSQSIHVHSGNTVLEWYLP 64
QY 65 GRAPKLLIYAASNLSEGVPSRFGSGSGTDFLTITSSLPEDFATYYCQSNEDPRTFGQ 124
DB 65 GOSPKLLIYKVSNRFGVPSRFGSGSGTDFLTITSRVEADGVVYFCQGHVPYTFGS 124
QY 125 GKVEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQ 184
DB 125 GYKLEIKRADAAPTIVFIFFPSDEQLTSGGASVVCFLNNFYPRDINVKWIDGSEQRNGYL 184
QY 185 ESVTEODSKDSTYSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 185 NSWTQDSKSTYSMSSTLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 238

RESULT 2
ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH5292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 59.7%; Score 739; DB 11; Length 234;
Best Local Similarity 60.1%; Pred. No. 6.6e-57;
Matches 143; Conservative 33; Mismatches 58; Indels 4; Gaps 1;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYMNY 60
DB 1 MMSAQFLGILLLCFGTQCDTQMTQTSSLSASLGDRVTISCRASQDI----SNLYNY 56
QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDFLTITSSLPEDFATYYCQSNEDPR 120
DB 57 QOKPDGTVKLLIYYTSRLVGVPSRFGSGSGTDFLTITSSLPEDFATYYCQSGNTPPF 116
QY 121 TFGQGTKEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQS 180
DB 117 TFGSGTKLEVKRADAAAPTIVFIFFPSDEQLTSGGASVVCFLNNFYPRDINVKWIDGSE 176
QY 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 177 NGVLSNWTQDSKSTYSMSSTLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234

RESULT 3
ID Q91WS9 PRELIMINARY; PRT; 233 AA.
AC Q91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH5292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 59.7%; Score 739; DB 11; Length 234;
Best Local Similarity 60.1%; Pred. No. 6.6e-57;
Matches 143; Conservative 33; Mismatches 58; Indels 4; Gaps 1;

QY 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYMNY 60
DB 1 MMSAQFLGILLLCFGTQCDTQMTQTSSLSASLGDRVTISCRASQDI----SNLYNY 56
QY 61 QOKPGKAPKLLIYAASNLSEGVPSRFGSGSGTDFLTITSSLPEDFATYYCQSNEDPR 120
DB 57 QOKPDGTVKLLIYYTSRLVGVPSRFGSGSGTDFLTITSSLPEDFATYYCQSGNTPPF 116
QY 121 TFGQGTKEIKRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQS 180
DB 117 TFGSGTKLEVKRADAAAPTIVFIFFPSDEQLTSGGASVVCFLNNFYPRDINVKWIDGSE 176
QY 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 177 NGVLSNWTQDSKSTYSMSSTLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 234

RESULT 4
ID Q91A5 PRELIMINARY; PRT; 214 AA.
AC Q91A5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Wilder K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FEJ.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Igv_1.
DR SMART; SM00410; Ig_Like_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 58.6%; Score 725; DB 11; Length 214;
Best Local Similarity 63.3%; Pred. No. 9.8e-56;
Matches 138; Conservative 30; Mismatches 46; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYMNYQQRPKAPKLLIYAASNLSE 80
DB 1 DIQLTQSPSSMYASLGERTVITCKASQDI----NSYLSWFFQKPGKSPKTLIYRANRLVD 56
QY 81 GVPFRFGSGSGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 59.7%; Score 738; DB 11; Length 233;
Best Local Similarity 63.2%; Pred. No. 8e-57;
Matches 144; Conservative 28; Mismatches 52; Indels 4; Gaps 1;

QY 11 LLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYMNYQQRPKAPKL 70
DB 10 LLLCFGSGRCDTQMTQTSSLSASLGDRVTISCSGSGI----ANYLNYQQKPDGTVKL 65
QY 71 LIYAASNLSEGVPSRFGSGSGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEI 130
DB 66 LIYTTSSLHSGVPSRFGSGSGTDFLTITSSLPEDFATYYCQRYLPWTFGGTKEI 125
QY 131 KRTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWVDNALQSGNSQSVTEQ 190
DB 126 KRADAAPTIVFIFFPSSEQLTSGGASVVCFLNNFYPRDINVKWIDGSEQRNGVLSNWTQ 185
QY 191 DSKDSTYSLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 186 DSKDSTYSMSSTLTLTCKDEYERHNSYTCETHKSTSTSPIVKSFNRNEC 233

RESULT 4
ID Q91A5 PRELIMINARY; PRT; 214 AA.
AC Q91A5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Wilder K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FEJ.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; Igv_1.
DR SMART; SM00410; Ig_Like_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 58.6%; Score 725; DB 11; Length 214;
Best Local Similarity 63.3%; Pred. No. 9.8e-56;
Matches 138; Conservative 30; Mismatches 46; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDSYMNYQQRPKAPKLLIYAASNLSE 80
DB 1 DIQLTQSPSSMYASLGERTVITCKASQDI----NSYLSWFFQKPGKSPKTLIYRANRLVD 56
QY 81 GVPFRFGSGSGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
```

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Db 57 GVPFRSGSGQDYSITISSLEYEDMGYYCLQYDEFFPFGSGTKLEIKRADAAPTVS 116
Qy 141 IFPPSDEQLKSGTASVCLLNFFPREAKVQWVDNALQSGNSQESVTEQDSKDSYSL 200
Db 117 IFPPSSQLTSGGASVVCFLNFFPKDINVKWKIDGSRQGVLSWTDQDSKDSYSMS 176
Qy 201 STLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 TLTLTKDEYERHNSYTCEATHKTSTSPIVKCFNRNEC 214

RESULT 5
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AA006643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 57.0%; Score 705.5; DB 11; Length 235;
Best Local Similarity 61.8%; Pred. No. 5.7e-54;
Matches 135; Conservative 31; Mismatches 50; Indels 5; Gaps 1;

Qy 18 STGDIVLTQSPSSLSASVGRVITTCASQSDVDGDSYNNWYQKPGKAPKLLIYAASN 77
Db 20 SRGQIVLTQSPAIMSASPGERVITTCASQSV-----SHMHYQKQSGTSPKRIYDTFK 74
Qy 78 LESGVPFRSGSGGTDTFTLTISLQPEDFATYQCQSNEDPRTFGQGTKEIKRTVAAP 137
Db 75 LTSGVPRFRSGSGGTGYSLTISNWEADVATYQCQWSRNPRTFGVGTGLELRADAAP 134
Qy 138 SVFIFFPSDEQLKSGTASVCLLNFFPREAKVQWVDNALQSGNSQESVTEQDSKDSY 197
Db 135 TVSIFPPSSEQLTSGGASVVCFLNFFPKDINVKWKIDGSRQGVLSWTDQDSKDSY 194
Qy 198 SLSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 195 SMSSTLTLTDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 235

RESULT 6
Q91XL0 PRELIMINARY; PRT; 211 AA.
ID Q91XL0;
AC Q91XL0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiramoto T., Horii F.,
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RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kizama M., Nishino T., Harada A.,
RA Sumi N., Ishii Y., Nakamura S., Hatsumi T., Ikegami T., Kashiwagi K.,
RA Yamamoto R., Matsunoto H., Sakauchi S., Izawa M., Ohara E., Watahiki M.,
RA Fujiwaka S., Inoue K., Togawa Y., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Yoneda Y., Ishikawa T., Inoue Y., Kira A., Hayashizaki Y.;
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL: AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 56.9%; Score 704; DB 11; Length 211;
Best Local Similarity 61.8%; Pred. No. 6.7e-54;
Matches 134; Conservative 32; Mismatches 43; Indels 8; Gaps 2;

Qy 24 LTQSPSSLSASVGRVITTCASQSDVDGDSYNN--WYQKPGKAPKLLIYAASNLSEG 81
Db 1 MTQSPASLSVSGVETVITCRASENI-----YNSLAWYQKQKSPQLLYAATNLADG 54
Qy 82 VPSRFRSGSGGTDTFTLTISLQPEDFATYQCQSNEDPRTFGQGTKEIKRTVAAPSVEI 141
Db 55 VPSRFRSGSGGTGYSLKINSLSQSEDFGSYFCQHFHWGTPRTFGGTTKLEIKRADAAPTYSI 114
Qy 142 FPPSDEQLKSGTASVCLLNFFPREAKVQWVDNALQSGNSQESVTEQDSKDSYSLSS 201
Db 115 FPPSSEQLTSGGASVVCFLNFFPKDINVKWKIDGSRQGVLSWTDQDSKDSYSMS 174
Qy 202 TLTLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
Db 175 TLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 211

RESULT 7
Q9UL77
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ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 38.1%; Score 471; DB 4; Length 108;
Best Local Similarity 83.0%; Pred. No. 6.8e-34;
Matches 93; Conservative 7; Mismatches 8; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLNWYQKPGKAPKLLIYAAS 56
QY 81 GVPFRFSGSGGTDTLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDTLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 108

RESULT 8
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 37.5%; Score 463.5; DB 4; Length 107;
Best Local Similarity 83.9%; Pred. No. 3e-33;
Matches 94; Conservative 6; Mismatches 7; Indels 5; Gaps 2;

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QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLNWYQKPGKAPKLLIYAAS 56
QY 81 GVPFRFSGSGGTDTLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDTLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 108

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 36.4%; Score 450; DB 4; Length 108;
Best Local Similarity 78.6%; Pred. No. 4.7e-32;
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQGI-----SNYLNWYQKPGKAPKLLIYAAS 56
QY 81 GVPFRFSGSGGTDTLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDTLTITSSLPQEDFATYQQSNEDPRTFGQGTKEIKR 108

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81;
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 35.4%; Score 438.5; DB 4; Length 107;
Best Local Similarity 78.6%; Pred. No. 4.7e-31;
Matches 88; Conservative 9; Mismatches 10; Indels 5; Gaps 2;
QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYNNWYQKPKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGRVTITCKASQSI---SNLYNWYQKPKAPNLLIYAASLQS 56
QY 81 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQOS-YSALTFGQGTKEIKR 107

RESULT 11
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.3%; Score 437; DB 4; Length 108;
Best Local Similarity 77.7%; Pred. No. 6.4e-31;
Matches 87; Conservative 7; Mismatches 14; Indels 4; Gaps 1;
QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYNNWYQKPKAPKLLIYAASNL 80
Db 1 DIVMTQSPSSLSASVGRVTITCKASQGI---SSLYLWYQKPKAPPELLIYAASLQS 56
QY 81 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQOYFFPFTFGQGTKEIKR 108

RESULT 12

Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
contributions of Ig V(L) germ line gene use and clonal plasma cell
burden."
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 35.0%; Score 433; DB 4; Length 116;
Best Local Similarity 70.8%; Pred. No. 1.6e-30;
Matches 85; Conservative 14; Mismatches 17; Indels 4; Gaps 1;
QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYNNWYQKPKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGRVTITCKASQDI---ANHLYWYQKPKAPKLLIYDGSFLKT 56
QY 81 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 57 GVPFRFSGSGSGTNTVTISSLQPEDFATYYCQVHHLPFTFGQGTKEIKRTVAAPSVF 116

RESULT 13
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.4 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_ci.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IG; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.9%; Score 431.5; DB 11; Length 235;

Best Local Similarity 42.6%; Pred. No. 5.4e-30;
Matches 101; Conservative 37; Mismatches 86; Indels 13; Gaps 7;

QY 7 LLWLLWVPGSGDVLVLTQSPSSLSASVGDRTVTICKASQSYVDYDGSYMNWYQKPKG 66
DB 6 LLLVFLHHTGSCAQVLVLTQ-PPSSVSTSLGSTAKLPKA--STGNIGDSYVWYQYMG 62
QY 67 APKLLIYAASNLSEGVPSRFGSG--GSGTDFLTITISSLOPEDFATYVCOQSNEDPRTFGQ 124
DB 63 STNMIYGGDLPSPGVSDRFSSIDSSNSAFLTIONVQADDEADYVCOYSGGIRVFGG 122
QY 125 GTKVEI-KRTVAAPSVFIPPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNALQSGNS 183
DB 123 GTKLVLSQPKTSPVTLFPSPSEELTNKATLVCTISDFYPCGVTVTDWKADG---TPVT 179
QY 184 QSVTEQDSK--DSYISLSTLTLSKADYEKHKVYACEVTHOGLSPVTKSFNRGEC 238
DB 180 QGVETQPSKQNNKYMASSTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234

RESULT 14

Q96E61
ID Q96E61 PRELIMINARY; PRT; 236 AA.
AC Q96E61;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:17259).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -.
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 34.7%; Score 429; DB 4; Length 236;

Best Local Similarity 42.4%; Pred. No. 9e-30;
Matches 100; Conservative 39; Mismatches 87; Indels 10; Gaps 7;

QY 7 LLWLLWVPGSGDVLVLTQSPSSLSASVGDRTVTICKASQSYVDYDGSYMNWYQKPKG 66
DB 6 LLLTLLAHTGSAQSVLAQ-PPSVSGAPGQVITISCTGS-STNIGAGYAVHWYQQFPGA 63
QY 67 APKLLIYAASNLSEGVPSRFGSGSGTDFLTITISSLOPEDFATYVCOQ--QSNEDPRTFGQ 124
DB 64 APKVLIIYGNYNRPSGVDPDRFSGSKGTSASLAITGLQADEADYVCOYSGLSGSVFCA 123
QY 125 GTKVEI-KRTVAAPSVFIPPPSDEQLKSGTASVVCLLNFPYPREAKVQWKVDNA-LQSGN 182
DB 124 GTKVTVLGQPKRANVTVTLFPSPSEELQANKATLVCLISDFYPCAVTVAMKADGSPVKAG- 182
QY 183 SOEVSTEQDSKSTLSLSTLSKADYEKHKVYACEVTHOGLSPVTKSFNRGEC 238
DB 183 -VETTKPSQSNKNYAASSTLTTPQWKSHRSYSCQVTHEG--STVEKTVAPTEC 235

RESULT 15

Q920E9
ID Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOLOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
FT NON_TER 1 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 33.5%; Score 415; DB 11; Length 111;

Best Local Similarity 72.1%; Pred. No. 5.6e-29;
Matches 80; Conservative 12; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVTICKASQSYVDYDGSYMNWYQKPKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRTISCRASKSYSTSGSYMHYQKPGQPPKLLIYASNL 60
QY 81 GVPSPRFGSGSGTDFLTITISSLOPEDFATYVCOQSNEDPRTFGQTKVEIK 131
DB 61 GVPARFSGSGTDFLTINHPVEEDATYVCOHSRELPTYFGGKLEIK 111

Search completed: August 14, 2002, 15:22:14

Job time: 682 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:34 ; Search time 230.21 Seconds
(without alignments)
114.832 Million cell updates/sec

Title: US-09-499-662-129
Perfect score: 1237
Sequence: 1 METDTILLWLLWVPGTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:
BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
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11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
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20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1237	100.0	238	21	AAW90931 Humanised anti-Fas
2	1233	99.7	238	21	AAW90930 Humanised anti-Fas
3	1232	99.6	238	21	AAW90932 Humanised anti-Fas
4	1177	95.1	238	19	AAW83034 Anti-Fas humanised
5	1177	95.1	238	21	AAW83033 Humanised anti-Fas
6	1177	95.1	238	21	AAW83031 Humanised anti-Fas
7	1172	94.7	238	19	AAW83031 Humanised anti-Fas
8	1172	94.7	238	21	AAW83032 Humanised anti-Fas
9	1172	94.7	238	19	AAW83032 Humanised anti-Fas
10	1159	93.7	238	19	AAW83032 Anti-Fas humanised
11	1159	93.7	238	21	AAW83032 Humanised anti-Fas

12	1159	93.7	238	21	AAW90923 Humanised anti-Fas
13	1158	93.6	238	19	AAW83035 Anti-Fas humanised
14	1158	93.6	238	21	AAW83035 Humanised anti-Fas
15	1158	93.6	238	21	AAW90928 Humanised HFE7A de
16	1157	93.5	238	19	AAW83033 Anti-Fas humanised
17	1157	93.5	238	21	AAW83033 Humanised anti-Fas
18	1157	93.5	238	21	AAW83033 Humanised anti-Fas
19	1108	89.6	218	18	AAW13563 Humanised anti-L-s
20	1096	88.6	218	21	AAW95658 Mus musculus anti-
21	1096	88.6	218	21	AAW85200 Light chain amino
22	1096	88.6	218	21	AAW76947 Full variable ligh
23	1089	88.0	218	14	AAW33312 Humanised MaE11 Ve
24	1073	86.7	218	20	AAW50030 Human 227 anti-IgE
25	1073	86.7	218	20	AAW95660 Mus musculus anti-
26	1073	86.7	218	21	AAW95662 Mus musculus anti-
27	1073	86.7	218	21	AAW07472 Amino acid sequenc
28	1073	86.7	218	22	AAW74211 E27 anti-IgE antib
29	1070	86.5	218	20	AAW95669 Mus musculus anti-
30	1070	86.5	218	20	AAW95664 Mus musculus anti-
31	1070	86.5	218	22	AAW47087 Anti-IgE antibody,
32	1070	86.5	218	22	AAW76949 Full length light
33	1070	86.5	218	22	AAW76951 Full length light
34	1070	86.5	218	22	AAW76953 Variable light cha
35	1070	86.5	218	22	AAW76958 Variable light cha
36	1049.5	84.8	237	21	AAW96298 Human IGFAM-10 imm
37	1048	84.7	240	20	AAW50161 Human reshaped F19
38	1045.5	84.5	237	21	AAW96289 Human IGFAM-1 immu
39	1043.5	84.4	241	22	AAW82912 Human immune respo
40	1041.5	84.2	234	14	AAW38162 Sequence of the ka
41	1037.5	83.9	237	21	AAW96301 Human IGFAM-13 imm
42	1036	83.8	234	18	AAW11638 Human anti-RSV mon
43	1033	82.7	240	22	AAW63665 Amino acid sequenc
44	1021	82.5	237	20	AAW73873 Human antifer epsil
45	1019	82.4	236	16	AAW77614 Humanised 5G1.1 VL

ALIGNMENTS

RESULT 1

AAW90931

ID AAW90931 standard; Protein; 238 AA.

XX AAW90931;

AC AAW90931;

XX 08-AUG-2000 (first entry)

DT Humanised anti-Fas designed light chain Leu 2 protein.

XX Pas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antinfertility; neuroprotective; antirheumatic; anti-Fas;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

XX EP990663-A2.

PN 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 DR N-PSDB; AA11632.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 PS Claim 2; Page 159; 263pp; English.
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 2
 CC which is described in the method of the invention.
 XX Sequence 238 AA;

Query Match 100.0%; Score 1237; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.1e-60;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVTITCKASQSDYDGDSTYNNY 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 metdtillwvllwpgstgdivltqspsslsasvgdrtvtitckasqsdvdygdsymwy 60
 QY 61 QQKPGQAPKLLIYAASNLSESGVPSRFSGSGCTDFTLTSSLPQEDFATYQCQSDNEPR 120
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 qqkpgqapklliyasnlsesgvpsrfsgsgctdftltsslpqedfatyqcqsdnepr 120
 QY 121 TFCQGTKEIKRTVAAPSVFIFPPQDEQLKSGTASVIVCLNNFYPREAKVQKVDNALQS 180
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 tfcgtkeikrtvaapsvfifppqdeqlksgtasvivilnnfypreakvqkvdnalqs 180
 QY 181 GNSQSVTEQDSKDTYSLSSTLTLSKADYKHVKYACEVTHQGLSSPVTKSFNRGEC 238
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 181 gnsqsvteqdskdtsyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 2
 AAW90930
 ID AAW90930 standard; Protein: 238 AA.
 XX
 AC AAW90930;
 XX
 DT 08-AUG-2000 (first entry)
 XX

DE Humanised anti-Fas designed light chain Leu 1 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS EP950663-A2.
 PN EP950663-A2.
 XX 05-APR-2000.
 PD 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AA11631.
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX Claim 3; Page 156-157; 263pp; English.
 PS This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 1
 CC which is described in the method of the invention.
 XX Sequence 238 AA;

Query Match 99.7%; Score 1233; DB 21; Length 238;
 Best Local Similarity 99.6%; Pred. No. 6.7e-60;
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVTITCKASQSDYDGDSTYNNY 60

||||| 1 metdtillwllvwpvgstgdivltqspsslsasvgsdrvtitckasqsvdydgsymwmy 60
 Qy 61 OQKPGQAPKLLIYAASNLSESGVPSRFSGSGTDFTLTSSQLQPDFAFYCCQSQNEDPR 120
 Db 61 qkpgkqkalliyaasnlsgvpsrfsqsgtdftltisslqpedfatyyccqsgnedpr 120
 Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180
 Db 121 tfgggtkeikrtvaapsvfifppsqdeqlksgtasvcllnnfypreakvqkvdnalq 180
 Qy 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqdsksdystslstltlskadyekhyacevthqglsspvtksfnrgec 238

RESULT 3
 ID AAW90932 standard; Protein: 238 AA.
 XX AAW90932;
 AC AAW90932;
 DT 08-AUG-2000 (first entry)
 XX Humanised anti-Fas designed light chain Leu 3 protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.
 OS
 XX EP990663-A2.
 XX
 XX 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 XX
 XX 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 XX
 XX N-PSDB; AAL11633.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems
 XX
 XX Claim 3; Page 161-162; 263pp; English.
 PS
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 3
 CC which is described in the method of the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.6%; Score 1232; DB 21; Length 238;
 Best Local Similarity 99.2%; Pred. No. 7.6e-60;
 Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVWPVGSTGDIVLTQSPSSLSASVGSdrvtITCKASQSVdydgsymwmy 60
 Db 1 metdtillwllvwpvgstgdivltqspsslsasvgsdrvtitckasqsvdydgsymwmy 60
 Qy 61 OQKPGQAPKLLIYAASNLSESGVPSRFSGSGTDFTLTSSQLQPDFAFYCCQSQNEDPR 120
 Db 61 qkpgkqkalliyaasnlsgvpsrfsqsgtdftltisslqpedfatyyccqsgnedpr 120
 Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQKVDNALQ 180
 Db 121 tfgggtkeikrtvaapsvfifppsqdeqlksgtasvcllnnfypreakvqkvdnalq 180
 Qy 181 GNSQSVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqsvteqdsksdystslstltlskadyekhyacevthqglsspvtksfnrgec 238

RESULT 4
 AAW83034
 ID AAW83034 standard; Protein: 238 AA.
 XX AAW83034;
 AC AAW83034;
 DT 15-MAR-1999 (first entry)
 XX
 XX Anti-Fas humanised antibody HFE7A light chain PDHH type.
 XX
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 XX Peptide 1..20
 XX /label= Sig_peptide
 XX Protein 21..238
 XX /label= Mat_protein
 XX Region 21..131
 XX /label= variable
 FT

FT Region 132..238
 FT /label= Constant
 FT 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 XX 01-APR-1997; 97JP-0082953.
 XX 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 XX N-PSDB; AAV70077.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 XX used to evaluate drugs in animal models and to treat Fas-associated
 XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 XX myocarditis, hepatitis and AIDS
 XX Claim 21; Page 218; 292pp; English.
 XX This is the amino acid sequence of the PDHH type humanised light
 XX chain of murine anti-human Fas monoclonal antibody HFE7A.
 XX Humanisation of the murine sequence (see AAW83042) entailed making
 XX D1E, P47A, K49R, H80S, P81R, V82L, E84P, A87F, T89V and R107K
 XX amino acid substitutions; these residues are conserved in the
 XX human light chain (kappa chain). Host cell Escherichia coli
 XX PHSH5 SANK 70398 harbors plasmid PHSH5 carrying a fusion
 XX fragment of the humanised PDHH type HFE7A light chain and DNA
 XX encoding the region of human immunoglobulin kappa chain, and is
 XX deposited as FERM BP-6274 (claimed). The invention provides
 XX methods for producing humanised antibodies by culturing host
 XX cells. Humanised versions of HFE7A (see AAW83031-37), like native
 XX HFE7A, are capable of inducing apoptosis in abnormal cells
 XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 XX cells. The humanised antibodies are used to evaluate, in animal
 XX models, treatments of diseases that involve Fas/Fas ligand
 XX interactions, and also to treat such diseases, including autoimmune
 XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
 XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 XX rejection (all claimed).
 XX Sequence 238 AA:
 Query Match 95.1%; Score 1177; DB 19; Length 238;
 Best Local Similarity 93.3%; Pred. NO. 7.2e-57;
 Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWPGSTGDIIVLTQSPGSLSPGERATLSCASQSVYDGDSDYMMWY 60
 |||||||||||||||||||:|||||:|:|:|:|||||||||||||

Db 1 metdtillwvllwpgstgeivltqspgslslsperatlscasqsvdydgsymwv 60
 QY 61 QQRPGQAPKLLIYAASNLESQVPSRFSGSGSGTDFLTITISSLPQEPFATVYCOQSNEDPR 120
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 Db 61 qkpgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepefavyycqgsnedpr 120
 |||||||:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||
 QY 121 TFGQGTKEIKRTVAAPSFIIPPDSDEQKSGTASVVCLLNNFYPREAKVQWVDNALQS 180
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 Db 121 tfgggtkleikrtvaapsvfifppsdeqiksgtasvvcillnnfypreakvqwkvdnalqs 180
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 QY 181 GNSQESVTEQDSKDSYSLSSLTILSKADYKHKYACEVTHQGLSSPVTKSNRGEC 238
 |||||||:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||
 Db 181 gnsqesvteqdkdstyslssltitiskadyekhkvyacevthqglsspvtksnrgec 238
 |||||||:|||||:|:|:|:|||||:|:|:|:|||||:|:|:|:|||||
 RESULT 5
 AAB14777
 ID AAB14777 standard; Protein; 238 AA.
 XX
 AC AAB14777;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 XX Humanised anti-Fas antibody light chain, SEQ ID NO:107.
 DE
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 XX 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAW2176.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 101; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC of diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 95.1%; Score 1177; DB 21; Length 238;

CC	antirheumatic, nephrotropic, antifertility, neuroprotective.
CC	antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
CC	apoptosis by binding to cell surface Fas or inhibit it by competitive
CC	inhibition of ligand binding. (I) are used to treat and/or prevent
CC	diseases associated with the Fas/Fas ligand system, especially systemic
CC	lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC	versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC	anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC	disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC	multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC	dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC	cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC	(B, C or D) or alcoholical, and transplant rejection. (I) selectively
CC	inhibit apoptosis in normal cells but selectively induce it in abnormal
CC	cells. They bind to both human and murine Fas, so can be evaluated in
CC	murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC	the native ligand, do not induce liver disease, and have reduced risk of
CC	inducing a human anti-murine antibody response. This sequence represents
CC	a humanised anti-Fas antibody HFE7A designed light chain which is used in
CC	the method described in the invention.
XX	
SQ	Sequence 238 AA;
	Query Match 95.1%; Score 1177; DB 21; Length 238;
	Best Local Similarity 93.3%; Pred. No. 7.2e-57;
	Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
QY	1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCRKASQSDYDGDSYMNY 60
DB	1 metdtillwlllwpvgstgeivltqspgtlslspgeratiscasqsdvdygdSYMNY 60
QY	61 QKQPGQAPKLLIYAASNLSEGVPSRFSGSGSGTDFTLTITISLQPEDFATYYCQOSNEDPR 120
DB	61 qkpgqgprlliyaasnlesgipdrfsgsgsgtdftltisrlepedfavyycqgsnedpr 120
QY	121 TFGOGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQS 180
DB	121 tfgggtkleikrtvaapsvfifppsdeqlksgtasvcllnnfypreakvqwkvdnalqs 180
QY	181 GNSQESTYEDSKDSTYSLSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB	181 gnsqesvteqgskdstyslsstltlskadyekhkvacevthgglspsvtksfnrgec 238
RESULT 7	
AAW83031	
ID	AAW83031 standard; Protein; 238 AA.
XX	AAW83031;
DT	15-MAR-1999 (first entry)
XX	
DE	Anti-Fas humanised antibody HFE7A light chain HH type.
XX	
KW	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW	apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW	systemic lupus erythematosus; graft versus host disease;
KW	Sjogren syndrome; pernicious anaemia; Addison's disease;
KW	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW	rheumatoid arthritis; autoimmune haemolytic anaemia;
KW	myasthenia gravis; multiple sclerosis; Basedow's disease;
KW	thrombopenia purpura; insulin-dependent diabetes; allergy;
KW	acrop; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW	transplant rejection; therapy.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..20
FT	/label= Sig peptide

FT Protein 21...238
 FT /label= Mat_protein
 FT Region 21...131
 FT /label= Variable
 FT Region 132...238
 FT /label= Constant
 FT Region 44...58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT Region 74...80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT Region 113...121
 FT /label= CDR_L3
 FT /note= "claim 9"
 XX AU9859701-A.
 XX
 PD 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70074.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21: Page 199-199; 292pp; English.
 XX
 CC This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AAW83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain and DNA encoding the region of human
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AAW83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX Sequence 238 AA;
 SQ

QY 1 METDTILLWLLVLPVGGTGDIVLTQSPSSLSASVGDRTVITCKASQSYDYDGDSYMNY 60
 DB 1 metdtillwlllvpggstgdivltqspgtlslsgeratlsckasqsvdygdsgymny 60
 QY 61 QOKPGQAPKLLIYAASNLESVPSFSGSGGTDTLTITSSLOPEDFATYYCOQSNEDPR 120
 DB 61 qkpgqaprllyaaanlesgipdrfsgsgsgtdltltsrlslepafavyycqgsnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSFIPTSPDEOLKSGTASVCLNNFYPREAKVOKVDNALOS 180
 DB 121 tfgggrleikrtvaapsvfiptpsdeqlksgtasvcllnnfybreakvqkvdnals 180
 QY 181 GNSQSVTEQDSKDYSLSTLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqsvteqdskdystylsstltlskadyekhkyacevthqglsspytksfnrgec 238
 RESULT 8
 AAB14772
 ID AAB14772 standard; Protein; 238 AA.
 XX
 AC AAB14772;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAA72124.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 78-79; 139pp; Japanese.
 CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX Sequence 238 AA;
 SQ

Query Match 94.7%; Score 1172; DB 19; Length 238;
 Best Local Similarity 92.98; Pred. No. 1.3e-56;
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Query Match 94.7%; Score 1172; DB 21; Length 238;
 Best Local Similarity 92.9%; Pred. No. 1.3e-56;
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWLLVWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
 DB 1 metdtillwllwpgstgdivltqspgtlslspgeratlsckasqsdvdygdsmnwy 60

QY 61 QOKPGQAPKLLIYAASNLGSPVSRFSGSGSGTDTLTITISLOPEDFATYCCQSNEDPR 120
 DB 61 qkpgqaprllyiaasnlesgipdrfsgsgsgdtftltisrlepadvfayvcqsgnedpr 120

QY 121 TFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQS 180
 DB 121 tfggktrleikrtvaapsvfifppsdqksgtasvvcvllnnfypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 9
 AAW90922 standard; Protein; 238 AA.

XX AAW90922;
 AC AAW90922;
 DT 08-AUG-2000 (first entry)
 DE Humanised anti-Fas antibody HFE7A light chain HH type protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 XX nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 XX Sjogren's syndrome; anemia; Addison's disease; sterility; myasthenia gravis;
 XX Goodpasture syndrome; Crohn's disease; scleroderma; purpura; allergy;
 XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.

XX EP990663-A2.
 XX 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 XX 30-SEP-1998; 98JP-0276881.
 XX 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPT; 2000-258930/23.
 XX N-PSDB; AAA11562.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems -
 XX Example reference 14; Page 114-115; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX ligand system, by binding to Fas on the cell surface, and prevents
 XX apoptosis in cells with a normal system, by inhibiting binding between

CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 XX the method described in the invention.

XX Sequence 238 AA;

Query Match 94.7%; Score 1172; DB 21; Length 238;
 Best Local Similarity 92.9%; Pred. No. 1.3e-56;
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWLLVWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
 DB 1 metdtillwllwpgstgdivltqspgtlslspgeratlsckasqsdvdygdsmnwy 60

QY 61 QOKPGQAPKLLIYAASNLGSPVSRFSGSGSGTDTLTITISLOPEDFATYCCQSNEDPR 120
 DB 61 qkpgqaprllyiaasnlesgipdrfsgsgsgdtftltisrlepadvfayvcqsgnedpr 120

QY 121 TFGGKTVEIKRTVAAPSVFIFFPSDEQLKSGTASVVCVLLNNFYPREAKVQKVDNALQS 180
 DB 121 tfggktrleikrtvaapsvfifppsdqksgtasvvcvllnnfypreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKDYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 DB 181 gnsqesvteqdsksdystslstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 10
 AAW83032 standard; Protein; 238 AA.

XX AAW83032;
 AC AAW83032;
 DT 15-MAR-1999 (first entry)
 DE Anti-Fas humanised antibody HFE7A light chain HM type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 XX systemic lupus erythematosus; graft versus host disease;
 XX Sjogren syndrome; pernicious anaemia; Addison's disease;
 XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 XX rheumatoid arthritis; autoimmune haemolytic anaemia;
 XX myasthenia gravis; multiple sclerosis; Basedow's disease;
 XX thrombopenia purpura; insulin-dependent diabetes; allergy;
 XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 XX transplant rejection; therapy.

XX Homo sapiens.
 XX Synthetic.

FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= Sig_peptide
FT Region 21..238
FT Region /label= Mat_protein
FT Region 21..131
FT Region /label= Variable
FT Region 132..238
FT Region /label= Constant
FT Region 44..58
FT Region /label= CDR_L1
FT Region /note= "claim 9"
FT Region 74..80
FT Region /label= CDR_L2
FT Region /note= "claim 9"
FT Region 113..121
FT Region /label= CDR_L3
FT Region /note= "claim 9"
XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX
XX 01-APR-1997; 97JP-0082953.
XX
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI: 1998-543440/47.
XX N-PSDB; AAV70075.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 200; 292pp; English.
XX
XX This is the amino acid sequence of the HM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A.
XX Humanisation of the murine sequence (see AAW83042) entailed making
XX P47A and K49R amino acid substitutions; these residues are
XX conserved in the human light (kappa) chain. Host cell E. coli
XX PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
XX fragment of the humanised HM type HFE7A light chain and DNA
XX encoding the region of human immunoglobulin kappa chain, and is
XX deposited as FERM BP-6072 (claimed). The invention provides
XX methods for producing humanised antibodies by culturing host
XX cells. Humanised versions of HFE7A (see AAW83031-37), like native
XX HFE7A, are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. The humanised antibodies are used to evaluate, in animal
XX models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).
XX
XX Sequence 238 AA;

Query Match 93.7%; Score 1159; DB 19; Length 238;
Best Local Similarity 92.0%; Pred. No. 6.8e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDYDGDSTYNNWY 60
Db 1 metdtillwvllwpgstgdivltqspgltslspgeratlsckasgsdydgdsgymwy 60
QY 61 QOKPGOAPKLLIYAASNLSEGPSRFSGGSGTDFLTITSSLOPEDFATVYCOQSNEDPR 120
Db 61 qkpgqaprllyaaanlesgipdrfs9sgtcdfltlthpveedaatyyccqgsnedpr 120
QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLNNFYPREAKVQWKVDNALQS 180
Db 121 tfgqgtrleikrtvaapsvfifppsdeqlksgtasvvcclnnfypreakvqwkvdnalqs 180
QY 181 GNSQESVTEODSKDSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdakdstysstltlskadyekhkvyacevthgglsspvtksfnrgec 238
RESULT 11
AAB14773
ID AAB14773 standard; Protein; 238 AA.
XX
XX AC AAB14773;
XX
XX DT 24-NOV-2000 (first entry)
XX
XX DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.
XX
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pannyelophthisis;
XX hepatitis; AIDS; graft rejection; light chain.
XX
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX
XX PN JP2000169393-A.
XX
XX PD 20-JUN-2000.
XX
XX PF 30-SEP-1999; 99JP-0278301.
XX
XX PR 30-SEP-1998; 98JP-0276883.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI: 2000-485645/43.
XX N-PSDB; AAA72125.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX
XX Claim 20; Page 80-81; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
XX represent the light chains of several humanised HFE7A-derived anti-Fas

CC antibodies.
XX Sequence 238 AA;
SQ

Query Match 93.78; Score 1159; DB 21; Length 238;
Best Local Similarity 92.08; Pred. No. 6.8e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDVDGDSYNNWY 60
Db 1 metdtillwllwpgstgdivltqspgtlslpgeratlsckasvdydgdsmwny 60

Qy 61 QOKPGQAPKLLIYAASNLSEGVPRFSGSGSDTFTLTISLQPEDFATYYCQSQSNEDEPR 120
Db 61 qkpgqaprllyaaasnlsegipdrfsgsgtdftltihpveeadaatyycqgsnedpr 120

Qy 121 TFGOGTKVEIKRTVAASVTFPPSDQLKSGTASVCLLNFFPREAKVQKVDNALQS 180
Db 121 tfgogtgleikrtvaasvtfppsdqlksgtasvcllnffpreakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKSTYSLSTLTSLKADYEKHKVYACEVTHOGLSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdstyslsltltlslkadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 12
AAW90923
ID AAW90923 standard; Protein; 238 AA.
XX
AC AAW90923;
XX
XX 08-AUG-2000 (first entry)
DT
XX Humanised anti-Fas antibody HFE7A light chain HM type protein.
DE
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EF990663-A2.
XX
XX 05-APR-2000.
PD
XX 29-SEP-1999; 99EP-0307711.
PF
XX 30-SEP-1998; 98JP-0276881.
PR
XX 30-SEP-1998; 98JP-0276882.
PR
XX (SANY) SANKYO CO LTD.
PA
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI; 2000-258930/23.
XX N-PSDB; AAA11563.
DR
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
XX Example reference 14; Page 117-118; 263pp; English.
PS
XX This invention describes a novel humanized anti-Fas antibody-like
CC

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
CC the method described in the invention.
XX
SQ Sequence 238 AA;

Query Match 93.78; Score 1159; DB 21; Length 238;
Best Local Similarity 92.08; Pred. No. 6.8e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITTCASQSDVDGDSYNNWY 60
Db 1 metdtillwllwpgstgdivltqspgtlslpgeratlsckasvdydgdsmwny 60

Qy 61 QOKPGQAPKLLIYAASNLSEGVPRFSGSGSDTFTLTISLQPEDFATYYCQSQSNEDEPR 120
Db 61 qkpgqaprllyaaasnlsegipdrfsgsgtdftltihpveeadaatyycqgsnedpr 120

Qy 121 TFGOGTKVEIKRTVAASVTFPPSDQLKSGTASVCLLNFFPREAKVQKVDNALQS 180
Db 121 tfgogtgleikrtvaasvtfppsdqlksgtasvcllnffpreakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKSTYSLSTLTSLKADYEKHKVYACEVTHOGLSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdstyslsltltlslkadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 13
AAW83035
ID AAW83035 standard; Protein; 238 AA.
XX
AC AAW83035;
XX
XX 15-MAR-1999 (first entry)
DT
XX Anti-Fas humanised antibody HFE7A light chain PDHM type.
DE
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX

OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= Sig_peptide
FT Protein 21..238
FT /label= Mat_protein
FT Region 21..131
FT /label= Variable
FT Region 132..238
FT /label= Constant
FT Region 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT Region 74..80
FT /label= CDR_L2
FT /note= "claim 9"
FT Region 113..121
FT /label= CDR_L3
FT /note= "claim 9"
XX
PN AU9859701-A.
XX
PD 08-OCT-1998.
XX
PF 30-MAR-1998; 98AU-0059701.
XX
PR 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
DR WPI: 1998-543440/47.
DR N-PSDB; AAV70078.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX
PS Claim 21; Page 220-221; 292pp; English.
XX
CC This is the amino acid sequence of the PDHM type humanised light
CC chain of murine anti-human Fas monoclonal antibody HFE7A.
CC Humanisation of the murine sequence (see AAW83042) entailed making
CC D1E, P47A, K49R and R107K amino acid substitutions; these
CC residues are conserved in the human light (kappa) chain. Host
CC cell Escherichia coli pSHM2 SANK 70198 harbors plasmid pSHM2
CC carrying a fusion of the humanised PDHM type HFE7A light chain and
CC DNA encoding the region of human immunoglobulin kappa chain, and is
CC deposited as FERM BP-6272 (claimed). The invention provides
CC methods for producing humanised antibodies by culturing host
CC cells. Humanised versions of HFE7A (see AAW83031-37), like native
CC HFE7A, are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. The humanised antibodies are used to evaluate, in animal
CC models, treatments of diseases that involve Fas/Fas ligand
CC interactions, and also to treat such diseases, including autoimmune
CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
CC thrombopenia purpura and insulin-dependent diabetes), allergies,
CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
CC rejection (all claimed).
XX

SQ Sequence 238 AA;
Query Match 93.6%; Score 1158; DB 19; Length 238;
Best Local Similarity 92.0%; Pred. No. 7.7e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWVLLIWPVSGTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDGSDYNNWY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 metdtillwvlllwpvgstgeivltspgtlspsgeratlsckasqsdvdgdsymnw 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 QKPGQAPKLLIYAASNLESGVPSRFGSGSGTDFLTITSSIQPEDFAFYCCQSNEDPR 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 qkpgqaprllyaaenlesgipdrfsgsgtdftltihpveedaatyccqgsnedpr 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 TFCQGTKVEIKRTVAAPSVFIPTPSDEQLKSGTASVVCLLNNFPPREAKVQWKVDNALQS 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 tfgggtklleikrtvaapsvfiptpsdeqiksgtasvvcilnnfybreakvqwkvdnalqs 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 GNSQESVTEQDSKDSYSLSSSTLTLSKADYEHKVVACEVTHQGLSPVTKSFNRGEC 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 gnsqesvteqdsksdystslsstltlskadyekhkvyacevthqglssptvtksfnrgec 238
RESULT 14
AAB14778
ID AAB14778 standard; Protein; 238 AA.
XX
AC AAB14778;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody light chain, SEQ ID NO:109.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; light chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-0278301.
XX
PR 30-SEP-1998; 98JP-0276883.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI: 2000-485645/43.
DR N-PSDB; AAA72177.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
PS Claim 20; Page 103; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy.

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
CC antibodies.
XX
SQ Sequence 238 AA;

Query Match 93.6%; Score 1158; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 7.7e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
Qy 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYMWY 60
Db 1 metdtillwllvpgstgeivltqspgtlsipgeratlsckasqsdvdygdsgymwy 60
Qy 61 OOKPGQAPKLLIYAASNLSESGVPSRFGSGGTDFTLTSSLOPEDFATYYCQSQSNEEDPR 120
Db 61 qkpgqaprllyaaashlesgipdrfsgsgsgtdftlihpveedaatyyccqsgnedpr 120
Qy 121 TFGQGTKEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180
Db 121 tfgggtkleikrtvaapsvfifppdsdeqlksgtasvcllnnfybreakvqwkvdnalqs 180
Qy 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqsvteqdsksdyslsstltlskadyekhkyacevthqglsppvtsksfnrgec 238

RESULT 15
AAW90928
ID AAW90928 standard; Protein; 238 AA.
XX
AC AAW90928;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed light chain protein #2.

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antifertility; neuroprotective; antirheosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
XX WPI; 2000-258930/23.
XX
XX N-PSDB; AAA11615.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems

PS
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC anti-rheumatic, nephrotropic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
CC the method described in the invention.

XX Sequence 238 AA;
SQ
Query Match 93.6%; Score 1158; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 7.7e-56;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSTYMWY 60
Db 1 metdtillwllvpgstgeivltqspgtlsipgeratlsckasqsdvdygdsgymwy 60
Qy 61 OOKPGQAPKLLIYAASNLSESGVPSRFGSGGTDFTLTSSLOPEDFATYYCQSQSNEEDPR 120
Db 61 qkpgqaprllyaaashlesgipdrfsgsgsgtdftlihpveedaatyyccqsgnedpr 120
Qy 121 TFGQGTKEIKRTVAAPSVFIFFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQS 180
Db 121 tfgggtkleikrtvaapsvfifppdsdeqlksgtasvcllnnfybreakvqwkvdnalqs 180
Qy 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqsvteqdsksdyslsstltlskadyekhkyacevthqglsppvtsksfnrgec 238

Search completed: August 14, 2002, 15:15:35
Job time: 833 sec

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0
.

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:03 ; Search time 82.88 Seconds
(without alignments)
70.141 Million cell updates/sec

Title: US-09-499-662-129

Perfect score: 1237

Sequence: 1 METDRILLWVLLLVPGSTG.....EVTHOGLSPPVTKSFNRGEC 238

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1108	89.6	218	5	PCT-US96-13152-2
2	1096	88.6	218	2	US-08-887-352B-13
3	1096	88.6	218	3	US-08-466-151-9
4	1096	88.6	218	4	US-09-109-207C-13
5	1096	88.6	218	4	US-09-296-005-13
6	1096	88.6	218	4	US-08-466-163B-9
7	1073	86.7	218	4	US-09-282-505-1
8	1073	86.7	218	4	US-09-084-255-1
9	1070	86.5	218	2	US-08-887-352B-15
10	1070	86.5	218	2	US-08-887-352B-17
11	1070	86.5	218	2	US-08-887-352B-19
12	1070	86.5	218	2	US-08-887-352B-24
13	1070	86.5	218	4	US-09-109-207C-15
14	1070	86.5	218	4	US-09-109-207C-17
15	1070	86.5	218	4	US-09-109-207C-19
16	1070	86.5	218	4	US-09-109-207C-24
17	1070	86.5	218	4	US-09-296-005-15
18	1070	86.5	218	4	US-09-296-005-17
19	1070	86.5	218	4	US-09-296-005-19
20	1070	86.5	218	4	US-09-296-005-24
21	1018.5	82.3	233	2	US-07-934-373C-25
22	1018.5	82.3	233	3	US-08-437-642B-25
23	1018.5	82.3	233	5	PCT-US93-07832-25
24	1015	82.1	214	2	US-07-934-373C-39
25	1015	82.1	214	3	US-08-437-642B-39
26	1015	82.1	214	5	PCT-US93-07832-39
27	1010	81.6	214	2	US-07-934-373C-40

28 1010 81.6 214 2 US-08-788-800-11 Sequence 11, Appl
29 1010 81.6 214 3 US-08-437-642B-40 Sequence 40, Appl
30 1010 81.6 214 3 US-09-097-309-2 Sequence 2, Appl
31 1010 81.6 214 4 US-09-097-171A-2 Sequence 2, Appl
32 1010 81.6 214 5 PCT-US93-07832-40 Sequence 40, Appl
33 1010 81.6 237 3 US-09-097-309-6 Sequence 6, Appl
34 1010 81.6 237 4 US-09-097-171A-10 Sequence 10, Appl
35 1010 81.6 237 4 US-09-422-712B-2 Sequence 2, Appl
36 1010 81.6 237 4 US-09-607-756-2 Sequence 2, Appl
37 1006.5 81.4 242 3 US-09-027-449-62 Sequence 62, Appl
38 1006.5 81.4 242 4 US-09-026-985-62 Sequence 62, Appl
39 1005.5 81.3 235 4 US-09-171-945-97 Sequence 97, Appl
40 1005.5 81.3 242 3 US-09-027-449-51 Sequence 51, Appl
41 1005.5 81.3 242 3 US-08-804-444A-51 Sequence 51, Appl
42 1005.5 81.3 242 4 US-09-026-985-51 Sequence 51, Appl
43 1002.5 81.0 219 3 US-09-027-449-72 Sequence 72, Appl
44 1002.5 81.0 219 4 US-09-026-985-72 Sequence 72, Appl
45 1002.5 81.0 242 3 US-09-027-449-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1

PCT-US96-13152-2

; Sequence 2, Application PC/TUS9613152

; GENERAL INFORMATION:

; APPLICANT: Martin, Ulrich, et al.

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; ADDRESSEE: Attn: Norman D. Hanson

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Computer Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/13152

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/578,953

; FILING DATE: 27-Dec-95

; APPLICATION NUMBER: EP 95 112 895.8

; FILING DATE: 17-Aug-95

; APPLICATION NUMBER: EP 95 114 969.9

; FILING DATE: 19-Sep-95

; ATTORNEY/AGENT INFORMATION:

; NAME: Norman D. Hanson

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; PCT-US96-13152-2

Query Match 89.6%; Score 1108; DB 5; Length 218;
Best Local Similarity 97.7%; Pred. NO. 1.6e-87;

QY 141 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200
Db 121 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4

US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123r1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 88.6%; Score 1096; DB 4; Length 218;
Best Local Similarity 97.2%; Pred. No. 1.7e-86;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGSYMNWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPFRFSGSGSGTDFTLTSSIQPEDFAFYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSGTDFTLTSSIQPEDFAFYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200
Db 121 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 88.6%; Score 1096; DB 4; Length 218;
Best Local Similarity 97.2%; Pred. No. 1.7e-86;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGSYMNWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPFRFSGSGSGTDFTLTSSIQPEDFAFYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSGTDFTLTSSIQPEDFAFYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200
Db 121 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-08-466-163B-9
; Sequence 9, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardiieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1d1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1, light chain
US-08-466-163B-9

Query Match 88.6%; Score 1096; DB 4; Length 218;
Best Local Similarity 97.2%; Pred. No. 1.7e-86;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYVDYDGSYMNWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCKASQSYVDYDGSYMNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPFRFSGSGSGTDFTLTSSIQPEDFAFYCCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGSGTDFTLTSSIQPEDFAFYCCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 200
Db 121 IFPPDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTYLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238

Db 181 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 7
US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match 86.7%; Score 1073; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 1.6e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCRASKPVDSYDGDSDSYNNWYQKPGAPKLLIYAASVLES 80
|||
Db 1 DIQLTQSPSSLSASVGRVITITCRASKPVDSYDGDSDSYNNWYQKPGAPKLLIYAASVLES 60
QY 81 GVPFRSGSGSGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140
|||
Db 61 GVPFRSGSGSGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
|||
Db 181 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 8
US-09-054-255-1
; Sequence 1, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match 86.7%; Score 1073; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 1.6e-84;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCRASKPVDSYDGDSDSYNNWYQKPGAPKLLIYAASVLES 80
|||

Db 1 DIQLTQSPSSLSASVGRVITITCRASKPVDSYDGDSDSYNNWYQKPGAPKLLIYAASVLES 60
QY 81 GVPFRSGSGSGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140
|||
Db 61 GVPFRSGSGSGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
|||
Db 181 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218

RESULT 9
US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match 86.5%; Score 1070; DB 2; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCRASKPVDSYDGDSDSYNNWYQKPGAPKLLIYAASVLES 80
|||
Db 1 DIQLTQSPSSLSASVGRVITITCRASKPVDSYDGDSDSYNNWYQKPGAPKLLIYAASVLES 60
QY 81 GVPFRSGSGSGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140
|||
Db 61 GVPFRSGSGSGDTFTLTISLQPEDFATYYCQSNEDPRTFGOGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYSLS 180
QY 201 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 238
|||

Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 10

US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-17

Query Match 86.5%; Score 1070; DB 2; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGDGYNNWYQKPGQAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGRVTITCKASRPVGDGDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQSNEDPRFTFGGKTVEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 11

US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-19

Query Match 86.5%; Score 1070; DB 2; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGDGYNNWYQKPGQAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGRVTITCKASRPVGDGDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 81 GVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQSNEDPRFTFGGKTVEIKRTVAAPSVF 140
Db 61 GVPSRFSGSGSGTDFTLTITSSLPEDFATYYCQSHEDPYTFGGTKVEIKRTVAAPSVF 120
QY 141 IFPPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 12

US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887.352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-24

Query Match 86.5%; Score 1070; DB 2; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTITCRASKQSDVDGDSYMNWYQKPGQAPKLLIYAASNLES 80
|||
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60
|||
QY 81 GVPFRFSGSGGTDTLTISSLPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
|||
Db 61 GVPFRFSGSGGTDTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
|||
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
|||

QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||

RESULT 13
US-09-109-207C-15
; Sequence 15, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 15
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-15

Query Match 86.5%; Score 1070; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTITCRASKQSDVDGDSYMNWYQKPGQAPKLLIYAASNLES 80
|||
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60
|||
QY 81 GVPFRFSGSGGTDTLTISSLPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
|||

Db 61 GVPFRFSGSGGTDTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
|||
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
|||
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||

RESULT 14
US-09-109-207C-17
; Sequence 17, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 17
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-17

Query Match 86.5%; Score 1070; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTITCRASKQSDVDGDSYMNWYQKPGQAPKLLIYAASNLES 80
|||
Db 1 DIQLTQSPSSLSASVGDRTITCRASKPVDGEGDSYLNWYQKPGKAPKLLIYAASYLE 60
|||
QY 81 GVPFRFSGSGGTDTLTISSLPEDFATYYCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
|||
Db 61 GVPFRFSGSGGTDTLTISSLPEDFATYYCQSHEDPYTFGQGTKEIKRTVAAPSVF 120
|||
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 200
|||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLS 180
|||
QY 201 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
|||
Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218
|||

RESULT 15
US-09-109-207C-19
; Sequence 19, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 19
; LENGTH: 218
; TYPE: PRT

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; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

Query Match      86.5%; Score 1070; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 2.9e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy  21 DIVLTQSPSSLASVSGDRVTITCKASQSDYDGDSDYMMWYQOKPGQAPKLLIYAASNLES 80
    |||
Db  1 DIQLTQSPSSLASVSGDRVTITCRASKPVDGSDSYLWYQOKPGKAPKLLIYAASYLES 60
    |||
Qy  81 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSQSNEDPRTFGGQTKVEIKRTVAAPSVF 140
    |||
Db  61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQSQSHEDPYTFGGQTKVEIKRTVAAPSVF 120
    |||
Qy  141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
    |||
Db  121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
    |||
Qy  201 STLTLKADYEKKHYACEVTHQGLSPVTKSFNRGEC 238
    |||
Db  181 STLTLKADYEKKHYACEVTHQGLSPVTKSFNRGEC 218
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Search completed: August 14, 2002, 15:17:03
Job time: 686 sec

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A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 60.88; Score 752; DB 2; Length 234;

Best Local Similarity 60.1%; Pred. No. 3.3e-42;
Matches 143; Conservative 35; Mismatches 56; Indels 4; Gaps 1;

QY 1 METDTILLWVLLWPGSTGDIVLTSPLSASVGDRTVITCKASQSDVDYDGDGYNNWY 60
DB 1 MRPAPFLGILLWVFGIKDKIWTSPSSWYASLGERVTVITCKASODI----NSLWSI 56
QY 61 QKPGQAPKLLIYAASNLGSGVSRFSGSGGTDFTITISSLOPEDFATYYCQSNEDPR 120
DB 57 QKPGKSPKTLIYRNLVAGVSRFSGSGGDSITISSLEVEDGVYVYCLRYDEFFP 116
QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 180
DB 117 TFGSGTKLEIKRAADAAPTIVSIFPPSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQ 176
QY 181 GNSQESVTEQDSKDSYSLSTLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 177 NGVLNSWTQDSKDSYSSSTLTLTKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 234

RESULT 10

JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-34/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 751; DB 2; Length 218;
Best Local Similarity 65.1%; Pred. No. 3.5e-42;
Matches 142; Conservative 28; Mismatches 48; Indels 0; Gaps 0;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDVDYDGDGYNNWYQKPGQAPKLLIYAASNL 80
DB 1 NIVLTQSPASLAVSLQGRATISCRASKSVASGYIYMHVYQKPGQPPKLLISLANLES 60
QY 81 GVPFRSGSGGTDFTLTITSSLOPEDFATYYCQSNEDPRTFQGTKEIKRTVAAPSVF 140
DB 61 GVPAREFGSGGTDFTLTINHPVEEDVATYYCQHSRELPLTFAGTKLEIKRAADAAPT 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
DB 121 IFPPSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTQDSKDSYSS 180
QY 201 STLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 181 STLTLTKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 218

RESULT 11

A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kente, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an anti-
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 59.0%; Score 730; DB 2; Length 220;
Best Local Similarity 62.3%; Pred. No. 8.3e-41;
Matches 137; Conservative 32; Mismatches 49; Indels 2; Gaps 1;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDVDYDGD--DSYNNWYQKPGQAPKLLIYAASNL 78
DB 1 DIVMTQSPSLVTAGEKVTMCTSSQSLSNSGKQKNLYTWYQKPGQPPKLVLIYWA 60
QY 79 ESGVPSRFSGSGGTDFTLTITSSLOPEDFATYYCQSNEDPRTFQGTKEIKRTVAAP 138
DB 61 ESGVPSRFSGSGGTDFTLTITSSVQAEADLAVYCYNDYSNPLTFEGGCKLELRADA 120
QY 139 VTFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 198
DB 121 VSIFPPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTQDSKDS 180
QY 199 LSSTLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 181 MSSTLTLTKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 220

RESULT 12

S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A:Reference number: S01320; MUID:88329081
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234 <DE1>
A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 58.6%; Score 725; DB 2; Length 234;
Best Local Similarity 57.9%; Pred. No. 1.9e-40;
Matches 139; Conservative 38; Mismatches 55; Indels 8; Gaps 2;

QY 1 METDTILLWVLLWPGSTGDIVLTSPLSASVGDRTVITCKASQSDVDYDGDGYNN-- 58
DB 1 MSVPTQVLGLLLWLTDAKDQIOMTQSPASLSVSGESVITCRASENI-----YSNLA 54
QY 59 WYQKPGQAPKLLIYAASNLGSGVSRFSGSGGTDFTLTITSSLOPEDFATYYCQSNED 118
DB 55 WYQKPGKSPQLLYVYATKLVGVPFRFSGSGGTQYSLKINSLSQSDFGSYCQHWDT 114
QY 119 PRTFQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 178
DB 115 PRTFSGTKLEIKRAADAAPTIVSIFPPSEQLTSGGASVVCFLNFPYKIDINVKWKID 174
QY 179 QSGNSQESVTEQDSKDSYSLSTLTSLKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 175 RQNGVLNSWTQDSKDSYSSSTLTLTKDEYERHNSYTCETHATKSTSPIVKSFNRNEC 234

RESULT 13

A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C;Accession: A56169
R;Moffardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454
A;Accession: A56169
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-210 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 58.4%; Score 722; DB 2; Length 210;
Best Local Similarity 65.6%; Pred. No. 2.6e-40;
Matches 137; Conservative 27; Mismatches 45; Indels 0; Gaps 0;
Qy 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGD SYMNWYQKPGQAPKLLIYAASNLES 80
Db 1 DIVLTQSPASLTSLGQRATISCRASKSVSSGYSYMHWYQKPGQPKVLIYLAASNLES 60
Qy 81 GVPFRFSGSGGTDTLTITSLQPEDPATYCCQSNEDPRTFGOGTKVEIKRTVAAPSVF 140
Db 61 GVPFRFSGSGGTDTLTINHPVEEDAATYICQHSRELPTWTFGGTRLEIKRADAAPTVS 120
Qy 141 IFPPSDQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLS 200
Db 121 IFPPSEQLTSGGASVYVCLNFFPKDINVKWKIDGSEKQNGVLSWTDQDSKDSYMS 180
Qy 201 STLTLSKADYEKHKVYACEVTHQGLSPV 229
Db 181 STLTLTDEYERHNSYTCETHKTSTSPI 209

RESULT 14
S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 58.2%; Score 720.5; DB 2; Length 225;
Best Local Similarity 62.3%; Pred. No. 3.5e-40;
Matches 142; Conservative 28; Mismatches 53; Indels 5; Gaps 2;
Qy 11 LLLVWPGSTGDIVLTQSPSSLSASVGRVITITCKASQSDYDGD SYMNWYQKPGQAPKL 70
Db 3 LLLCVSGAHGSIYMTQPKFLLISAGRVITITCKASQSVND---VANWYQKPGQSPKL 58
Qy 71 LIYAASNLESGVPRFSGSGGTDTLTITSLQPEDPATYCCQSNEDPRTFGOGTKVEI 130
Db 59 LIYYASSRYTGVPDRFGSGVGTDTFTISTVQAEDLAVYFCQQ-DYSSVTFGGGTKLEI 117
Qy 131 KRTVAAPSVIFPPSDQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQ 190
Db 118 KRADAAPTIVSIFPPSEQLTSGGASVYVCLNFFPKDINVKWKIDGSEKQNGVLSWTDQ 177
Qy 191 DSKDSTYLSLSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 178 DSKDSTYMSSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNREC 225

RESULT 15
PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A;Reference number: PC4202; MUID:97082978
A;Accession: PC4203
A;Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:gl594225; PIDN:AAC52821.1; PID:gl594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

Query Match 57.7%; Score 713.5; DB 2; Length 219;
Best Local Similarity 60.3%; Pred. No. 9.7e-40;
Matches 132; Conservative 36; Mismatches 50; Indels 1; Gaps 1;
Qy 21 DIVLTQSPSSLSASVGRVITITCKASQSDY-DGD SYMNWYQKPGQAPKLLIYAASNLE 79
Db 1 DVLMTQTPLSLPVSLGDAQISCRSSQSIHTNGNTYLEWYLQKPGQSPKLLIYKVSNR 60
Qy 80 SGVPSRFSGSGGTDTLTITSLQPEDPATYCCQSNEDPRTFGOGTKVEIKRTVAAPSV 139
Db 61 SGVPDRFSGSGGTDTLTIKSRVEAEDLGVIYCFQGSHPRTFGGTGKLEIKRADAAPT 120
Qy 140 FIFPPSDQLKSGTASVYVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 199
Db 121 SIFPPSEQLTSGGASVYVCLNFFPKDINVKWKIDGSEKQNGVLSWTDQDSKDSYMS 180
Qy 200 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 181 SSTLTLTDEYERHNSYTCETHKTSTSPIVKSFNREC 219

Search completed: August 14, 2002, 15:18:59
Job time: 687 sec

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:13 ; Search time 53.64 Seconds
(without alignments)
171.798 Million cell updates/sec

Title: US-09-499-662-129

Perfect score: 1237

Sequence: 1 METDTILLWVLLWVPGSTG.....EVTHOGLSSPVTKSFNRGEC 238

Scoring table:
BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	548	44.3	106	1 KAC_HUMAN	P01834 homo sapien
2	536	43.3	131	1 KV3I_MOUSE	P01661 mus musculus
3	521	42.1	132	1 KV3F_MOUSE	P01658 mus musculus
4	487	39.4	111	1 KV3M_MOUSE	P01665 mus musculus
5	485	39.2	111	1 KV3N_MOUSE	P01666 mus musculus
6	483	39.0	111	1 KV3O_MOUSE	P01667 mus musculus
7	482.5	39.0	129	1 KV3L_HUMAN	P18135 homo sapien
8	480	38.8	111	1 KV3Q_MOUSE	P01669 mus musculus
9	476	38.5	129	1 KV1W_HUMAN	P04431 homo sapien
10	472	38.2	111	1 KV3L_MOUSE	P01664 mus musculus
11	462.5	37.4	110	1 KV3P_MOUSE	P01668 mus musculus
12	460.5	37.2	129	1 KV3M_HUMAN	P18136 homo sapien
13	457	36.9	108	1 KV1H_HUMAN	P01600 homo sapien
14	452	36.5	134	1 KV4C_HUMAN	P06314 homo sapien
15	449	36.3	108	1 KV1M_HUMAN	P01605 homo sapien
16	448	36.2	108	1 KV1G_HUMAN	P01599 homo sapien
17	444	35.9	108	1 KV1K_HUMAN	P01603 homo sapien
18	442	35.7	108	1 KV1B_HUMAN	P01594 homo sapien
19	441	35.7	108	1 KV1E_HUMAN	P01597 homo sapien
20	441	35.7	108	1 KV1F_HUMAN	P01598 homo sapien
21	441	35.7	108	1 KV1N_HUMAN	P01606 homo sapien
22	440	35.6	111	1 KV3H_MOUSE	P01660 mus musculus
23	438	35.4	108	1 KV1V_HUMAN	P04430 homo sapien
24	437	35.3	108	1 KV1A_HUMAN	P01593 homo sapien
25	437	35.3	117	1 KV1J_HUMAN	P01602 homo sapien
26	436.5	35.3	133	1 KV4B_HUMAN	P06313 homo sapien
27	435.5	35.2	129	1 KV3H_HUMAN	P04207 homo sapien
28	434	35.1	108	1 KV1Y_HUMAN	P80362 homo sapien
29	431	34.8	108	1 KV1Q_HUMAN	P01607 homo sapien
30	431	34.8	111	1 KV3J_MOUSE	P01662 mus musculus
31	430	34.8	108	1 KV1P_HUMAN	P01608 homo sapien
32	430	34.8	111	1 KV3K_MOUSE	P01663 mus musculus
33	429	34.7	108	1 KV1R_HUMAN	P01610 homo sapien

RESULT 1

ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig kappa chain C region..			
GN	IGKC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064023; PubMed=5489770;			
RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";			
RL	Biochemistry 9:3155-3161(1970).			
RN	[2]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			
RL	Biochemistry 9:3188-3196(1970).			
RN	[3]			
RP	SEQUENCE (BENCE-JONES PROTEIN TI).			
RX	MEDLINE=72188439; PubMed=5027703;			
RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;			
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81042304; PubMed=6775818;			
RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;			
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";			
RL	Cell 22:197-207(1980).			
RN	[5]			
RP	SEQUENCE (BENCE-JONES PROTEIN ROY).			
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;			
RL	(In) Franek F., Shugar D. (eds.);			
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).			
RN	[6]			
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).			
RX	MEDLINE=68242259; PubMed=5586923;			
RA	Hilschmann N.;			
RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";			

ALIGNMENTS

34	429	34.7	128	1 KV3K_HUMAN	P06311 homo sapien
35	426	34.4	111	1 KV3R_MOUSE	P01670 mus musculus
36	425	34.4	108	1 KV1S_HUMAN	P01611 homo sapien
37	425	34.4	129	1 KV1X_HUMAN	P04432 homo sapien
38	421.5	34.1	109	1 KV1T_HUMAN	P01612 homo sapien
39	420.5	34.0	133	1 KV2F_HUMAN	P06310 homo sapien
40	420	33.8	115	1 KV3I_HUMAN	P04433 homo sapien
41	418	33.8	108	1 KV1L_HUMAN	P01604 homo sapien
42	418	33.8	111	1 KV3S_MOUSE	P01671 mus musculus
43	416	33.6	108	1 KV1O_HUMAN	P01609 homo sapien
44	415.5	33.6	107	1 KV1D_HUMAN	P01596 homo sapien
45	415	33.5	112	1 KV3G_MOUSE	P01659 mus musculus

```
RL Hoppe-Seyley's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS; THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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DR EMBL: J00241; AAA58989.1; -
DR EMBL: V00557; CAA23823.1; -
DR PIR: A02116; K3HU.
DR HSSP: P01842; 7FAB.
DR MIM: 147200; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00407; Igcl; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIG=VAR_003897.
FT CONFLICT 14 14
FT CONFLICT 57 57
FT CONFLICT 57 57
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 44.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.5e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 133 TVAPSVFFPPSDEQLKSTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDS 192
DB 1 TVAPSVFFPPSDEQLKSTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDS 60
QY 193 KOSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
DB 61 KOSTYLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 106
RESULT 2
KV3F_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
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RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR: A01935; KVM5M6.
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131
FT DOMAIN 21 43
FT DOMAIN 44 58
FT DOMAIN 59 73
FT DOMAIN 74 80
FT DOMAIN 81 112
FT DOMAIN 113 121
FT DOMAIN 122 131
FT DISULFID 43 112
FT NON_TER 131 131
FT SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
SQ
Query Match 43.3%; Score 536; DB 1; Length 131;
Best Local Similarity 76.3%; Pred. No. 3e-36;
Matches 100; Conservative 17; Mismatches 14; Indels 0; Gaps 0;
QY 1 METDTILLWVLLWVPGSGDIVLTQSPSLSASVGDVRVITCKASQSDYDGDSDYNNWY 60
DB 1 METDTILLWVLLWVPGSGTGNIVLTQSPASLAVSLGORATISCRASESDVSGNSFMHWY 60
QY 61 QOKPGQAPKLLIYAASNLGSGVPSRFGSGGTDFTLTISLSLOPEDFATYTCQSNEDPR 120
DB 61 QOKPGQAPKLLIYLANLGSQVPSRFGSGGRTDFTLTIDPVEADDAATYTCQNNEDPW 120
QY 121 TFGQGTKEIK 131
DB 121 TFGGQGTKEIK 131
RESULT 3
KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
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RN  SEQUENCE OF 1-37.
RX  MEDLINE=7823587; PubMed=98179;
RA  Burstein Y., Schechter I.;
RT  "Primary structures of N-terminal extra peptide segments linked to
RT  the variable and constant regions of immunoglobulin light chain
RT  precursors: implications on the organization and controlled
RT  expression of immunoglobulin genes.";
RL  Biochemistry 17:2392-2400(1978).
RN  SEQUENCE OF 21-132.
RX  MEDLINE=7314024; PubMed=4120629;
RA  McKean D.J., Potter M., Hood L.E.;
RT  "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT  chain.";
RL  Biochemistry 12:749-759(1973).
CC  -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC  BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC  REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC  RESIDUES.
DR  PIR; A01933; KVM532.
DR  HSSP; P01607; IREI.
DR  InterPro; IPR003006; Ig_MHC.
DR  InterPro; IPR003596; Ig_V.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; IgV; 1.
KW  Immunoglobulin V region; Bence-Jones protein; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT  DOMAIN 21 43 FRAMEWORK-1.
FT  DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 59 73 FRAMEWORK-2.
FT  DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 81 112 FRAMEWORK-3.
FT  DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 122 131 FRAMEWORK-4.
FT  DISULFID 43 112 BY SIMILARITY.
FT  NON_TER 132 132
SQ  SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 42.18; Score 521; DB 1; Length 132;
Best Local Similarity 68.28; Pred. No. 4.7e-35;
Matches 90; Conservative 27; Mismatches 15; Indels 0; Gaps 0;

Qy 1 METDTILLVLLWLVPGSTGDIVLTQSPSSLSASVGRVITTCRASQSDVDGDSYMMWY 60
Db 1 METDTLLVLLWLVPGSTGDIVLTQSPASLAVSLGQRATISCRASKSVNTYGNFMZWY 60

Qy 61 QOKPGQAPKLIYASNLSEGVSRFSGSGSDTFTLTISLQPEDFATYYCQSQSNEDPR 120
Db 61 ZZKPGCPKLIYASNLZSGIPARFSGSGSRBTBTLTBVPZABDVATYFCZZSB2BFW 120

Qy 121 TFGGQTKVEIKR 132
Db 121 TFGSGTKLEIKR 132

RESULT 4
KV3M_MOUSE
ID KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT  DOMAIN 1 23
FT  DOMAIN 24 38
FT  DOMAIN 39 53
FT  DOMAIN 54 60
FT  DOMAIN 61 92
FT  DOMAIN 93 101
FT  DOMAIN 102 111
FT  DISULFID 23 92
FT  NON_TER 111 111
SQ  SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
"Rearrangement of genetic information may produce immunoglobulin
diversity.";
Nature 276:785-790(1978).
PIR; A01937; KVM543.
HSSP; P01789; IMCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT  DOMAIN 1 23
FT  DOMAIN 24 38
FT  DOMAIN 39 53
FT  DOMAIN 54 60
FT  DOMAIN 61 92
FT  DOMAIN 93 101
FT  DOMAIN 102 111
FT  DISULFID 23 92
FT  NON_TER 111 111
SQ  SEQUENCE 111 AA; 12002 MW; 7A5FCB586C306D29 CRC64;

Query Match 39.4%; Score 487; DB 1; Length 111;
Best Local Similarity 82.0%; Pred. No. 2e-32;
Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVITTCRASQSDVDGDSYMMWYQKPGAPKLLIYASNLSE 80
Db 1 DIVLTQSPASLAVSLGQRATISCRASKSQSDVDGDSYMMWYQKPGPPKLLIYASNLSE 60

Qy 81 GVPSRFSGSGSDTFTLTISLQPEDFATYYCQSQSNEDPRTFGQGTKEIK 131
Db 61 GIPARFSGSGSDTFTLTNIHPVEEDAATYYCQSQSNEDPFTFGSGTKLEIK 111

RESULT 5
KV3N_MOUSE
ID KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR PIR; B01937; KVM583.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT  DOMAIN 1 23
FT  DOMAIN 24 38
FT  DOMAIN 39 53
FT  DOMAIN 54 60
FT  DOMAIN 61 92
FT  DOMAIN 93 101
FT  DOMAIN 102 111
FT  DISULFID 23 92
FT  NON_TER 111 111
SQ  SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;
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Query Match      39.2%; Score 485; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 2.8e-32;
Matches 90; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGDSTYNNYQKPGQAPKLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTYNNYQKPGQAPKLLIYAASNLES 60

QY 81 GVPFRSGSGSGTDFLTITSSLPQEPFATYCCQSNEDPRTFGQGNKVEIK 131
DB 61 GIPARFSGSGSGTDFLTINHPVEEDAAATYCCQSNEDPRTFGAGTKLEIK 111

RESULT 6
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM508.
DR HSSP: P01789; LMCP.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match      39.0%; Score 483; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 4.1e-32;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGDSTYNNYQKPGQAPKLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGORATISCKASQSDYDGDSTYNNYQKPGQAPKLLIYTASNLES 60

QY 81 GVPFRSGSGSGTDFLTITSSLPQEPFATYCCQSNEDPRTFGQGNKVEIK 131
DB 61 GIPARFSGSGSGTDFLTINHPVEEDAAATYCCQSNEDPRTFGAGTKLEIK 111

RESULT 7
KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR: PL0022; K3HUHA.
DR HSSP: P01789; LMCP.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;

Query Match      39.0%; Score 482.5; DB 1; Length 129;
Best Local Similarity 69.7%; Pred. No. 5.4e-32;
Matches 92; Conservative 16; Mismatches 21; Indels 3; Gaps 1;

QY 1 METDTILLWLLVLLWPGSGDIVLTQSPSSLSASVGRVTITCKASQSDYDGDSTYNNY 60
DB 1 METPAQLLFLLLLWLPDITGTEIVLTQSPGTLSPGERATLSCRASQSV---SSSYLAWY 57

QY 61 QKQPGQAPKLLIYAASNLESQVPSRFSGSGSGTDFLTITSSLPQEPFATYCCQSNEDPR 120
DB 58 QKQPGQAPRLIYVASSRATGIPDRFSGSGSGTDFLTITSRLEPEDFAVYVCOQYGTSPR 117

QY 121 TFGQGTKEIKR 132
DB 118 TFGQGTKEIKR 129

RESULT 8
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: E01937; KVM569.
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DR HSP: P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 38.8%; Score 480; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 7.1e-32;
Matches 89; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWYQOKPGQAPKLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQOKPGQAPKLLIYAASNLES 60
QY 81 GVPFRFGSGSGTDFTLTISSLPEDFATYYCQSNEDPRTFGQGTKEIK 131
DB 61 GIPARFSGSGTDFTLNIHPVEEDAATYYCQSNEDPRTFGSGTKLEIK 111

RESULT 9
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P0431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combratio G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related."
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUK.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129
FT DOMAIN 23 45
FT DOMAIN 23 45
FT DOMAIN 46 56
FT DOMAIN 57 71
FT DOMAIN 72 78
IG KAPPA CHAIN V-I REGION WALKER.
FRAMEWORK-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-1.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
FRAMEWORK-4.
BY SIMILARITY.
Gaps 0;
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FT DOMAIN 79 110
FT DOMAIN 111 119
FT DOMAIN 120 129
FT DISULFID 45 110
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 38.5%; Score 476; DB 1; Length 129;
Best Local Similarity 73.3%; Pred. No. 1.8e-31;
Matches 96; Conservative 13; Mismatches 18; Indels 4; Gaps 1;

QY 1 METDTILLWLLVPGSTGDIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWY 60
DB 3 MRVPAQLLGLLLWLRGARCIDIQTQSPSSLSASVGRVITITCKASQSI----SNLWNY 58
QY 61 QOKPGQAPKLLIYAASNLESVPSRFGSGSGTDFTLTISSLPEDFATYYCQSNEDPRT 120
DB 59 QOKPGKAPKLLIYAASLSQSGVTSRFGSGSGTDFTLTISSLPEDSATYYCQSYSTLI 118
QY 121 TFGQGTKEIK 131
DB 119 TFGQGTKEIK 129

RESULT 10
KV3L_MOUSE STANDARD; PRT; 111 AA.
ID KV3L_MOUSE
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVMSC1.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BLAD98AD965962 CRC64;

Query Match 38.2%; Score 472; DB 1; Length 111;
Best Local Similarity 79.3%; Pred. No. 3.1e-31;
Matches 88; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVITITCKASQSDYDGDSDYNNWYQOKPGQAPKLLIYAASNLES 80
DB 1 DIVLTQSPASLAVSLGQRATISCKASQSDYDGDSDYNNWYQONPGQSPKLLIYAASNLES 60
QY 81 GVPFRFGSGSGTDFTLTISSLPEDFATYYCQSNEDPRTFGQGTKEIK 131
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Query Match      37.4%; Score 462.5; DB 1; Length 110;
Best Local Similarity 79.3%; Pred. No. 1.7e-30;
Matches 88; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

QY   21 DIVLTQSPSSLSASVGDRVTITCKASQSDVDGSYNNWYQQKGPAPKLIIYAASNLES 80
Db    1 DIVLTQSPASVLSLGRATISCKASQSLDYGDSYNWYQQKGPQPPLIYAASNLES 60
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY   81 GVPSRFSGSGLTFTLTITISLPQDEPATYYCOQSNEPRTFFGGTKVEIK 131
Db    1 : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY   61 GIPARFSGSGTDFTLNHIHPVEEDAATYYCHQS-EDPWTFGSSTKLEIK 110
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12
KV3M_HUMAN
ID KV3M_HUMAN STANDARD; PRT; 129 AA.
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IIJ region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RM MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
```

ET	DOMAIN	24	34	COMPLEMENTARITY-DETERMINING-1.
FT	DOMAIN	35	49	FRAMEWORK-2.
FT	DOMAIN	50	56	COMPLEMENTARITY-DETERMINING-2.
FT	DOMAIN	57	88	FRAMEWORK-3.
FT	DOMAIN	89	97	COMPLEMENTARITY-DETERMINING-3.
FT	DOMAIN	98	107	FRAMEWORK-4.
FT	DISULFID	23	88	BY SIMILARITY.
FT	NON_TER	108	108	
SQ	SEQUENCE	108 AA:	11671 MW:	08D3A61608D8D0618 CRC64:

		Query Match	36.9%	Score 457;	DB 1;	Length 108;
		Best Local Similarity	79.5%;	Pred. No. 4.7e-30;		
		Matches	89;	Conservative	12;	Mismatches 7;
					Indels	4; Gaps
						1;
Qy	21	DIVITQTSPSSLSASVGDRTVTTCRASQSVVDYDGSYMNWYQQKPGQPAPKLIIYAASNLES	80			
		: :				
Db	1	DIQMTQSPSSLSASVGDRTVTTCRASQSI-----SSYLSSWYQQKPKAPQVLIIYAASLPS	56			
Qy	81	GVPFRFSGSGGTDFTLTIISSLQPEDPATYYCQQSNEDPRFTGGTKVKEIKR	132			
Db	57	GVPFRFSGSGGTDFTLTIISSLQPEDPATYYCQONYIPTPTSFGRGTRVEIKR	108			

RESULT	14
KV4C_HUMAN	
ID	KV4C.HUMAN STANDARD; PRT; 134 AA.
DI	P06314;
DT	01-JAN-1988 (Rel. 06, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig kappa chain V-IV region B17 precursor.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RX	SEQUENCE FROM N.A.
RX	MEDLINE=86041854; PubMed=2997713;
RA	Marsh P., Mills F., Gould H.;
RT	"Detection of a unique human V kappa IV germline gene by a cloned
RT	cDNA probe."
RL	Nucleic Acids Res. 13:6531-6544(1985).
RN	[2]
RP	REVISION TO 76.
RA	Marsh P.;
RL	Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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EMBL: X02990; CAA26733.1; -.
PIR: A01905; K4HU17.
HSP: P01789; IMCP.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam: PF00047; Ig: 1.
SMART: SM00406; Igv: 1.
Immunoglobulin V region; Signal.
-----
              1      20
FT  CHAIN      21  134
FT  DOMAIN     41  43
FT  FT         44  60
FT  DOMAIN     61  75
FT  DOMAIN     76  82
FT  DOMAIN     83  114
FT  DOMAIN     115  121
FT  DOMAIN     122  133
FT  DOMAIN

```

[illegible]

RESULT	15			
ID	KV1M_HUMAN	STANDARD;	PRT;	108 AA.
AC	P01605;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	15-JUL-1999	(Rel. 38, Last annotation update)		
DE	Ig kappa chain V-I region Lay.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
{1}	RN			
RP	SEQUENCE.			
RX	MEDLINE=77038198; PubMed=824717;			
RA	Capra J.D., Klapper D.G.;			
RT	"Complete amino acid sequence of the variable domains of two human			
RT	IgM anti-gamma globulins (Lay/Pom) with shared idiotype			
RT	specificities.";			
RL	Scand. J. Immunol. 5:677-684(1976).			
CC	-1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS			
CC	CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,			
CC	WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.			
CC	-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA			
CC	GLOBULIN ACTIVITY.			

DR	PTB: A01871; KIHULY.	
DR	HSP; P01607; IREI.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_V.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	Immunoglobulin V region.	
KW		
FT	DOMAIN	1
FT	DOMAIN	23
FT	DOMAIN	24
FT	DOMAIN	34
FT	DOMAIN	35
FT	DOMAIN	49
FT	DOMAIN	50
FT	DOMAIN	56
FT	DOMAIN	57
FT	DOMAIN	89
FT	DOMAIN	97
FT	DOMAIN	98
FT	DOMAIN	107
FT	DISULFID	23
FT	NON_TER	88
FT	SEQUENCE	108
SQ	SEQUENCE	108 AA; 118334 MW; 739993A95431434A CRC64;

[illegible]

Qy 81 GVPFRFSGSGTDFTLTIISSLPEDFATYYCQSNEDPRTFGQTKVEIKR 132
|||||
Db 57 GVPFRFSGSGTDFTLTIISSLPEDATYYCQYNNWPTFGQTKVEIKR 108
|||||

Search completed: August 14, 2002, 15:23:13
Job time: 686 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:14 ; Search time 187.61 Seconds
(without alignments)
219.459 Million cell updates/sec

Title: US-09-499-662-129

Perfect score: 1237

Sequence: 1 METDTILLWLLLVPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750.5	60.7	238	11 Q99M37	Q99M37 mus musculus
2	739	59.7	234	11 Q91WF8	Q91WF8 mus musculus
3	738	59.7	233	11 Q91WS9	Q91WS9 mus musculus
4	721	58.3	214	11 Q9RIA5	Q9RIA5 mus musculus
5	705.5	57.0	235	11 Q91W12	Q91W12 mus musculus
6	700	56.6	211	11 Q91XL0	Q91XL0 mus musculus
7	467	37.8	108	4 Q9UL77	Q9UL77 homo sapien
8	459.5	37.1	107	4 Q96SA9	Q96SA9 homo sapien
9	446	36.1	108	4 Q9UL70	Q9UL70 homo sapien
10	434.5	35.1	107	4 Q9UL81	Q9UL81 homo sapien
11	434	35.1	116	4 Q96PF6	Q96PF6 homo sapien
12	433	35.0	108	4 Q9UL79	Q9UL79 homo sapien
13	430.5	34.8	235	11 Q99M11	Q99M11 mus musculus
14	429	34.7	236	4 Q96E61	Q96E61 homo sapien
15	419	33.9	111	11 Q920E9	Q920E9 mus musculus
16	398.5	32.2	109	4 Q9UL78	Q9UL78 homo sapien

17	386.5	31.2	233	4	Q96I69	Q96I69 homo sapien
18	384	31.0	108	4	Q9UL83	Q9UL83 homo sapien
19	378	30.6	233	11	Q91V32	Q91V32 m adult mal
20	375.5	30.4	109	4	Q9UL86	Q9UL86 homo sapien
21	375.5	30.4	109	4	Q9UL85	Q9UL85 homo sapien
22	375	30.3	238	11	Q9QYF0	Q9QYF0 mus musculus
23	370	29.9	103	11	Q9UL80	Q9UL80 mus musculus
24	361	29.2	109	11	Q920E6	Q920E6 mus musculus
25	354	28.6	114	4	Q9UL80	Q9UL80 homo sapien
26	351	28.4	127	11	Q925S9	Q925S9 mus musculus
27	350	28.3	107	11	Q9ER29	Q9ER29 mus musculus
28	349	28.2	99	11	Q9JL74	Q9JL74 mus musculus
29	346.5	28.0	106	5	Q9U410	Q9U410 schistosoma
30	335	27.1	101	11	Q9JL78	Q9JL78 mus musculus
31	328	26.5	97	11	Q9JL76	Q9JL76 mus musculus
32	325.5	26.3	104	11	Q9JL82	Q9JL82 mus musculus
33	324.5	26.2	241	11	Q921A6	Q921A6 mus musculus
34	302	24.4	109	6	Q9N0W5	Q9N0W5 oryctolagus
35	297	24.0	107	11	Q9JL84	Q9JL84 mus musculus
36	279.5	22.6	218	11	Q925S1	Q925S1 mus musculus
37	247	20.0	107	4	Q9UL82	Q9UL82 homo sapien
38	242.5	19.6	107	4	Q9NSD6	Q9NSD6 homo sapien
39	236.5	19.1	108	4	Q96SB0	Q96SB0 homo sapien
40	236	19.1	130	4	Q9NP29	Q9NP29 homo sapien
41	225	18.2	130	11	Q9B8W4	Q9B8W4 mus musculus
42	215	17.4	112	4	Q96JD1	Q96JD1 homo sapien
43	212	17.1	267	13	Q90529	Q90529 ginglymosto
44	208.5	16.9	112	4	Q96JD2	Q96JD2 homo sapien
45	207.5	16.8	116	4	Q96JD0	Q96JD0 homo sapien

ALIGNMENTS

RESULT 1
Q99M37 ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC TISSUE.;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -;
DR HSSP; P01679; 2FBJ
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 60.7%; Score 750.5; DB 11; Length 238;
Best Local Similarity 59.0%; Pred. No. 1e-57;
Matches 138; Conservative 39; Mismatches 56; Indels 1; Gaps 1;

QY	6	ILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYD-DGDSYMNWYQOKP	64
Db	5	VRLLVLMFWIPASSDVMWTPQLSLPVLGQASISQSVHSNGNTVLEWYLOKP	64
QY	65	GOAPKLLIYAASNLSEGVPSRFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFQ	124
Db	65	GOSPGLLIYKVNRFSGVPSRFGSGSGTDFLTISRVAEDLVGVYFCQGHVPYFGS	124
QY	125	GKVEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKNALQSGNSQ	184
Db	125	GKLEIKRADAAPTVSIIPPSPDEQLKSGTASVVCFLNNFYPKDINVKWIDGSEKQNGVL	184
QY	185	ESVTEODSKDSYSSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	238
Db	185	NSWTQDSKDSYSSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRNEC	238
RESULT	2		
QY1WF8		PRELIMINARY; PRT; 234 AA.	
AC	Q91WF8;		
DT	01-DEC-2001 (TRENBLrel. 19, Created)		
DT	01-DEC-2001 (TRENBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TRENBLrel. 19, Last annotation update)		
DE	HYPOTHETICAL 25.9 KDA PROTEIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=COLON;		
RA	Strausberg R.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC015292; AAH15292.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;		
Query Match	59.7%;	Score 739;	DB 11; Length 234;
Best Local Similarity	60.1%;	Pred. No. 1e-56;	
Matches	143;	Conservative 33;	Mismatches 58; Indels 4; Gaps 1;
QY	1	METDILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDYMNWY	60
Db	1	MMSSAQFLGLLILCFQGTCDIQMTTSSLSASLGDRVTISCRASQDI----SNLWNY	56
QY	61	QOKPGQAPKLLIYAASNLSEGVPSRFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPR	120
Db	57	QOKPGTAKLLIYTRSLVGVPSRFGSGSGTDFLTISNLEQEDFATYFCQGNTPPF	116
QY	121	TFGQGTKEIKRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKNALQ	180
Db	117	TFGSGTKLEVKRADAAPTVSIIPPSPDEQLKSGTASVVCFLNNFYPKDINVKWIDGSE	176
QY	181	GNQSVTEQDSKDSYSSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	238
Db	177	NGVLNSWTQDSKDSYSSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRNEC	234
RESULT	3		
QY1WS9		PRELIMINARY; PRT; 233 AA.	
AC	Q91WS9;		
DT	01-DEC-2001 (TRENBLrel. 19, Created)		
DT	01-DEC-2001 (TRENBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TRENBLrel. 19, Last annotation update)		
DE	HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		

RP	SEQUENCE FROM N.A.		
RC	TISSUE=COLON;		
RA	Strausberg R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC013496; AAH13496.1; -		
KW	Hypothetical protein.		
FT	NON_TER 1		
SQ	SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;		
Query Match	59.7%;	Score 738;	DB 11; Length 233;
Best Local Similarity	63.2%;	Pred. No. 1.2e-56;	
Matches	144;	Conservative 28;	Mismatches 52; Indels 4; Gaps 1;
QY	11	LLLVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDYMNWYQOKPGAPKL	70
Db	10	LLLCFQSGKCDIQMTTSSLSASLGDRVTISCSQGI----ANYLWYQKPDGTVKL	65
QY	71	LIYAASNLSEGVPSRFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQPKVEI	130
Db	66	LIYTTSSLHSGVPSRFGSGSGTDFLTISNLEPEDFATYYQVRYLPWTFGGGTKLEI	125
QY	131	KRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNNFYPREAKVQWKNALQSGNSQSVTEQ	190
Db	126	KRAAAPTIVFIIPPSPDEQLKSGTASVVCFLNNFYPKDINVKWIDGSEKQNGVLNSWTQ	185
QY	191	DSKDTYSSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC	238
Db	186	DSKDTYSSSTLTLSKADYKHKVYACEVTHQGLSPVTKSFNRNEC	233
RESULT	4		
QY1A5		PRELIMINARY; PRT; 214 AA.	
AC	Q91A5;		
DT	01-MAY-2000 (TRENBLrel. 13, Created)		
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TRENBLrel. 19, Last annotation update)		
DE	KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Wildie K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;		
RT	"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF152371; AAD40242.1; -		
DR	HSSP; P01679; 2FBJ.		
DR	InterPro; IPR003600; Ig_Like.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig; 2.		
DR	SMART; SM00406; IGV; 1.		
DR	SMART; SM00410; IG_Like; 1.		
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.		
FT	NON_TER 1		
FT	NON_TER 214		
SQ	SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;		
Query Match	58.3%;	Score 721;	DB 11; Length 214;
Best Local Similarity	62.8%;	Pred. No. 3.3e-55;	
Matches	137;	Conservative 31;	Mismatches 46; Indels 4; Gaps 1;
QY	21	DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDYMNWYQOKPGAPKLLIYAASNLSE	80
Db	1	DIOLTQSPSSMYASLGERTVITCKASQDI----NSYLSWFQOKPGKSPKTLIYRANRLVD	56
QY	81	GVPSRFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQPKVEIKRTVAAPSVF	140

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||||| 57 GVPFRFSGSGSQDYSLTISLEVEDMGYYCLQYDEFFTFGGTGKLEIKRADAPTVS 116
||||| 141 IFPPSDEOLKSGTASVVCLLNNFYPREAKVQMYDNALQSGNSQESVTEQDQSKDSTYSLS 200
||||| 117 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSNWTQDQSKDSTYSMS 176
QY 201 STLTLKADYEHKKYACEVTHQGLSPVTKSFNRGEC 238
Db 177 STLTLKDEYERHNSYTCETHKTKTSTPIVKCFNRNEC 214

RESULT 5
Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:6582).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AAH06643.1; -.
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 57.0%; Score 705.5; DB 11; Length 235;
Best Local Similarity 61.1%; Pred. No. 8.5e-54;
Matches 135; Conservative 31; Mismatches 50; Indels 5; Gaps 1;

QY 18 STGDIVLTQSPSSLSASVGRVTTTCASQVDYDGSYNNWYQKQGPAPKLIYAASN 77
Db 20 SRGQIVLTQSPALMSASPGERVTTTCASSSV-----SHMHYQKSGTSPKRIYDTFK 74
QY 78 LESGVPFRFSGSGSTDTFTLTISLQDPFATYQCQSNEDPRTFGGQTKVEIKRTVAAP 137
Db 75 LTSGVPRFSGSGSTGTSIFSLISNMEADVATYTCQWSRNPFTGVTGKLELRADAAP 134
QY 138 SVFIFFPSDEOLKSGTASVVCLLNNFYPREAKVQMYDNALQSGNSQESVTEQDQSKDSTY 197
Db 135 TVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSNWTQDQSKDSTY 194
QY 198 SLSTLTLSKADYEHKKYACEVTHQGLSPVTKSFNRGEC 238
Db 195 SMSSTLTLTKDEYERHNSYTCETHKTKTSTPIVKCFNRNEC 235

RESULT 6
Q91XL0 PRELIMINARY; PRT; 211 AA.
AC Q91XL0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

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RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda K., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Numata K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai K., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL: AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 56.6%; Score 700; DB 11; Length 211;
Best Local Similarity 61.3%; Pred. No. 2.2e-53;
Matches 133; Conservative 33; Mismatches 43; Indels 8; Gaps 2;

QY 24 LTQSPSSLSASVGRVTTTCASQVDYDGSYNN--WYQKQGPAPKLIYAASNLESG 81
Db 1 MTQSPASLSVSVGETVTTTCRASENI-----YSLNLAWYQKQKSPOLLVYATNLDAG 54
QY 82 VPSRFSGSGSTDTFTLTISLQDPFATYQCQSNEDPRTFGGQTKVEIKRTVAAPSVEFI 141
Db 55 VPSRFSGSGSTQYSLKINSQSEDFSGYFCQHFHWGTPRTFGGQTKLEIKRADAAPTYSI 114
QY 142 FPPSDEOLKSGTASVVCLLNNFYPREAKVQMYDNALQSGNSQESVTEQDQSKDSTYSLS 201
Db 115 FPPSSEQLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSNWTQDQSKDSTYSMS 174
QY 202 TLTLSKADYEHKKYACEVTHQGLSPVTKSFNRGEC 238
Db 175 TLTLTKDEYERHNSYTCETHKTKTSTPIVKCFNRNEC 211

RESULT 7
Q9UL77

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ID Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 37.1%; Score 467; DB 4; Length 108;
Best Local Similarity 82.1%; Pred. No. 2e-33;
Matches 92; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLNWYQKPGKAPKLLIYAAS 56

QY 81 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 108

RESULT 8
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ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody v region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 37.1%; Score 459.5; DB 4; Length 107;
Best Local Similarity 83.0%; Pred. No. 8.8e-33;
Matches 93; Conservative 7; Mismatches 7; Indels 5; Gaps 2;

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QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SSYLNWYQKPGKAPKLLIYAAS 56

QY 81 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 108

RESULT 9
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 36.1%; Score 446; DB 4; Length 108;
Best Local Similarity 77.7%; Pred. No. 1.3e-31;
Matches 87; Conservative 9; Mismatches 12; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGQAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQGI-----SNFLAWYQKPGKVPKSLIYAAS 56

QY 81 GVPFRFSGSGGTDFLTITSSLPEDFATYYCQSNEDPRTFGQGTKEIKR 132
Db 57 GVPFRFSGSGGTDFLTITSSLPEDVATYYCQKYNAPRTFGPGTKLEIKR 108

RESULT 10
Q9UL81 PRELIMINARY; PRT; 107 AA.
ID Q9UL81;
AC Q9UL81;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
DR Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
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DR SMART; SM00406; IGV; 1.
FT NON_TER 1
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SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

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Best Local Similarity 77.7%; Pred. No. 1.3e-30;
Matches 87; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 21 DIVLTQSPSSLSASVGRVTTTCRASQSDYDGSYNNWYQKPGQAPKLLIYAASNL 80
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Db 1 DIQMTQSPSSLSASVGRVTTTCRASQSI----SNLWYQKPGKAPFLIYAASLS 56

QY 81 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGGTKVEIKR 132
  |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSS--YSALTFGGTKVDIIR 107

RESULT 11
Q96PF6 ID Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1
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FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

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Best Local Similarity 70.8%; Pred. No. 1.6e-30;
Matches 85; Conservative 14; Mismatches 17; Indels 4; Gaps 1;

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QY 81 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGGTKVEIKRTVAAPSV 140
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Db 57 GVPFRFSGSGSATFTVTTISLQPEDFATYYCQYHLPFTFGPTKVDKRTVAAPSV 116

RESULT 12
Q9UL79 ID Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.0%; Score 433; DB 4; Length 108;
Best Local Similarity 76.8%; Pred. No. 1.8e-30;
Matches 86; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

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QY 81 GVPFRFSGSGSGTDFTLTISLQPEDFATYYCQSNEDPRTFGGTKVEIKR 132
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RESULT 13
Q99M11 ID Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.4 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFB6782A3FB CRC64;

Query Match 34.8%; Score 430.5; DB 11; Length 235;

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GenCore version 4.5	
Copyright (c) 1993 - 2000 CompuGen Ltd.	
OM protein - protein search, using sw model	
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(without alignments)	
114.832 Million cell updates/sec	
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16	1154	93.3	238	19	AAW83033	Anti-Fas humanised
17	1154	93.3	238	21	AAW14774	Humanised anti-Fas
18	1154	93.3	238	21	AAW90924	Humanised anti-Fas
19	1113	90.0	218	18	AAW13563	Humanised anti-L-s
20	1099	88.8	218	21	AAW95658	Mus musculus anti-
21	1099	88.8	218	21	AAW85200	Light chain amino
22	1099	88.8	218	21	AAW76947	Full variable ligh
23	1092	88.3	218	14	AAW33312	Humanised MaEl1 Ve
24	1076	87.0	218	20	AAW50030	Human E27 anti-IgE
25	1076	87.0	218	20	AAW95660	Mus musculus anti-
26	1076	87.0	218	20	AAW95662	Mus musculus anti-
27	1076	87.0	218	21	AAW07472	Amino acid sequenc
28	1076	87.0	218	22	AAW74211	E27 anti-IgE antib
29	1073	86.7	218	20	AAW95669	Mus musculus anti-
30	1073	86.7	218	20	AAW95664	Mus musculus anti-
31	1073	86.7	218	22	AAW47087	Anti-IgE antibody,
32	1073	86.7	218	22	AAW76949	Full length light
33	1073	86.7	218	22	AAW76951	Full length light
34	1073	86.7	218	22	AAW76953	Variable light cha
35	1073	86.7	218	22	AAW76958	Variable light cha
36	1052.5	85.1	237	21	AAW96238	Human IGFAM-10 imm
37	1048.5	84.8	237	21	AAW96289	Human IGFAM-1 immu
38	1046.5	84.6	241	22	AAW82912	Human immune respo
39	1044.5	84.4	234	14	AAW38162	Sequence of the ka
40	1043	84.3	240	20	AAW50161	Human reshaped F19
41	1040.5	84.1	237	21	AAW96301	Human IGFAM-13 imm
42	1039	84.0	234	18	AAW11638	Human anti-RSV mon
43	1026	82.9	240	22	AAW63665	Amino acid sequenc
44	1022	82.6	236	16	AAW77614	Humanised 5G1.1 VL
45	1021.5	82.6	233	14	AAW30777	pH52-9.0 humanised

ALIGNMENTS

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ID	AAW90932 standard; Protein; 238 AA.
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AC	AAW90932;
DT	08-AUG-2000 (first entry)
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DE	Humanised anti-Fas designed light chain Leu 3 protein.
XX	
KW	Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW	anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW	dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW	nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW	hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW	Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW	Storjen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW	Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW	multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW	insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW	cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX	
OS	Synthetic.
XX	
PN	EP990663-A2.
XX	
PD	05-APR-2000.
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PF	29-SEP-1999; 99EP-0307711.
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PR	30-SEP-1998; 98JP-0276881.
PR	30-SEP-1998; 98JP-0276882.
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SUMMARIES

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1	1237	100.0	238	21	AAW90932	Humanised anti-Fas
2	1236	99.9	238	21	AAW90930	Humanised anti-Fas
3	1232	99.6	238	21	AAW90931	Humanised anti-Fas
4	1174	94.9	238	19	AAW83034	Anti-Fas humanised
5	1174	94.9	238	21	AAW14777	Humanised anti-Fas
6	1174	94.9	238	21	AAW90927	Humanised HFE7A de
7	1169	94.5	238	19	AAW83031	Anti-Fas humanised
8	1169	94.5	238	21	AAW14772	Humanised anti-Fas
9	1169	94.5	238	21	AAW90922	Humanised anti-Fas
10	1156	93.5	238	19	AAW83032	Anti-Fas humanised
11	1156	93.5	238	21	AAW14773	Humanised anti-Fas

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AA11633.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 PT
 PS Claim 3; Page 161-162; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antirheumatic,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antihypertensive, nephrotropic, antiinfertility, neuroprotective,
 CC antidiabetic, cardiatic and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 3
 CC which is described in the method of the invention.
 XX Sequence 238 AA;
 SQ
 Query Match 100.0%; Score 1237; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 4.3e-62;
 Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLVLLWVPGSGDVLVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWY 60
 DB 1 metdtillvllwvpgsgtdvlvtqspsslsasvgsdrtvitckasqsdvdygdsgymwv 60
 QY 61 OQKPKAKPLLIYAASNLSEGIPIRFGSGSGTDFLTITSSIQPEDFATYYCQSQNEDPR 120
 DB 61 qkpkakplliyaasnlesgipirfsgsgsgtdftltisslqpedfatyycqsqnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCVLLNFFYPREAKVQMKVDNALQS 180
 DB 121 tfgqgtkeikrtvaapsvfifppdsdeqlksgtasvvcvllnffypreakvqmkvdnals 180
 QY 181 GNSQSVTEQDSKDSYSLSSLTLSKADYKHKYACVTHQGLSSPYTKSFNRGEC 238
 DB 181 gnsqsvteqdsksyslsstltlskadyekhyacvthqglsspytksfnrgec 238
 RESULT 2
 ID AAW90930 standard; Protein; 238 AA.
 XX
 AC AAW90930;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed light chain Leu 1 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antidiabetic; antirheumatic;
 KW Hashimoto disease; rheumatoid arthritis; systemic lupus erythematosus;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX Synthetic.
 OS
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-0307711.
 PF
 XX 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AA11631.
 XX
 CC New humanized anti-Fas antibody, useful for treating or preventing e.g.
 CC inflammatory or autoimmune disease, induces apoptosis selectively in
 CC cells with abnormal Fas-Fas ligand systems -
 CC
 PS Claim 3; Page 156-157; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antidiabetic, cardiatic and hepatotropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 1
 CC which is described in the method of the invention.
 XX Sequence 238 AA;
 SQ
 Query Match 99.9%; Score 1236; DB 21; Length 238;
 Best Local Similarity 99.6%; Pred. No. 4.9e-62;
 Matches 237; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 METDTILLVLLWVPGSGDVLVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWY 60

Db 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtltckasqsvdydgsymnw 60
 Qy 61 QOKPKAPKLLIYAASNLSEIPSRFSGSGSDTFTLTISLQPEDFATYTCQSQSNEEDPR 120
 Db 61 qkpgkpklllyaaasnlsgvpsrfsgsgsgtdftltisslqpedfatytcqsgsnepr 120
 Qy 121 TFGOGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180
 Db 121 tfgggtkveikrtvaapsvfippsdeqlksgtasvcllnffpreakvqkvdnalqs 180
 Qy 181 GNSQESVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystlsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 3
 AAW90931
 ID AAW90931 standard; Protein: 238 AA.
 XX
 AC AAW90931;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed light chain Leu 2 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 XX EP990663-A2.
 XX
 XX 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 XX
 XX 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 XX WPI: 2000-258930/23.
 XX
 XX N-PSDB: AAA11632.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems
 XX
 XX Claim 2; Page 159; 263pp; English.
 XX
 XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX ligand system, by binding to Fas on the cell surface, and prevents
 XX apoptosis in cells with a normal system, by inhibiting binding between
 XX Fas and its ligand. The products of the invention have anti-inflammatory,
 XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 XX antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 XX antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
 XX apoptosis by binding to cell surface Fas or inhibit it by competitive
 XX inhibition of ligand binding. (I) are used to treat and/or prevent

CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody light chain construct designated Leu 2
 CC which is described in the method of the invention.
 XX
 SQ Sequence 238 AA;

Query Match 99.6%; Score 1232; DB 21; Length 238;
 Best Local Similarity 99.2%; Pred. No. 8.1e-62;
 Matches 236; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METDTILLWLLWVPGSTGDIVLTQSPSSLSASVSGDRVTITCKASQSVDYDGSYMMWY 60
 Db 1 metdtillwllwvpgstgdivltqspsslsasvsgdrvtitckasqsvdydgsymnw 60
 Qy 61 QOKPKAPKLLIYAASNLSEIPSRFSGSGSDTFTLTISLQPEDFATYTCQSQSNEEDPR 120
 Db 61 qkpgkpklllyaaasnlsgvpsrfsgsgsgtdftltisslqpedfatytcqsgsnepr 120
 Qy 121 TFGOGTKVEIKRTVAAPSVFIPPSDEQLKSGTASVCLLNFFPREAKVQKVDNALQS 180
 Db 121 tfgggtkveikrtvaapsvfippsdeqlksgtasvcllnffpreakvqkvdnalqs 180
 Qy 181 GNSQESVTEQDSKDYSTLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqdsksdystlsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 4
 AAW83034
 ID AAW83034 standard; Protein: 238 AA.
 XX
 AC AAW83034;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas humanised antibody HFE7A light chain PDHH type.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease; sterility;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; anemia;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..20 /label= Sig_peptide
 FT Protein 21..238 /label= Mat_protein
 FT Region 21..131 /label= Variable

Best Local Similarity 93.3%; Pred. No. 1.4e-58;
Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwllwpgstgeivltqspgtislsppgeratiscasqsdvdgdsymnw 60

QY 61 QOKPGKAPKLLIYAASNLGSGIPRFGSGSGTDTLTITISLQPEDFATYYCQOSNEDPR 120
Db 61 qqkpgqprlliyaasnlsgipdrfsgsgtdftltisrlepedfayyccsqsdpr 120

QY 121 TFGOGTKVEIKRTVAASVFIFFPSDQLKSGTASVCLLNFFPRPRAKVQKVDNALQS 180
Db 121 tfgogtkleikrtvaasvfiifpsdqksgtasvcllnffprpreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdskstyslstltlskadyekhyacevthgglsspvtksfnrgec 238

RESULT 6
AAW90927
ID AAW90927 standard; Protein; 238 AA.

XX AC AAW90927;
DT 08-AUG-2000 (first entry)
XX Humanised HFE7A designed light chain protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antirheiosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
OS Synthetic.

XX EP990663-A2.
XX 05-APR-2000.
XX 29-SEP-1999; 99EP-0307711.
XX 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
XX N-PSDB; AAAL1614.
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX Claim 3; Page 141-142; 263pp; English.
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,

CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
CC the method described in the invention.

XX SQ Sequence 238 AA;

Query Match 94.9%; Score 1174; DB 21; Length 238;
Best Local Similarity 93.3%; Pred. No. 1.4e-58;
Matches 222; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 METDTILLWLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwllwpgstgeivltqspgtislsppgeratiscasqsdvdgdsymnw 60

QY 61 QOKPGKAPKLLIYAASNLGSGIPRFGSGSGTDTLTITISLQPEDFATYYCQOSNEDPR 120
Db 61 qqkpgqprlliyaasnlsgipdrfsgsgtdftltisrlepedfayyccsqsdpr 120

QY 121 TFGOGTKVEIKRTVAASVFIFFPSDQLKSGTASVCLLNFFPRPRAKVQKVDNALQS 180
Db 121 tfgogtkleikrtvaasvfiifpsdqksgtasvcllnffprpreakvqkvdnalqs 180

QY 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdskstyslstltlskadyekhyacevthgglsspvtksfnrgec 238

RESULT 7
AAW83031
ID AAW83031 standard; Protein; 238 AA.
XX AC AAW83031;
DT 15-MAR-1999 (first entry)
XX Anti-Fas humanised antibody HFE7A light chain HH type.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.

XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
XX Peptide 1..20
XX /label= Sig_peptide

FT Protein 21..238
 FT /label= Mat_protein
 FT Region 21..131
 FT /label= Variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT Region 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT Region 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 PN AU9859701-A.
 XX 08-OCT-1998.
 PD 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 PA
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 DR WPI; 1998-543440/47.
 DR N-PSDB; AAV70074.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 199-199; 292pp; English.
 XX
 CC This is the amino acid sequence of the HH type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AA83042) entailed making
 CC P47A, K49R, H80S, P81R, V82L, E84P, E85A, A87F and T89V amino acid
 CC substitutions; these residues are conserved in the human light
 CC chain (kappa chain). Host cell Escherichia coli PHSGH7 SANK 73497
 CC harbors plasmid PHSGH7 carrying a fusion fragment of the humanised
 CC HH type HFE7A light chain, and is deposited as FERM BP-6073
 CC immunoglobulin kappa chain, and is deposited as FERM BP-6073
 CC (claimed). The invention provides methods for producing humanised
 CC antibodies by culturing host cells. Humanised versions of HFE7A
 CC (see AA83031-37), like native HFE7A, are capable of inducing
 CC apoptosis in abnormal cells expressing Fas, and of inhibiting
 CC Fas-induced apoptosis in normal cells. The humanised antibodies
 CC are used to evaluate, in animal models, treatments of diseases that
 CC involve Fas/Fas ligand interactions, and also to treat such
 CC diseases, including autoimmune disease (e.g. systemic lupus
 CC erythematosus, Hashimoto's disease, graft versus host disease,
 CC Sjogren syndrome, pernicious anaemia, Addison's disease,
 CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
 CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
 CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
 CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
 CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 94.5%; Score 1169; DB 19; Length 238;
 Best Local Similarity 92.9%; Pred. No. 2.7e-58;
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVITRTCKASQSDYDGDSTNNWY 60
 |||||
 Db 1 metdtillwvllwpgstgdivltqspgtslspgeratlsckasqsdvdygdsgymwy 60
 |||||
 QY 61 QOKPKAPKLLIYAASNLSESGIPSRPSGSGTDFTLTITSSLOPEDFATYYCQOSNEDPR 120
 |||||
 Db 61 gqkgqaprllyaaanlesgipdrfsgsgsgtdftltisrlepafavyyccqsgnedpr 120
 |||||
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS 180
 |||||
 Db 121 tfggtrleikrtvaapsvfifppsqdeqksgtasvvccllnnfyppreakvqwkvdnals 180
 |||||
 QY 181 GNSQESVTEQDSKDSYSLSTLTLSKADYEHKHVYACEVTHQGLSSPVTKSFNRGEC 238
 |||||
 Db 181 gnsqesvteqdsksdstyslsstltiskadyekkhvyacevthqglsspvtksfnrgec 238
 |||||
 RESULT 8
 AAB14772
 ID AAB14772 standard; Protein; 238 AA.
 XX
 AC AAB14772;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:50.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 2000-485645/43.
 DR N-PSDB; AAA72124.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 PS Claim 20; Page 78-79; 139pp; Japanese.
 CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The compositions of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas
 CC antibodies.
 XX
 SQ Sequence 238 AA;

Query Match 94.5%; Score 1169; DB 21; Length 238;
 Best Local Similarity 92.9%; Pred. No. 2.7e-58;
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDGDSYMMWY 60
 Db 1 metdtillwvllwvpgstgdivltqspgtlsispggeratlsckasqsvdydgdsmwmy 60

Qy 61 QOKPKAPKLIYAASNLSEGIPTSPFSGSGSGTDFTLTISLQPDFTATYTCQSSNEQDP 120
 Db 61 qkqpgqaprllyaaasnlsegiptspfgsgsgtfdtlisrlpadfafvvyqcgsgnepr 120

Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQ 180
 Db 121 tfgggttrleikrtvaapsvfifppdeqlksgtasvvcclnnfyprkavqwkvdnalq 180

Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqgskdstyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 9
 ID AAW90922 standard; Protein; 238 AA.
 AC AAW90922;
 DT 08-AUG-2000 (first entry)
 DE Humanised anti-Fas antibody HFE7A light chain HH type protein.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.
 OS
 XX EP990663-A2.
 XX
 XX 05-APR-2000.
 XX
 XX 29-SEP-1999; 99EP-0307711.
 XX
 XX 30-SEP-1998; 98JP-0276881.
 XX
 XX 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 XX
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 XX WPI: 2000-258930/23.
 XX
 XX N-PSDB; AAA11562.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 XX inflammatory or autoimmune disease, induces apoptosis selectively in
 XX cells with abnormal Fas-Fas ligand systems
 XX
 XX Example reference 14; Page 114-115; 263pp; English.
 XX
 XX This invention describes a novel humanized anti-Fas antibody-like
 XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 XX ligand system, by binding to Fas on the cell surface, and prevents
 XX apoptosis in cells with a normal system, by inhibiting binding between

Fas and its ligand. The products of the invention have anti-inflammatory,
 anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
 apoptosis by binding to cell surface Fas or inhibit it by competitive
 inhibition of ligand binding. (I) are used to treat and/or prevent
 diseases associated with the Fas/Fas ligand system, especially systemic
 lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 inhibit apoptosis in normal cells but selectively induce it in abnormal
 cells. They bind to both human and murine Fas, so can be evaluated in
 murine disease models. (I) act on the active site of Fas, i.e. they mimic
 the native ligand, do not induce liver disease, and have reduced risk of
 inducing a human anti-murine antibody response. This sequence represents
 a humanised anti-Fas antibody HFE7A light chain HH type which is used in
 the method described in the invention.

XX
 SQ Sequence 238 AA;

Query Match 94.5%; Score 1169; DB 21; Length 238;
 Best Local Similarity 92.9%; Pred. No. 2.7e-58;
 Matches 221; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWVPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDGDSYMMWY 60
 Db 1 metdtillwvllwvpgstgdivltqspgtlsispggeratlsckasqsvdydgdsmwmy 60

Qy 61 QOKPKAPKLIYAASNLSEGIPTSPFSGSGSGTDFTLTISLQPDFTATYTCQSSNEQDP 120
 Db 61 qkqpgqaprllyaaasnlsegiptspfgsgsgtfdtlisrlpadfafvvyqcgsgnepr 120

Qy 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRKAVQWKVDNALQ 180
 Db 121 tfgggttrleikrtvaapsvfifppdeqlksgtasvvcclnnfyprkavqwkvdnalq 180

Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 238
 Db 181 gnsqesvteqgskdstyslsstltlskadyekhkyacevthqglsspvtksfnrgec 238

RESULT 10
 ID AAW83032 standard; Protein; 238 AA.
 AC AAW83032;
 XX
 XX 15-MAR-1999 (first entry)
 XX
 XX Anti-Fas humanised antibody HFE7A light chain HM type.
 XX
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 XX apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 XX systemic lupus erythematosus; graft versus host disease;
 XX Sjorgen syndrome; pernicious anaemia; Addison's disease;
 XX scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 XX rheumatoid arthritis; autoimmune haemolytic anaemia;
 XX myasthenia gravis; multiple sclerosis; Basedow's disease;
 XX thrombopenia purpura; insulin-dependent diabetes; allergy;
 XX atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 XX glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 XX transplant rejection; therapy.
 XX
 XX Homo sapiens.
 XX Synthetic.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..20
 FT Protein /label= Sig_peptide
 FT 21..238
 FT /label= Mat_protein
 FT Region 21..131
 FT /label= Variable
 FT Region 132..238
 FT /label= Constant
 FT Region 44..58
 FT /label= CDR_L1
 FT /note= "claim 9"
 FT Region 74..80
 FT /label= CDR_L2
 FT /note= "claim 9"
 FT Region 113..121
 FT /label= CDR_L3
 FT /note= "claim 9"
 PN AU9859701-A.
 XX
 XX 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-0059701.
 XX
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX
 PI WPI: 1998-543440/47.
 DR N-PSDB; AA70075.
 DR
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS
 XX
 PS Claim 21; Page 200; 292pp; English.
 XX
 CC This is the amino acid sequence of the HM type humanised light
 CC chain of murine anti-human Fas monoclonal antibody HFE7A.
 CC Humanisation of the murine sequence (see AA83042) entailed making
 CC P47A and K49R amino acid substitutions; these residues are
 CC conserved in the human light (kappa) chain. Host cell E. coli
 CC PHSGHM17 SANK 73597 harbors plasmid PHSGHM17 carrying a fusion
 CC fragment of the humanised HM type HFE7A light chain and DNA
 CC encoding the region of human immunoglobulin kappa chain, and is
 CC deposited as FERM BP-6072 (claimed). The invention provides
 CC methods for producing humanised antibodies by culturing host
 CC cells. Humanised versions of HFE7A (see AA83031-37), like native
 CC HFE7A, are capable of inducing apoptosis in abnormal cells
 CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
 CC cells. The humanised antibodies are used to evaluate, in animal
 CC models, treatments of diseases that involve Fas/Fas ligand
 CC interactions, and also to treat such diseases, including autoimmune
 CC disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
 CC graft versus host disease, Sjogren syndrome, pernicious anaemia,
 CC Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
 CC sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
 CC thrombopenia purpura and insulin-dependent diabetes), allergies,
 CC atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
 CC nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
 CC rejection (all claimed).
 XX
 SQ Sequence 238 AA;

Query Match 93.5%; Score 1156; DB 19; Length 238;
 Best Local Similarity 92.0%; Pred. No. 1.4e-57;
 Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
 QY 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSYNNWY 60
 DB 1 metdtillwvllwpgstgdivltqspgtlsipgeratlsckasqsvdygdsgsynwyy 60
 QY 61 QOKPGKAPKLLIYAASNLGSGIPSRFSGSGTDFLTITSSLOPEDFATVYCOQSNEDPR 120
 DB 61 qkpggaprlllyaaanlesgipdrfsgsgsgtcdftlthpveedaatyyccqsgnedpr 120
 QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
 DB 121 tfgggtrleikrtvaapsvfifppsdeqlksgtasvvcllnnfyreakvqwkvdnalqs 180
 QY 181 GNSQSVTEQDSKDSYSLSSLTLSKADYEKHKVACEVTHOGLSSPVTYKSNRREC 238
 DB 181 gnsqsvteqdsksdyslsstltskadyekkhkvyacevthoglspsvtksnrgec 238
 RESULT 11
 AAB14773
 ID AAB14773 standard; Protein; 238 AA.
 XX
 AC AAB14773;
 XX
 DT 24-NOV-2000 (first entry)
 XX
 DE Humanised anti-Fas antibody light chain, SEQ ID NO:52.
 XX
 KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
 KW murine; humanised antibody; complementarity determining region; CDR;
 KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
 KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
 KW hepatitis; AIDS; graft rejection; light chain.
 XX
 OS Chimeric - Mus musculus.
 OS Chimeric - Homo sapiens.
 XX
 PN JP2000169393-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 30-SEP-1999; 99JP-0278301.
 XX
 PR 30-SEP-1998; 98JP-0276883.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI: 2000-485645/43.
 DR N-PSDB; AA72125.
 XX
 PT Preventive or treating agent for the diseases caused by an abnormality
 PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
 PT anti-Fas antibody -
 XX
 PS Claim 20; Page 80-81; 139pp; Japanese.
 XX
 CC The invention relates to compositions for the prevention or treatment
 CC or diseases caused by an abnormality in the Fas/Fas ligand system
 CC containing an anti-Fas antibody as the active component. The anti-Fas
 CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
 CC or a humanised version of HFE7A containing identical CDRs
 CC (complementarity determining regions) to antibody HFE7A. Via its
 CC interaction with Fas, the antibody of the invention acts as a modulator
 CC of apoptosis. The composition of the invention may therefore be used in
 CC the treatment or prevention of conditions such as autoimmune diseases,
 CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
 CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
 CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
 CC represent the light chains of several humanised HFE7A-derived anti-Fas

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CC antibodies.
XX
SQ Sequence 238 AA;

Query Match 93.5%; Score 1156; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4e-57;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwvllwpgstgdivltqspgtlslpgeratiscasqsdvdgdsynnwy 60

Qy 61 QOKFGKAPKLLIYAASNLSEGIPIRFGSGSGTDTFTITSLQPEDFATYYCQSQSNEQPR 120
Db 61 qkpgqaprllyaaasnlsegiiprfsgsgsgtdftitlhpvveedaatyycqsgsneqpr 120

Qy 121 TFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRAKYQKVDNALQS 180
Db 121 tfggktleikrtvaapsvfifppsdqksgtasvvcclnnfyprakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdstylstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 12
AAW90923
ID AAW90923 standard; Protein; 238 AA.
AC AAW90923;
XX
XX 08-AUG-2000 (first entry)
XX
XX Humanised anti-Fas antibody HFE7A light chain HM type protein.
DE
DE Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW hepatotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
XX
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
XX
XX 30-SEP-1998; 98JP-0276882.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX
XX N-PSDB; AAA11563.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems
XX
XX Example reference 14; Page 117-118; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
XX

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CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A light chain HM type which is used in
CC the method described in the invention.
XX
SQ Sequence 238 AA;

Query Match 93.5%; Score 1156; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4e-57;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDTILLWVLLWPGSTGDIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
Db 1 metdtillwvllwpgstgdivltqspgtlslpgeratiscasqsdvdgdsynnwy 60

Qy 61 QOKFGKAPKLLIYAASNLSEGIPIRFGSGSGTDTFTITSLQPEDFATYYCQSQSNEQPR 120
Db 61 qkpgqaprllyaaasnlsegiiprfsgsgsgtdftitlhpvveedaatyycqsgsneqpr 120

Qy 121 TFGGKTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPRAKYQKVDNALQS 180
Db 121 tfggktleikrtvaapsvfifppsdqksgtasvvcclnnfyprakvqkvdnalqs 180

Qy 181 GNSQESVTEQDSKDYSLSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdstylstltlskadyekhkvyacevthqglsspvtksfnrgec 238

RESULT 13
AAW83035
ID AAW83035 standard; Protein; 238 AA.
XX
XX AAW83035;
XX
XX 15-MAR-1999 (first entry)
XX
XX Anti-Fas humanised antibody HFE7A light chain PDHM type.
XX
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjorgen syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX

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OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT Peptide
FT /label= Sig_peptide
FT 21..238
FT Protein
FT /label= Mat_protein
FT 21..131
FT Region
FT /label= Variable
FT 132..238
FT Region
FT /label= Constant
FT 44..58
FT /label= CDR_L1
FT /note= "claim 9"
FT 74..80
FT Region
FT /label= CDR_L2
FT /note= "claim 9"
FT 113..121
FT Region
FT /label= CDR_L3
FT /note= "claim 9"
XX
XX AU9859701-A.
XX
XX 08-OCT-1998.
XX
XX 30-MAR-1998; 98AU-0059701.
XX
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
XX WPI; 098-543440/47.
XX N-PSDB; AAV70078.
XX
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX
XX Claim 21; Page 220-221; 292pp; English.
XX
XX This is the amino acid sequence of the PDHM type humanised light
XX chain of murine anti-human Fas monoclonal antibody HFE7A.
XX Humanisation of the murine sequence (see AAW83042) entailed making
XX D1E, P47A, K49R and R107K amino acid substitutions; these
XX residues are conserved in the human light (kappa) chain. Host
XX cell Escherichia coli pSHM2 SANK 70198 harbors plasmid pSHM2
XX carrying a fusion of the humanised PDHM type HFE7A light chain and
XX DNA encoding the region of human immunoglobulin kappa chain, and is
XX deposited as FERM BP-6272 (claimed). The invention provides
XX methods for producing humanised antibodies by culturing host
XX cells. Humanised versions of HFE7A (see AAW83031-37), like native
XX HFE7A, are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. The humanised antibodies are used to evaluate, in animal
XX models, treatments of diseases that involve Fas/Fas ligand
XX interactions, and also to treat such diseases, including autoimmune
XX disease (e.g. systemic lupus erythematosus, Hashimoto's disease,
XX graft versus host disease, Sjogren syndrome, pernicious anaemia,
XX Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, rheumatoid arthritis, autoimmune haemolytic anaemia,
XX sterility, myasthenia gravis, multiple sclerosis, Basedow's disease,
XX thrombopenia purpura and insulin-dependent diabetes), allergies,
XX atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
XX nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant
XX rejection (all claimed).

SQ Sequence 238 AA;
Query Match 93.4%; Score 1155; DB 19; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.6e-57;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
QY 1 METDTILLWVLLWPGSTGDIVLTQSPSLSASVSGDRVTITCKASQSDYDGDSDYNNWY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 metdtillwvllwpgstgeivltqspgtlsipgeratlsckasqsdvdygdsgymwy 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 QQKPGKAPKLLIYAASNLESGIPSRFSGSGGTDFLTITSSLPEDFATYYCOOSNEDPR 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 qqkpgqaprlliyaasnlesgipdrfsgsggtfdltitphveedaatyycqgsnedpr 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 TFGQGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNYPREAKVQWKVDNALQS 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 tfgggtkleikrtvaapsvfifppsdeqiksgtasvvcllnnfyreakvqwkvdnalqs 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 GNSQESVTEQDSKDSYSLSSSTLTLSKADYERKHVYACEVTHQGLSPVTKSFNRGEC 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 gnsqesvteqdsksdyslsstltlskadyekhkvacevthqglspvtksfnrgec 238
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
RESULT 14
AA14778
ID AAB14778 standard; Protein; 238 AA.
XX
XX AAB14778;
XX
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody light chain, SEQ ID NO:109.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX hepatitis; AIDS; graft rejection; light chain.
XX
XX Chimeric - Mus musculus.
XX Chimeric - Homo sapiens.
XX
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
XX (SANY) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72177.
XX
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX
XX Claim 20; Page 103; 139pp; Japanese.
XX
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14772-B14774 and AAB14777-B14778
CC represent the light chains of several humanised HFE7A-derived anti-Fas
XX antibodies.
SQ Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.6e-57;
Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
Qy 1 METDPTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGSYMNWY 60
Db 1 metdtillwvllwpgstgeivltqspgtislsperatlsckasqsvdydgsymnw 60
Qy 61 QOKPKAKPLLIYAASNLESIGPSRFGSGGTDFTLTISSLOPEDFATYYCQOSNEQDPR 120
Db 61 qkpgqaprllyaaasnlesigpdrfsgsgsgtdftltihpveedaatyccqsgnedpr 120
Qy 121 TFGQGTKEIKRTVAAPSVFIPPPDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQS 180
Db 121 tfgggtkleikrtvaapsvfifppsdqqlksgtasvvcvllnnfybreakvqkvdnalqs 180
Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdystslstltlskadyekkhkyvacevthqglsppvtskfnrgec 238

RESULT 15

AAW90928
ID AAW90928 standard; Protein; 238 AA.

AC AAW90928;

DT 08-AUG-2000 (first entry)

XX Humanised HFE7A designed light chain protein #2.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antirheosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; sterility;
KW Goodpasture syndrome; Crohn's disease; scleroderma; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

XX 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

XX 30-SEP-1998; 98JP-0276881.

XX 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX WPI; 2000-258930/23.

XX N-PSDB; AAA11615.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems

PS Example reference 21; Page 144-145; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, arteriosclerosis, myocarditis,
CC dependent diabetes mellitus, allergy, thrombopenia purpura, insulin
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed light chain which is used in
XX the method described in the invention.

SQ Sequence 238 AA;

Query Match 93.4%; Score 1155; DB 21; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.6e-57;

Matches 219; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 METDPTILLWVLLWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSVVDYDGSYMNWY 60
Db 1 metdtillwvllwpgstgeivltqspgtislsperatlsckasqsvdydgsymnw 60
Qy 61 QOKPKAKPLLIYAASNLESIGPSRFGSGGTDFTLTISSLOPEDFATYYCQOSNEQDPR 120
Db 61 qkpgqaprllyaaasnlesigpdrfsgsgsgtdftltihpveedaatyccqsgnedpr 120
Qy 121 TFGQGTKEIKRTVAAPSVFIPPPDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQS 180
Db 121 tfgggtkleikrtvaapsvfifppsdqqlksgtasvvcvllnnfybreakvqkvdnalqs 180
Qy 181 GNSQESVTEQDSKSTYSLSSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 gnsqesvteqdsksdystslstltlskadyekkhkyvacevthqglsppvtskfnrgec 238

Search completed: August 14, 2002, 15:15:35
Job time: 833 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:03 ; Search time 82.88 Seconds
(without alignments)
70.141 Million cell updates/sec

Title: US-09-499-662-131

Perfect score: 1237

Sequence: 1 METDITLLWVLLWVPGSTG.....EVTHQGLSPVTKSFNRGEC 238

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	90.0	218	5	PCT-US96-13152-2
2	1099	88.8	218	2	US-08-887-352B-13
3	1099	88.8	218	3	US-08-466-151-9
4	1099	88.8	218	4	US-09-109-207C-13
5	1099	88.8	218	4	US-09-296-005-13
6	1099	88.8	218	4	US-08-466-163B-9
7	1076	87.0	218	4	US-09-282-505-1
8	1076	87.0	218	4	US-09-054-255-1
9	1073	86.7	218	2	US-08-887-352B-15
10	1073	86.7	218	2	US-08-887-352B-17
11	1073	86.7	218	2	US-08-887-352B-19
12	1073	86.7	218	2	US-08-887-352B-24
13	1073	86.7	218	4	US-09-109-207C-15
14	1073	86.7	218	4	US-09-109-207C-17
15	1073	86.7	218	4	US-09-109-207C-19
16	1073	86.7	218	4	US-09-109-207C-24
17	1073	86.7	218	4	US-09-296-005-15
18	1073	86.7	218	4	US-09-296-005-17
19	1073	86.7	218	4	US-09-296-005-19
20	1073	86.7	218	4	US-09-296-005-24
21	1021.5	82.6	233	2	US-07-934-373C-25
22	1021.5	82.6	233	3	US-08-437-642B-25
23	1021.5	82.6	233	5	PCT-US93-07832-25
24	1018	82.3	214	2	US-07-934-373C-39
25	1018	82.3	214	3	US-08-437-642B-39
26	1018	82.3	214	5	PCT-US93-07832-39
27	1013	81.9	214	2	US-07-934-373C-40

28	1013	81.9	214	2	US-08-788-800-11	Sequence 11, Appl
29	1013	81.9	214	3	US-08-437-642B-40	Sequence 40, Appl
30	1013	81.9	214	3	US-09-097-309-2	Sequence 2, Appl
31	1013	81.9	214	4	US-09-097-171A-2	Sequence 2, Appl
32	1013	81.9	214	5	PCT-US93-07832-40	Sequence 40, Appl
33	1013	81.9	237	3	US-09-097-309-6	Sequence 6, Appl
34	1013	81.9	237	4	US-09-097-171A-10	Sequence 10, Appl
35	1013	81.9	237	4	US-09-422-712B-2	Sequence 2, Appl
36	1013	81.9	237	4	US-09-607-756-2	Sequence 2, Appl
37	1009.5	81.6	242	3	US-09-027-449-62	Sequence 62, Appl
38	1009.5	81.6	242	4	US-09-026-985-62	Sequence 62, Appl
39	1008.5	81.5	235	4	US-09-171-945-97	Sequence 97, Appl
40	1008.5	81.5	242	3	US-09-027-449-51	Sequence 51, Appl
41	1008.5	81.5	242	3	US-08-804-444A-51	Sequence 51, Appl
42	1008.5	81.5	242	4	US-09-026-985-51	Sequence 51, Appl
43	1005.5	81.3	219	3	US-09-027-449-72	Sequence 72, Appl
44	1005.5	81.3	219	4	US-09-026-985-72	Sequence 72, Appl
45	1005.5	81.3	242	3	US-09-027-449-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1

PCT-US96-13152-2

; Sequence 2, Application PC/TUS9613152

; GENERAL INFORMATION:

; APPLICANT: Martin, Ulrich, et al.

; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ f

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; ADDRESSEE: Attn: Norman D. Hanson

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Computer Disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/13152

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/578,953

; FILING DATE: 27-Dec-95

; APPLICATION NUMBER: EP 95 112 895.8

; FILING DATE: 17-Aug-95

; APPLICATION NUMBER: EP 95 114 969.9

; FILING DATE: 19-Sep-95

; ATTORNEY/AGENT INFORMATION:

; NAME: Norman D. Hanson

; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 218

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US96-13152-2

Query Match 90.0%; Score 1113; DB 5; Length 218;
Best Local Similarity 98.6%; Pred. No. 5.3e-88;

Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITTKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 80
|| :|||||
Db 1 DIQMTQSPSSLSASVGDRTVITTKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 60

QY 81 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 140
:|||||
Db 61 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 120

QY 141 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLS 200
:|||||
Db 121 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLS 180

QY 201 STLTLSKADYEHKHYACVETHTQGLSSPVTKSFNRGEC 238
:|||||
Db 181 STLTLSKADYEHKHYACVETHTQGLSSPVTKSFNRGEC 218

RESULT 2
US-08-887-352B-13
; Sequence 13, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IGE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-13

Query Match 88.8%; Score 1099; DB 2; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.3e-87;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITTKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 80
|| :|||||
Db 1 DIQLTQSPSSLSASVGDRTVITTKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 60

QY 81 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 140
:|||||
Db 61 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 120

QY 141 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLS 200
:|||||

Db 121 IPPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYISLS 180

QY 201 STLTLSKADYEHKHYACVETHTQGLSSPVTKSFNRGEC 238
:|||||
Db 181 STLTLSKADYEHKHYACVETHTQGLSSPVTKSFNRGEC 218

RESULT 3
US-08-466-151-9
; Sequence 9, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P07182C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-9

Query Match 88.8%; Score 1099; DB 3; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.3e-87;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITTKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 80
|| :|||||
Db 1 DIQLTQSPSSLSASVGDRTVITTKASQSYDYGDSYMNWYQOKPGKAPKLLIYAASNLES 60

QY 81 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 140
:|||||
Db 61 GIPSRFSGSGSGTDFTLTITSSLOPEDFATYYCQSQNEDPRTFGQGTKEIKRTVAAPSVE 120

QY 141 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 4
US-09-109-207C-13
; Sequence 13, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-05-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-109-207C-13

Query Match 88.8%; Score 1099; DB 4; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.3e-87;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSYDYGDSYMNWYQKPGKAPKLLIYAASYLE 60
QY 81 GIPSRFSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5
US-09-296-005-13
; Sequence 13, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; CURRENT FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 08/887,352
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 13
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial

; LOCATION: 1-218
; OTHER INFORMATION: Light chain sequence derived from MAE11
US-09-296-005-13

Query Match 88.8%; Score 1099; DB 4; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.3e-87;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSYDYGDSYMNWYQKPGKAPKLLIYAASYLE 60
QY 81 GIPSRFSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 181 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6
US-08-466-163B-9
; Sequence 9, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64
; SEQ ID NO 9
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized mae11, version 1, light chain
US-08-466-163B-9

Query Match 88.8%; Score 1099; DB 4; Length 218;
Best Local Similarity 97.2%; Pred. No. 8.3e-87;
Matches 212; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQSYDYGDSYMNWYQKPGKAPKLLIYAASYLE 60
QY 81 GIPSRFSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPFRSGSGSTDFLTITSSLPQEDFATYYCQSHEDPRTFGQGTKEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSDEQLKSTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL 180
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238

Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 7

US-09-282-505-1
; Sequence 1, Application US/09282505A
; Patent No. 6194551
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-218
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-1

Query Match 87.0%; Score 1076; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 7.7e-85;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCRASKPVDGDSYNNWYQKPGKAPKLLIYAASVLS 80
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGDSYNNWYQKPGKAPKLLIYAASVLS 60
QY 81 GIPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTVEIKRTVAAPSVF 140
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 61 GVPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180

QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 8

US-09-054-255-1
; Sequence 1, Application US/09054255
; Patent No. 6242195
; GENERAL INFORMATION:
; APPLICANT: Esche Ekinaduese Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266
; CURRENT APPLICATION NUMBER: US/09/054,255
; CURRENT FILING DATE: 1998-04-02
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: E27 anti-IgE antibody light chain
US-09-054-255-1

Query Match 87.0%; Score 1076; DB 4; Length 218;
Best Local Similarity 95.4%; Pred. No. 7.7e-85;
Matches 208; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCRASKPVDGDSYNNWYQKPGKAPKLLIYAASVLS 80
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||

Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGDSYNNWYQKPGKAPKLLIYAASVLS 60
QY 81 GIPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTVEIKRTVAAPSVF 140
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 61 GVPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 181 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 218

RESULT 9

US-08-887-352B-15
; Sequence 15, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-15

Query Match 86.7%; Score 1073; DB 2; Length 218;
Best Local Similarity 95.0%; Pred. No. 1.4e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCRASKPVDGDSYNNWYQKPGKAPKLLIYAASVLS 80
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGDSYNNWYQKPGKAPKLLIYAASVLS 60
QY 81 GIPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTVEIKRTVAAPSVF 140
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 61 GVPSRFSGSGSGTDFLTITSSLOPEDFATYYCQSNEDPRTFGQGTVEIKRTVAAPSVF 120
QY 141 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 201 STLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||

Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 10

```

US-08-887-352B-17
; Sequence 17, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/887,352B
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-17

```

Query Match 86.7%; Score 1073; DB 2; Length 218;
 Best Local Similarity 95.0%; Pred. No. 1.4e-84;
 Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYMNWYQKPKAPKLLIYAASNLES 80
   |||
Db 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGSYMNWYQKPKAPKLLIYAASNLES 60
   |||
QY 81 GIPSRFSGSGGTDTLTITSLQPEDFATYTCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
   |||
Db 61 GVPFRFSGSGGTDTLTITSLQPEDFATYTCQSNEDPRTFGQGTKEIKRTVAAPSVF 120
   |||
QY 141 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
   |||
Db 121 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||
QY 201 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
   |||
Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

```

RESULT 11

```

US-08-887-352B-19
; Sequence 19, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA: US/08/887,352B
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-887-352B-19

```

Query Match 86.7%; Score 1073; DB 2; Length 218;
 Best Local Similarity 95.0%; Pred. No. 1.4e-84;
 Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

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QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDYDGSYMNWYQKPKAPKLLIYAASNLES 80
   |||
Db 1 DIQLTQSPSSLSASVGRVTITCRASQSDYDGSYMNWYQKPKAPKLLIYAASNLES 60
   |||
QY 81 GIPSRFSGSGGTDTLTITSLQPEDFATYTCQSNEDPRTFGQGTKEIKRTVAAPSVF 140
   |||
Db 61 GVPFRFSGSGGTDTLTITSLQPEDFATYTCQSNEDPRTFGQGTKEIKRTVAAPSVF 120
   |||
QY 141 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 200
   |||
Db 121 IFPPSDQLKSGTASVVCVLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
   |||
QY 201 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 238
   |||
Db 181 STLTSLKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 218

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RESULT 12

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US-08-887-352B-24
; Sequence 24, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

```



```

; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-218
; OTHER INFORMATION: Light chain F(ab) sequence derived from MAE11
US-09-109-207C-19

Query Match      86.7%; Score 1073; DB 4; Length 218;
Best Local Similarity 95.0%; Pred. No. 1.4e-84;
Matches 207; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASNLES 80
Db 1 DIQLTQSPSSLSASVGDRTVITCRASKPVDGSDSYLNWYQOKPGKAPKLLIYAASYLES 60

Qy 81 GIPSRFSGSGSDTFTLTISLQPEDFATYYCQOSNEDPRTFGQGTKEIKRTVAAPSVF 140
Db 61 GVPKRFSGSGSDTFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTVAAPSVF 120

Qy 141 IFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 200
Db 121 IFPPSDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSTLS 180

Qy 201 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 238
Db 181 STLTLKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 218
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Search completed: August 14, 2002, 15:17:04
Job time: 687 sec

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F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 927.5; DB 2; Length 215;
Best Local Similarity 83.6%; Pred. No. 1.5e-53;
Matches 183; Conservative 13; Mismatches 18; Indels 5; Gaps 2;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
Db 1 EVVLTQSPATLSVSPGERATLSCRASQSV---HSNLAWYQKPGQAPRLLIYRASTRAT 56
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 139
Db 57 GIPAREFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 116
QY 140 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 199
Db 117 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176
QY 200 SSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 177 SSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 215

RESULT 3
JE0243
Ig kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0243
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.0%; Score 902.5; DB 2; Length 215;
Best Local Similarity 81.3%; Pred. No. 6.3e-52;
Matches 178; Conservative 17; Mismatches 19; Indels 5; Gaps 2;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
Db 1 EIVMTQSPATLSVSPGERATLSCRASQSV---ATVWVYMQKLGQAPRLLIYDASTRAT 56
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIK-RTVAAPSV 139
Db 57 GVPAREFGSGSGTDFLTITSSLOPEDFATYYCOHNNAPPTFGQGTKEIKRTVAAPSV 116
QY 140 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 199
Db 117 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 176
QY 200 SSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 177 SSTLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 215

RESULT 4
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575
A:Accession: A23746

A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 71.7%; Score 886.5; DB 2; Length 215;
Best Local Similarity 82.0%; Pred. No. 6.9e-51;
Matches 178; Conservative 13; Mismatches 23; Indels 3; Gaps 1;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
Db 1 EIVLTQSPATLSVSPGERATLSGASQSV---SSNLAWYQKPGQAPRLLIYDASSRAT 57
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 140
Db 58 GIPDRFSGSGSGTDFLTITSRLEPEDFAVYGOQYSSPLTFGGGTKEIKRTVAAPSV 117
QY 141 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 118 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 177
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGE 237
Db 178 STLTLSKADYKHKYVAGEVTHQGLSSPVTKSFNRGE 214

RESULT 5
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 70.8%; Score 876; DB 2; Length 216;
Best Local Similarity 79.4%; Pred. No. 3.3e-50;
Matches 173; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
Db 1 DIVLTQSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQKPGQ-PKLLIW-ANVRS 58
QY 81 GIPRSFGSGSGTDFLTITSSLOPEDFATYYCOQSNEDPRTFGQGTKEIKRTVAAPSV 140
Db 59 GVPDRFSGSGTDFLTITSNLQALVAVYCYQYTYSTYPSFGQGRLEIKRTVAAPSV 118
QY 141 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 119 FIPPPDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 178
QY 201 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238
Db 179 STLTLSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 216

RESULT 6
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084

Best Local Similarity 61.8%; Pred. No. 7.9e-42;

Matches 144; Conservative 37; Mismatches 47; Indels 5; Gaps 2;

QY 7 LLVLLVLLW-VPGSTGDIVLTQSPSSLSASVGDRTVTITCKASQSYDYGDSYMNWYQKPG 65

Db 2 LGLLLVLLVLLVGGARCDIQVTQSPSSLSASLTERVSTRTSOSV-----SNYLNWYQKPG 57

QY 66 KAPKLLIYAASNLSEGISPRFSGSGSGTDTLTITISLQPEDFATYYCQSQNSNEDPRTFGGG 125

Db 58 QAPKLLIYYATRLHTDVPFRFSGSGSGTDYTLTISNLEANDATYYCQYESTPLAFGG 117

QY 126 TKVEIKRTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQE 185

Db 118 TNVEIKRSDAQPSVFLFKPSEQLRTGTGVVCLVNDVFPKDNVKKVGDVGTQNSFQN 177

QY 186 SYTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHOGLSPVTKSFNRGEC 238

Db 178 SFTQDSKSKSTYSLSSTLTLSSEYQSHNAYACEVSHKSLPTALVKSFNKNEC 230

RESULT 10

JC5810

monoclonal antibody 13-1 light chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: JC5810

R:Akashi, S.; Kato, K.; Torizawa, T.; Dobmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr

A:Reference number: JC5810; MUID:98063277

A:Accession: JC5810

A:Molecule type: protein

A:Residues: 1-218 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 746; DB 2; Length 218;

Best Local Similarity 64.2%; Pred. No. 9.3e-42;

Matches 140; Conservative 30; Mismatches 48; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVTITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80

Db 1 NIVLTQSPASLAVLQGRATISCRASKSVASGYIYMHYQKPGQPPKLLISLASNLES 60

QY 81 GIPSRFSGSGTDTLTITISLQPEDFATYYCQSQNSNEDPRTFGGTKEIKRTVAAPSVF 140

Db 61 GVPARFSGSGTDTLTINHPVEEDVAIYQHSRELPLTFGAGTKLEKLRADAAPTVS 120

QY 141 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQSVTEQDSKSTYSLS 200

Db 121 IFPPSSEQLTSGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTQDSKSTYSNS 180

QY 201 SLTILSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238

Db 181 SLTILTKDEYERHNSYTCEATHTKSTSPIVKSFNRNEC 218

RESULT 11

S01320

Ig kappa chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000

C:Accession: S01320

R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.

Eur. J. Biochem. 176, 287-295, 1988

A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a

A:Reference number: S01320; MUID:88329081

A:Accession: S01320

A:Molecule type: mRNA

A:Residues: 1-234

A:Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785

A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 728; DB 2; Length 234;

Best Local Similarity 57.9%; Pred. No. 1.5e-40;

Matches 139; Conservative 38; Mismatches 55; Indels 8; Gaps 2;

QY 1 METDTILLVLLWVPGSTGDIVLTQSPSSLSASVGDRTVTITCKASQSYDYGDSYMN-- 58

Db 1 MSVPTQVLGLLLLTARDCTQMTQSPASLSVSGESVITTCRASENI-----YSNLA 54

QY 59 WYQKPGKAPKLLIYAASNLSEGISPRFSGSGSGTDTLTITISLQPEDFATYYCQSQNSNED 118

Db 55 WYQKQKSPQLLVYVATKLVDPVSRFSGSGSGTQYSLKINSLSQSEDFGYYCQHFWD 114

QY 119 PRTFGGTKEIKRTVAAPSVFIFFPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNAL 178

Db 115 PTFSGSGTKLEMKRADAAPTVSIFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSE 174

QY 179 QSGNSQESVTEQDSKSTYSLSSTLTLSKADYEKKHYACEVTHOGLSPVTKSFNRGEC 238

Db 175 RQGVLSNWTQDSKSTYSMSSTLTLTDEYERHNSYTCEATHTKSTSPIVKSFNRNEC 234

RESULT 12

A31790

Ig kappa chain V region (17/9) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000

C:Accession: A31790

R:Schulze-Gahmen, U.; Rinkl, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A

J. Biol. Chem. 263, 17100-17105, 1988

A:Title: Preliminary crystallographic data, primary sequence, and binding data for an

A:Reference number: A92686; MUID:89034213

A:Accession: A31790

A:Molecule type: mRNA

A:Residues: 1-220 <SCH>

A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 58.6%; Score 725; DB 2; Length 220;

Best Local Similarity 61.4%; Pred. No. 2.2e-40;

Matches 135; Conservative 34; Mismatches 49; Indels 2; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVTITCKASQSYDYG--DSYMNWYQKPGKAPKLLIYAASNL 78

Db 1 DIVMTQSPSLIVTAGEKVTMSCTSSQSLFNSGKQKNYLTWTYQKPGQPKVILYVASTR 60

QY 79 ESGIPSRFSGSGSGTDTLTITISLQPEDFATYYCQSQNSNEDPRTFGGTKEIKRTVAAP 138

Db 61 ESGVDPDRFTGSGSGTDTLTITISVQAEDLAVYYCQNDYSNPLTFGGGTLEKLRADAA 120

QY 139 VFIFPPSDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDSKSTYS 198

Db 121 VSIFPPSSQELTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTQDSKSTYS 180

QY 199 LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 238

Db 181 MSSTLTLTDEYERHNSYTCEATHTKSTSPIVKSFNRNEC 220

RESULT 13

A56169

Ig kappa chain V region (clone 23.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C;Accession: A56169
R;Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
J. Biol. Chem. 270, 6628-6638, 1995
A;Title: Recombinant antibodies in bioactive peptide design.
A;Reference number: A56169; MUID:95204454
A;Accession: A56169
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-210 <MON>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;keywords: heterotetramer; immunoglobulin

Query Match 58.0%; Score 717; DB 2; Length 210;
Best Local Similarity 64.0%; Pred. No. 6.9e-40;
Matches 135; Conservative 29; Mismatches 45; Indels 0; Gaps 0;
Qy 21 DIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASNLES 80
Db 1 DIVLTQSPASLTSLVSLGORATISCRASKSVSSGYSYHWHYQOKPGQPKVLIYLASNLES 60
Qy 81 GIPSRFSGSGGTDTFTLTISLQPEDFATYCCQSNEDPRFTFGGTVKEIKRTVAAPSVF 140
Db 61 GVPRFSGSGGTDTFTLNIHPVEEDAATYCCQHSRELPTWTFGGTRELKRAADAPTVS 120
Qy 141 IFPPSDEQLKSGTASVYVCLLNFFYPRAKQVQKVDNALQSGNSQESVTEQDSKDSYSL 200
Db 121 IFPPSSQLTSGGASVYVCLNFFYKPDINVKWKIDGSRQGVLSNWTQDSKDSYSMS 180
Qy 201 STLTLSKADYEKKHVKYACEVTHOGLSSPV 229
Db 181 STLTLTKDEYERHNSYTCETHKTSTSPI 209

RESULT 14
S37484
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;keywords: heterotetramer; immunoglobulin

Query Match 57.8%; Score 715.5; DB 2; Length 225;
Best Local Similarity 61.4%; Pred. No. 9.2e-40;
Matches 140; Conservative 30; Mismatches 53; Indels 5; Gaps 2;
Qy 11 LLLVWPGSTGDIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGKAPKL 70
Db 3 LLLCVSGAHGSIWMTQPKFLLSAGDRVITTCASQSVND----VAVYQOKPGQSPKL 58
Qy 71 LIYAASNLESIGIPSRFSGSGGTDTFTLTISLQPEDFATYCCQSNEDPRFTFGGTVKEI 130
Db 59 LIYYASSRYTGVPDRFTGSGYGTDTFTISTVQAEDLAVYFCQQ-DYSSVTFGGGCTKLEI 117
Qy 131 KRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNFFYPRAKQVQKVDNALQSGNSQESVTEQ 190
Db 118 KRDAAPATVSIFPPSSQLTSGGASVYVCLNFFYKPDINVKWKIDGSRQGVLSNWTQD 177
Qy 191 DSKDSTYSLSTLTLSKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 238
Db 178 DSKDSTYMSSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNREC 225

RESULT 15

PC4203

Ig kappa chain (monoclonal antibody MAbA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a
A;Reference number: PC4202; MUID:97082978
A;Accession: PC4203
A;Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U29147; NID:gi1594225; PIDN:AAC52821.1; PID:gi1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

Query Match 57.3%; Score 708.5; DB 2; Length 219;
Best Local Similarity 59.4%; Pred. No. 2.6e-39;
Matches 130; Conservative 38; Mismatches 50; Indels 1; Gaps 1;
Qy 21 DIVLTQSPSSLSASVGRVITTCASQSDYDGDSDYNNWYQOKPGKAPKLLIYAASNLE 79
Db 1 DVLMTQTPLSLPSVLGDAQSISCRSSQSIVHTNGNTYLEWYIQKPGQSPKLLIYKVSNR 60
Qy 80 SGIPSRFSGSGGTDTFTLTISLQPEDFATYCCQSNEDPRFTFGGTVKEIKRTVAAPSV 139
Db 61 SGVPRFSGSGGTDTFTLTISRVAEDLGVIYFCGSHVPRFTGGTKLEIKRAADAPT 120
Qy 140 FIFPPSDEQLKSGTASVYVCLLNFFYPRAKQVQKVDNALQSGNSQESVTEQDSKDSYSL 199
Db 121 SIFPPSSEQLTSGGASVYVCLNFFYKPDINVKWKIDGSRQGVLSNWTQDSKDSYSL 180
Qy 200 SSTLTLSKADYEKKHVKYACEVTHOGLSSPVTKSFNRGEC 238
Db 181 SSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNREC 219

Search completed: August 14, 2002, 15:18:59
Job time: 687 sec

us-09-499-662-131.rpr

Thu Aug 15 07:56:01 2002

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:13 ; Search time 53.64 Seconds
(without alignments)
171.798 Million cell updates/sec

Title: US-09-499-662-131

Perfect score: 1237

Sequence: 1 METDTILLWLLWPGSTG.....EVTHQGLSSPVTKSFNRGEC 238

Scoring table:
BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	548	44.3	106	1	KAC_HUMAN	P01834 homo sapien
2	531	42.9	131	1	KV3J_MOUSE	P01661 mus musculus
3	520	42.0	132	1	KV3K_MOUSE	P01658 mus musculus
4	484	39.1	111	1	KV3M_MOUSE	P01665 mus musculus
5	482	39.0	111	1	KV3N_MOUSE	P01666 mus musculus
6	480	38.8	111	1	KV3O_MOUSE	P01667 mus musculus
7	479.5	38.8	129	1	KV3L_HUMAN	P18135 homo sapien
8	479	38.7	129	1	KV1W_HUMAN	P04431 homo sapien
9	477	38.6	111	1	KV3Q_MOUSE	P01669 mus musculus
10	469	37.9	111	1	KV3L_MOUSE	P01664 mus musculus
11	460	37.2	108	1	KV1H_HUMAN	P01600 homo sapien
12	459.5	37.1	110	1	KV3P_MOUSE	P01668 mus musculus
13	457.5	37.0	129	1	KV3M_HUMAN	P18136 homo sapien
14	451	36.5	108	1	KV1G_HUMAN	P01599 homo sapien
15	448	36.2	108	1	KV1M_HUMAN	P01605 homo sapien
16	447	36.1	108	1	KV1K_HUMAN	P01603 homo sapien
17	447	36.1	134	1	KV4C_HUMAN	P06314 homo sapien
18	445	36.0	108	1	KV1B_HUMAN	P01594 homo sapien
19	444	35.9	108	1	KV1E_HUMAN	P01597 homo sapien
20	444	35.9	108	1	KV1F_HUMAN	P01598 homo sapien
21	444	35.9	108	1	KV1N_HUMAN	P01606 homo sapien
22	441	35.7	108	1	KV1A_HUMAN	P04430 homo sapien
23	440	35.6	108	1	KV1A_HUMAN	P01593 homo sapien
24	440	35.6	117	1	KV1J_HUMAN	P01602 homo sapien
25	437	35.3	111	1	KV3H_MOUSE	P01660 mus musculus
26	434	35.1	108	1	KV1O_HUMAN	P01607 homo sapien
27	433	35.0	108	1	KV1P_HUMAN	P01608 homo sapien
28	432.5	35.0	129	1	KV3H_HUMAN	P04207 homo sapien
29	431.5	34.9	133	1	KV4B_HUMAN	P06313 homo sapien
30	429	34.7	108	1	KV1Y_HUMAN	P80362 homo sapien
31	428	34.6	108	1	KV1R_HUMAN	P01610 homo sapien
32	428	34.6	108	1	KV1S_HUMAN	P01611 homo sapien
33	428	34.6	129	1	KV1X_HUMAN	P04432 homo sapien

RESULT 1

KAC_HUMAN	ID	KAC_HUMAN	STANDARD;	PRT;	106 AA.
AC	P01834;	DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)	DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Ig kappa chain C region.	GN	IGKC.		
OS	Homo sapiens (Human).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	OX	NCBI_TaxID=9606;		
RN	[1]	RP	SEQUENCE (MYELOMA PROTEIN EU).		
RX	MEDLINE=71064023; PubMed=5489770;	RA	Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;		
RT	"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";	RL	Biochemistry 9:3155-3161(1970).		
RN	[2]	RP	DISULFIDE BONDS.		
RX	MEDLINE=71064027; PubMed=4923144;	RA	Gall W.E., Edelman G.M.;		
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";	RL	Biochemistry 9:3188-3196(1970).		
RN	[3]	RP	SEQUENCE (BENCE-JONES PROTEIN TI).		
RX	MEDLINE=72188439; PubMed=5027703;	RA	Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;		
RT	"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";	RL	Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).		
RN	[4]	RP	SEQUENCE FROM N.A.		
RX	MEDLINE=81042304; PubMed=6775818;	RA	Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;		
RT	"Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";	RL	Cell 22:197-207(1980).		
RN	[5]	RP	SEQUENCE (BENCE-JONES PROTEIN ROY).		
RA	Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H., Steinmetz-Kayne M., Suter L., Watanabe S.;	RL	(In) Franek F., Shugar D. (eds.);		
RL	Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).	RN	[6]		
RP	SEQUENCE (BENCE-JONES PROTEIN CUM).	RX	MEDLINE=68242259; PubMed=5586923;		
RA	Hilschmann N.;	RT	"The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";		

34	426	34.4	111	1	KV3J_MOUSE	P01662 mus musculus
35	426	34.4	128	1	KV3K_MOUSE	P06311 homo sapien
36	425	34.4	111	1	KV3K_MOUSE	P01663 mus musculus
37	424.5	34.3	109	1	KV1T_HUMAN	P01612 homo sapien
38	421	34.0	108	1	KV1L_HUMAN	P01604 homo sapien
39	421	34.0	111	1	KV3R_MOUSE	P01670 mus musculus
40	419	33.9	108	1	KV1Q_HUMAN	P01609 homo sapien
41	418.5	33.8	107	1	KV1D_HUMAN	P01596 homo sapien
42	418	33.8	117	1	KV1I_HUMAN	P01601 homo sapien
43	417	33.7	115	1	KV3I_HUMAN	P04433 homo sapien
44	415.5	33.6	133	1	KV2F_HUMAN	P06310 homo sapien
45	414	33.5	112	1	KV3G_MOUSE	P01659 mus musculus

ALIGNMENTS

```
RL Hoppe-Seyley's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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CC -----
DR EMBL; J00241; AAA58989.1; -
DR EMBL; V00557; CAA23823.1; -
DR PIR; A02116; K3HU.
DR HSP; P01842; 7FAB.
DR MIM; 147202; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86
FT DISULFID 106 106
FT VARIANT 83 83
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT V -> L (IN INV(1,2) MARKER).
FT /FTIG-VAR_003897.
FT D -> N (IN REF. 7 AND 8).
FT E -> Q (IN REF. 5 AND 6).
FT CONFLICT 14 14
FT CONFLICT 57 57
FT SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 44.3%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 133 TVAAPSVFTFPSPDEQLKSGTASVCLLNFPREAKVQKVDNALQSGNSQESVTEQDS 192
DB 1 TVAAPSVFTFPSPDEQLKSGTASVCLLNFPREAKVQKVDNALQSGNSQESVTEQDS 60
QY 193 KOSTYLSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
DB 61 KOSTYLSLSTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 2
KV3L_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
RT the variable and constant regions of immunoglobulin light chain
RT precursors: implications on the organization and controlled
RT expression of immunoglobulin genes."
RL Biochemistry 17:2392-2400(1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences."
RL Biochemistry 12:760-771(1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions."
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
DR PIR; A01935; KVM56.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 131
FT DOMAIN 21 43
FT DOMAIN 44 58
FT DOMAIN 59 73
FT DOMAIN 74 80
FT DOMAIN 81 112
FT DOMAIN 113 121
FT DOMAIN 122 131
FT DISULFID 43 112
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
Query Match 42.9%; Score 531; DB 1; Length 131;
Best Local Similarity 74.8%; Pred. No. 5.7e-36;
Matches 98; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 METDTLLWVLLWVPGSGDVLVTQSPSLASVSGDVRVITCKASQSDYDGDSTANWY 60
DB 1 METDTLLWVLLWVPGSGDVLVTQSPSLASVSGDVRVITCKASQSDYDGDSTANWY 60
QY 61 QOKPGKAPKLLIYAASNLESIGPSRSGSGTGDTFTLTISLQPEDAFATYCCQSNEDPR 120
DB 61 QOKPGKAPKLLIYAASNLESIGPSRSGSGTGDTFTLTIDPVEADDAATYCCQNNEDPW 120
QY 121 TFGGQTKVEIK 131
DB 121 TFGGQTKVEIK 131

RESULT 3
KV3F_MOUSE STANDARD; PRT; 132 AA.
AC P01658;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 321 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RA  SEQUENCE OF 1-37.
RX  MEDLINE=78235887; PubMed=981179;
RA  Burstein Y., Schechter I.;
RT  "Primary structures of N-terminal extra peptide segments linked to
FT  the variable and constant regions of immunoglobulin light chain
RT  precursors: implications on the organization and controlled
RL  expression of immunoglobulin genes.";
RL  Biochemistry 17:2392-2400(1978).
[2]
RX  SEQUENCE OF 21-132.
RX  MEDLINE=73140224; PubMed=4120629;
RA  McKean D.J., Potter M., Hood L.E.;
RT  "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
RT  chain.";
RL  Biochemistry 12:749-759(1973).
CC  -I- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
CC  BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
CC  REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
CC  RESIDUES.
DR  PIR: A01933; KVM532.
DR  HSSP: P01607; IRE1.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003596; Ig_V.
DR  Pfam: PF00047; Ig; 1.
DR  SMART: SM00406; IG; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL 1 20
FT  CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
FT  DOMAIN 21 43 FRAMEWORK-1.
FT  DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN 59 73 FRAMEWORK-2.
FT  DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
FT  DOMAIN 81 112 FRAMEWORK-3.
FT  DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
FT  DOMAIN 122 131 FRAMEWORK-4.
FT  DISULFID 43 112 BY SIMILARITY.
FT  NON_TER 132 132
SQ  SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;

Query Match 42.08; Score 520; DB 1; Length 132;
Best Local Similarity 68.98; Pred. No. 4.4e-35;
Matches 91; Conservative 26; Mismatches 15; Indels 0; Gaps 0;

Qy 1 METDTLLWVLLWVPGSTGDIVLTQSPSSLSASVGRVITTCASQSVVDGDSYMNWY 60
Dy 1 METDTLLWVLLWVPGSTGDIVLTQSPASLAVSLGQRATISCRASKSVNTYGSFMZWY 60
Qy 61 QOKPKGKAPLLIYAASNLSEGIPIRFGSGSGTDTFTLTSSLPQEDFATYYCQSNEDPR 120
Dy 61 ZZKPGZPPKLLIYRASNLZSGIPARFSGSGSRBTFTLTBPVABDVATYFCZS2BZBPW 120
Qy 121 TFGSGTKVEIKR 132
Dy 121 TFGSGTKLEIKR 132

RESULT 4
KV3M_MOUSE STANDARD; PRT; 111 AA.
AC P01665;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7043.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;

Query Match 39.18; Score 484; DB 1; Length 111;
Best Local Similarity 82.08; Pred. No. 2.7e-32;
Matches 91; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 21 DIVLTQSPSSLSASVGRVITTCASQSVVDGDSYMNWYQOKPKGKAPLLIYAASNLSE 80
Dy 1 DIVLTQSPASLAVSLGQRATISCRASKQSVVDGDSYMNWYQOKPGQPPKLLIYAASNLSE 60
Qy 81 GIPRFGSGSGTDTFTLTSSLPQEDFATYYCQSNEDPRTFGSGTKVEIK 131
Dy 61 GIPARFSGSGSGTDTFTLTNHPVEEDAATYYCQSNEDPRTFGSGTKLEIK 111

RESULT 5
KV3N_MOUSE STANDARD; PRT; 111 AA.
AC P01666;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7183.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
DR HSSP: P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IG; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11952 MW; 2058BB50CE306D31 CRC64;
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Query Match          39.0%; Score 482; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 3.8e-32;
Matches 90; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRTATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 60

QY 81 GIPRSFGSGSGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQTKVEIK 131
DB 61 GIPARESGSGTDFLTINHPVEEDAAATYYCQSNEDPRTFGAGTKLEIK 111

RESULT 6
KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01667;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790(1978).
DR PIR: C01937; KVM08.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 29 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match          38.8%; Score 480; DB 1; Length 111;
Best Local Similarity 81.1%; Pred. No. 5.5e-32;
Matches 90; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRTATISCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNL 60

QY 81 GIPRSFGSGSGTDFLTITSSLPQEDFATYYCQSNEDPRTFGQTKVEIK 131
DB 61 GIPARESGSGTDFLTINHPVEEDAAATYYCQSNEDPRTFGAGTKLEIK 111

RESULT 7
KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Antibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
LEUKEMIA.
CC PIR: P0022; K3HUHA.
DR HSSP: P01789; 1MCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match          38.8%; Score 479.5; DB 1; Length 129;
Best Local Similarity 69.7%; Pred. No. 7.3e-32;
Matches 92; Conservative 16; Mismatches 21; Indels 3; Gaps 1;

QY 1 METDTLLVLLWVPGSTGDI VLTQSPSSLSASVGDRTVITCKASQSDYDGDSDYNNWY 60
DB 1 METPAQLLFLLWLPDITGEIVLTQSPGTLSPGERATLSCRASQSV---SSSYLAWY 57

QY 61 QKPGKAPKLLIYAASNLGSGIPRSFGSGSGTDFLTITSSLPQEDFATYYCQSNEDP 120
DB 58 QKPGQAPRLIIYGASSRATGIPDRFSGSGSGTDFLTITISRLPEDFATYYCQYGTSP 117

QY 121 TFGQGTKEIKR 132
DB 118 TFGQGTKEIKR 129

RESULT 8
KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----

DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 23 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 38.7%; Score 479; DB 1; Length 129;
Best Local Similarity 73.3%; Pred. No. 8.1e-32;
Matches 96; Conservative 13; Mismatches 18; Indels 4; Gaps 1;

QY 1 METDTILLWLLWPGSTGDTITQSPSSLSASVGRVTITCKASQSDVDGDSYNNWY 60
DB 3 MRVPAQLGLLLWLGRARCDIQMTQSPSSLSASVGRVTITCKASQSI-----SNYLNWY 58
QY 61 QQKPGKAPKLLIYAASNLGSPRFGSGSGTDTLTITSSLOPEDFATYYCQSNEDPR 120
DB 59 QQKPGKAPKLLIYAASLSQSGVTSRFGSGSGTDTLTITSSLOPEDSATYCCQSYSTLI 118
QY 121 TFGQGTKEIK 131
DB 119 TFGQGTREIK 129

RESULT 9
KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity";
RL Nature 276:785-790(1978).
DR PIR; E01937; KVM569.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.

FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12011 MW; 6FAA345279356829 CRC64;

Query Match 38.6%; Score 477; DB 1; Length 111;
Best Local Similarity 80.2%; Pred. No. 9.6e-32;
Matches 89; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWYQKPGKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCRASQSDVDGDSYNNWYQKPGQPPKVLIFRASNLES 60
QY 81 GIPSRFGSGSGTDTLTITSSLOPEDFATYYCQSNEDPRTFGQGTKEIK 131
DB 61 GIPARFSGSGSGTDTLTNIHPVEEDAATYYCQSNEDPWTFGSGTKLEIK 111

RESULT 10
KV3L_MOUSE STANDARD; PRT; 111 AA.
AC P01664;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CBPC 101.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01936; KVM5C1.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11964 MW; E2BLAD98AD965962 CRC64;

Query Match 37.9%; Score 469; DB 1; Length 111;
Best Local Similarity 79.3%; Pred. No. 4.2e-31;
Matches 88; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 21 DIVLTQSPSSLSASVGRVTITCKASQSDVDGDSYNNWYQKPGKAPKLLIYAASNL 80
DB 1 DIVLTQSPASLAVSLGQRATISCRASQSDVDGDSYNNWYQQNFGQSPKLLIYAASNL 60
QY 81 GIPSRFGSGSGTDTLTITSSLOPEDFATYYCQSNEDPRTFGQGTKEIK 131

2

FT	DOMAIN	78	109
FRAMEWORK-3.			

vaccines
 00, conservative
 10, misadventures
 12, rulers
 1, cups

1 DIVLTQSPASLAVSLGORATISCKASQSLDYDGDSYMWNWYQQKPGQPPKLLIYAASNLES 60

db 61 GIPARFSGSGGTDETLNIHPVEEEDAATYYCHOS-EDPWTFGSGTKLEIK 110

FT	DOMAIN	78	109
FRAMEWORK-3.			

Search completed: August 14, 2002, 15:23:13
Job time: 686 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:15 ; Search time 187.61 Seconds
(without alignments)
219.459 Million cell updates/sec

Title: US-09-499-662-131
Perfect score: 1237
Sequence: 1 METDTFLWLWLLWVPGSTG.....EVTHQGLSPVTKSPNRGEC 238

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	745.5	60.3	238	11	Q99M37	Q99M37 mus musculus
2	738	59.7	234	11	Q91WF8	Q91WF8 mus musculus
3	737	59.6	233	11	Q91WS9	Q91WS9 mus musculus
4	724	58.5	214	11	Q91IA5	Q91IA5 mus musculus
5	704.5	57.0	235	11	Q91W12	Q91W12 mus musculus
6	703	56.8	211	11	Q91XL0	Q91XL0 mus musculus
7	470	38.0	108	4	Q9UL77	Q9UL77 homo sapien
8	462.5	37.4	107	4	Q96SA9	Q96SA9 homo sapien
9	449	36.3	108	4	Q9UL70	Q9UL70 homo sapien
10	437.5	35.4	107	4	Q9UL81	Q9UL81 homo sapien
11	436	35.2	108	4	Q9UL79	Q9UL79 homo sapien
12	432	34.9	116	4	Q96PF6	Q96PF6 homo sapien
13	430.5	34.8	235	11	Q99M11	Q99M11 mus musculus
14	428	34.6	236	4	Q96E61	Q96E61 homo sapien
15	414	33.5	111	11	Q920E9	Q920E9 mus musculus
16	395.5	32.0	109	4	Q9UL78	Q9UL78 homo sapien

17	383.5	31.0	233	4	Q96169	Q96169 homo sapien
18	381	30.8	108	4	Q9UL83	Q9UL83 homo sapien
19	378	30.6	298	11	Q9QYF0	Q9QYF0 mus musculus
20	376	30.4	233	11	Q91V32	Q91V32 m adult mal
21	372.5	30.1	109	4	Q9UL86	Q9UL86 homo sapien
22	372.5	30.1	109	4	Q9UL85	Q9UL85 homo sapien
23	365	29.5	103	11	Q9JL80	Q9JL80 mus musculus
24	364	29.4	109	11	Q920E6	Q920E6 mus musculus
25	350	28.3	127	11	Q925S9	Q925S9 mus musculus
26	349	28.2	114	4	Q9UL80	Q9UL80 homo sapien
27	345.5	27.9	106	5	Q9U410	Q9U410 schistosoma
28	345	27.9	107	11	Q9ERZ9	Q9ERZ9 mus musculus
29	344	27.8	99	11	Q9JL74	Q9JL74 mus musculus
30	334	27.0	101	11	Q9JL78	Q9JL78 mus musculus
31	329.5	26.6	241	11	Q921A6	Q921A6 mus musculus
32	327	26.4	97	11	Q9JL76	Q9JL76 mus musculus
33	320.5	25.9	104	11	Q9JL82	Q9JL82 mus musculus
34	305	24.7	109	6	Q9N0W5	Q9N0W5 oryctolagus
35	296	23.9	107	11	Q9JL84	Q9JL84 mus musculus
36	274.5	22.2	218	11	Q925S1	Q925S1 mus musculus
37	244	19.7	107	4	Q9UL82	Q9UL82 homo sapien
38	239.5	19.4	107	4	Q9NSD6	Q9NSD6 homo sapien
39	235.5	19.0	108	4	Q96SB0	Q96SB0 homo sapien
40	231	18.7	130	4	Q9NE29	Q9NE29 homo sapien
41	225	18.2	130	11	Q9B8W4	Q9B8W4 mus musculus
42	214	17.3	112	4	Q96JDI	Q96JDI homo sapien
43	211	17.1	267	13	Q90529	Q90529 ginglymosto
44	207.5	16.8	112	4	Q96JD2	Q96JD2 homo sapien
45	206.5	16.7	116	4	Q96JD0	Q96JD0 homo sapien

ALIGNMENTS

RESULT	1
Q99M37	
ID	Q99M37 PRELIMINARY; PRT; 238 AA.
AC	Q99M37;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	HYPOTHETICAL 26.3 KDA PROTEIN.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RC	TISSUE.;
RA	Strausberg R.;
RL	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; BC02035; AAH02035.1; -
DR	HSSP; P01679; 2FBJ
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR003597; Ig-cl.
DR	InterPro; IPR003600; Ig-like.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF00047; ig; 2.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGC1; 1.
DR	SMART; SM00406; IGV; 1.
DR	SMART; SM00410; IG_Like; 1.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 60.3%; Score 745.5; DB 11; Length 238;
Best Local Similarity 58.1%; Pred. No. 9.le-58;
Matches 136; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

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QY 6 ILLVLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDY-DGDSYMNWYQOKP 64
DB 5 VRLVLMFWIPASSSDVWMTQTPLSPVSLGDAQISCRSSQSIHVHNGNTYLEWYQKP 64
QY 65 GKAPKLLIYAASNLGSGIPRSGSGGTDFTLTITSSLOPEDFATYYCOOSNEDPRTFG 124
DB 65 GQSPKLLIYKVRSGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCGSHVPTFGS 124
QY 125 GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQ 184
DB 125 GTKLEIKRAADAAPTISFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVL 184
QY 185 ESVTEQDSKDSYSLSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 185 NSWTQDSKDSYSTMSSTLTLTDEYERHNSYTCEATHKTSPIVKSFRNEC 238

RESULT 2
Q91WF8 PRELIMINARY; PRT; 234 AA.
ID Q91WF8;
AC Q91WF8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 25.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6B7812D2 CRC64;

Query Match 59.7%; Score 738; DB 11; Length 234;
Best Local Similarity 59.7%; Pred. No. 4.1e-57;
Matches 142; Conservative 34; Mismatches 58; Indels 4; Gaps 1;

QY 1 METDTILLVLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDYSYNNY 60
DB 1 MMSAQFLGILLCFQGTCDIQMTQTSSLSASLGDRVTISCRASQDI----SNLYNY 56
QY 61 QOKPKAPKLLIYAASNLGSGIPRSGSGGTDFTLTITSSLOPEDFATYYCOOSNEDPR 120
DB 57 QOKPDGTVKKLLIYYSRLYGLVPSRFSGSGGTDYSLTISNLEQEDIATYFCQGGNTPPF 116
QY 121 TFGQGTVEIKRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQ 180
DB 117 TFGSGTKLEVKRAADAAPTISFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSE 176
QY 181 GNSQSVTEQDSKDSYSTMSSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 177 NGVLSNWTQDSKDSYSTMSSTLTLTDEYERHNSYTCEATHKTSPIVKSFRNEC 234

RESULT 3
Q91WS9 PRELIMINARY; PRT; 233 AA.
ID Q91WS9;
AC Q91WS9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013496; AAH13496.1; -.
KW Hypothetical protein.
SQ SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;

Query Match 59.6%; Score 737; DB 11; Length 233;
Best Local Similarity 62.7%; Pred. No. 4.9e-57;
Matches 143; Conservative 29; Mismatches 52; Indels 4; Gaps 1;

QY 11 LLLVWPGSTGDIVLTQSPSSLSASVGDRTVITCKASQSDYDGDYSYMNWYQOKPGRAPKL 70
DB 10 LLLCFQGSRCDIQMTQTSSLSASLGDRVTISCSQGI----ANYLWYQOKPDGTIVKL 65
QY 71 LIYAASNLGSGIPRSGSGGTDFTLTITSSLOPEDFATYYCOOSNEDPRTFGQTKVEI 130
DB 66 LIYTSLSHSGVPSRFSGSGGTDYSLTISNLEPEDIATYCCQYRYLPWTFGGTKLEI 125
QY 131 KRTVAAPSVFIFPPSDEQLKSGTASVYVCLLNNFYPREAKVQWKVDNALQSGNSQSVTEQ 190
DB 126 KRADAAPTISFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQ 185
QY 191 DSKDSTYSLSSTLTSLKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238
DB 186 DSKDSTYSMSSTLTLTDEYERHNSYTCEATHKTSPIVKSFRNEC 233

RESULT 4
Q9RIA5 PRELIMINARY; PRT; 214 AA.
ID Q9RIA5;
AC Q9RIA5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scFv).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 58.5%; Score 724; DB 11; Length 214;
Best Local Similarity 62.8%; Pred. No. 6.1e-56;
Matches 137; Conservative 31; Mismatches 46; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSDYDGDYSYMNWYQOKPGRAPKLLIYAASNL 80
DB 1 DIQLTQSPSSMWYASLGERVITCKASQDI----NSVLSHFQKPGKSPKTLIYRANLVD 56
QY 81 GIPSRFSGSGGTDFTLTITSSLOPEDFATYYCOOSNEDPRTFGQGTVEIKRTVAAPSVF 140
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Db 57 GVPSPSGSGGQDSTLTSSLEVEDAGIYCYLOYDEFFETFGSGTKLEIKRADAAPTVS 116
.OY 141 IFPPSDEOLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSL 200
Db 117 IFPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDSYMS 176
QY 201 STLFLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 177 STLTLTKDEYERHNSYTCATHKTSTSPIVKCFNRNEC 214

RESULT 5
Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:65842).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BREAST TUMOR;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006643; AA006643.1; - 5FC73BDEBD5E8FEF CRC64;
SQ SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC64;

Query Match 57.0%; Score 704.5; DB 11; Length 235;
Best Local Similarity 60.6%; Pred. No. 3.6e-54;
Matches 134; Conservative 33; Mismatches 50; Indels 5; Gaps 1;

QY 18 STGDIVITQSPSSLSASVGRVTTTCASQSDVDGSDYNNWYQKPGKAPKLIYAASN 77
Db 20 SRGQIVLTQSPAIMSASGERVTTWCSSSSV-----SHHWYQKSGTSPKRIYDTFK 74
QY 78 LESGIPRFGSGSGTDFTLTITSSLOPEDFATYTCQOSNEDPRTFGGTVKIKRTVAAP 137
Db 75 LTSVPPDRFSGSGSGTSTYLTISNWEADVATYTCQQWSRNPPTFGVTKLELRADAAP 134
QY 138 SVTIFPSPDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSY 197
Db 135 TVSIFPSPSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDSY 194
QY 198 SLSTLTLKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 195 SMSSTLTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 235

RESULT 6
Q91XL0 PRELIMINARY; PRT; 211 AA.
AC Q91XL0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
DE CLONE:0610010P20, FULL INSERT SEQUENCE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
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RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Soabe Y.,
RA Suzuki H., Tagami T., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL: AK002514; BAB22154.1; -.
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

Query Match 56.8%; Score 703; DB 11; Length 211;
Best Local Similarity 61.3%; Pred. No. 4.2e-54;
Matches 133; Conservative 33; Mismatches 43; Indels 8; Gaps 2;

QY 24 LTQSPSSLSASVGRVTTTCASQSDVDGSDYNN--WYQKPGKAPKLLIYAANLSESG 81
Db 1 MTQSPASLSVSGVTVTITCRASENI-----YSLAWYQKQKSGSPOLLVTAANLADG 54
QY 82 IPRFSFGSGSGTDFTLTITSSLOPEDFATYTCQOSNEDPRTFGGTVKIKRTVAAPSVEI 141
Db 55 VPSRFSFGSGSGTQYSLKINSLSQSEDFGSYFCQHFQWGTPTFGGCTKLEIKRADAAPTYSI 114
QY 142 FPPSDEQLKSGTASVCLLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSLSS 201
Db 115 FPPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLNSWTDQDSKDSYMS 174
QY 202 TLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238
Db 175 TLTLTKDEYERHNSYTCATHKTSTSPIVKSFNRNEC 211

RESULT 7
Q9UL77
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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
DR EMBL; AF035033; AAD56269.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 107
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 35.4%; Score 437.5; DB 4; Length 107;
Best Local Similarity 77.7%; Pred. No. 3.9e-31;
Matches 87; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
QY 81 GIPSRFSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKR 132
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
QY 57 GVPFRSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKR 107
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56

RESULT 11
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.2%; Score 436; DB 4; Length 108;
Best Local Similarity 76.8%; Pred. No. 5.3e-31;
Matches 86; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIVMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
QY 81 GIPSRFSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKR 132
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
QY 57 GVPFRSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKR 108
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56

RESULT 12
Q9UL79 PRELIMINARY; PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 35.2%; Score 436; DB 4; Length 108;
Best Local Similarity 76.8%; Pred. No. 5.3e-31;
Matches 86; Conservative 8; Mismatches 14; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIVMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
QY 81 GIPSRFSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKR 132
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
QY 57 GVPFRSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKR 108
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----SYLNWYQKPGKAPKLLIYAAS 56
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Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 116
FT NON_TER 116
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;

Query Match 34.9%; Score 432; DB 4; Length 116;
Best Local Similarity 70.0%; Pred. No. 1.3e-30;
Matches 84; Conservative 15; Mismatches 17; Indels 4; Gaps 1;

QY 21 DIVLTQSPSSLSASVGDRTVITCKASQSYDYGDSYMNWYQKPGKAPKLLIYAASNL 80
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----ANHLNWKYQKPGKAPKLLIYDGSFL 56
QY 81 GIPSRFSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKRTVAAPS 140
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----ANHLNWKYQKPGKAPKLLIYDGSFL 56
QY 57 GVPFRSGSGGTDFTLTISSLPQDFATYYCQSNEDPRTFGQTKVEIKRTVAAPS 116
Db 1 DIQMTQSPSSLSASVGDRTVITCKASQSI-----ANHLNWKYQKPGKAPKLLIYDGSFL 56

RESULT 13
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 25.4 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IGV_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 34.8%; Score 430.5; DB 11; Length 235;
```

Best Local Similarity 42.2%; Pred. No. 4.5e-30;
Matches 100; Conservative 38; Mismatches 86; Indels 13; Gaps 7;

QY 7 LLWVLLWVPGSGDIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGK 66
Db 6 LLLVFLHLLTGSCAQLVLTQ-PSVSTSLGSAKLPCKA--STGNIQSDSYNNWYQYQYMR 62
QY 67 APKLLIYAASNLGSGIPRSFGSG--GSGDTFTLTISLQPEDFATYCYCOQSNEDPRTFGQ 124
Db 63 SPINMIYGDLLRSGVSDRESGSIDSSNSAFLTIQNVQADDEADYCYQSYSGIRVFGG 122
QY 125 GTKVEI-KRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNPNYPREAKVQWKNALQSGNS 183
Db 123 GTRLTVLSPQKTPSPVTLFPSPSEELTKATLVCTISDFPGVTVDMKADG---TPVT 179
QY 184 QESVTEQDSK--DSTVSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 238
Db 180 QGVETTPQSKNNKYNKYNASSYLTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234

RESULT 14
Q96E61 PRELIMINARY; PRT; 236 AA.
AC Q96E61;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:17259).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012876; AAH12876.1; -
SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 34.6%; Score 428; DB 4; Length 236;
Best Local Similarity 41.9%; Pred. NO. 7.4e-30;
Matches 99; Conservative 40; Mismatches 87; Indels 10; Gaps 7;

QY 7 LLWVLLWVPGSGDIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGK 66
Db 6 LLLTLAHTGSAQSVLAQ-PPSVSGAPGQTVTISCTGS-STNIGAGYAVHWYQYPPGA 63
QY 67 APKLLIYAASNLGSGIPRSFGSGDTFTLTISLQPEDFATYCYCOQSNEDPRTFGQ 124
Db 64 APKVLIVGNYNRPGVPDRFSGSGSGTSASLAITGLQAEADYCYQSYDGLSGSVFGA 123
QY 125 GTKVEI-KRTVAAPSVFIIPPSPDEQLKSGTASVVCLLNPNYPREAKVQWKNALQSGN 182
Db 124 GTRVTLVGLQKANTPTVTLFPSPSEELQANKATLVCLISDFPGAVTVAMKADGSPVKAG- 182
QY 183 SQESVTEQDSKSTVSLSTLTLSKADYKHKVYACVTHQGLSSPVTKSFNRGEC 238
Db 183 -VETTPKSKNNKYAASSYLSLTLPQWKSRSYSCQVTHEG--STVEKTVAPTEC 235

RESULT 15
Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PTERIN-MIMICKING ANTI-IDIOPOPE KAPPA CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -
FT NON_TER 111
FT NON_TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

Query Match 33.5%; Score 414; DB 11; Length 111;
Best Local Similarity 71.2%; Pred. No. 4.7e-29;
Matches 79; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 21 DIVLTQSPSLSASVGDRTVITCKASQSDYDGDSDYNNWYQKPGKAPKLLIYAASNLG 80
Db 1 DIVLTQSPASLAVSLGORATISCRASKSVSTSGYSYMHYQKPGKPKLLIYLASNLG 60
QY 81 GIPSRFSGSGSGDTFTLTISLQPEDFATYCYCOQSNEDPRTFGQTKVEIK 131
Db 61 GVPARFSGSGSGDTFTLTNIHPVEEADAATYCOHSRELPTFTFGGTTKLEIK 111

Search completed: August 14, 2002, 15:22:15
Job time: 683 sec

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!!AA_MULTIPLE_ALIGNMENT 1.0
PileUp of: us*

Symbol comparison table: GenRunData:blosu62.comp CompCheck: 1102

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GapLengthWeight: 2

compare2.msf MSF: 470 Type: P August 15, 2002 08:33 Check: 2323 ..

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Name: us-09-499-662-147 Len: 470 Check: 2453 Weight: 1.00
Name: us-09-499-662-89 Len: 470 Check: 1182 Weight: 1.00
Name: us-09-499-662-157 Len: 470 Check: 2838 Weight: 1.00

//

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us-09-499-662-147 MWSCIIILFL VATATGVHSQ VOLVQSGAEV KKPASVKVYS CKASGYTTTS
us-09-499-662-89 MWSCIIILFL VATATGVHSQ VOLVQSGAEV KKPASVKVYS CKASGYTTTS
us-09-499-662-157 MWSCIIILFL VATATGVHSQ VOLVQSGAEV KKPASVKVYS CKASGYTTTS

51
us-09-499-662-143 YMWQVKQAP GQGLEWGEI DPDSYTNYN QKFKGKATLT VDTSTSTAYM 100
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us-09-499-662-117 YMWQVKQAP GQGLEWGEI DPDSYTNYN QKFKGKATLT VDTSTSTAYM
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us-09-499-662-157 YMWQVKQAP GQGLEWGEI DPDSYTNYN QKFKGKATLT VDTSTSTAYM

101
us-09-499-662-143 ELSLSRSED AVYICARNRD YSNWYFDVW GQGLTVTVSS ASTKGPSVFP 150
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us-09-499-662-117 ELSLSRSED AVYICARNRD YSNWYFDVW GQGLTVTVSS ASTKGPSVFP
us-09-499-662-147 ELSLSRSED AVYICARNRD YSNWYFDVW GQGLTVTVSS ASTKGPSVFP
us-09-499-662-89 ELSLSRSED AVYICARNRD YSNWYFDVW GQGLTVTVSS ASTKGPSVFP
us-09-499-662-157 ELSLSRSED AVYICARNRD YSNWYFDVW GQGLTVTVSS ASTKGPSVFP

151
us-09-499-662-143 LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPVAVLOSS 200
us-09-499-662-145 LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPVAVLOSS
us-09-499-662-117 LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPVAVLOSS
us-09-499-662-147 LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPVAVLOSS
us-09-499-662-89 LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPVAVLOSS
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201
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us-09-499-662-117 GLYSLSSVVT VPSSSLGTQT YICNVNHNKPS NTKVDRKRVEP KSCDKTHTCP
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us-09-499-662-89 GLYSLSSVVT VPSSSLGTQT YICNVNHNKPS NTKVDRKRVEP KSCDKTHTCP
us-09-499-662-157 GLYSLSSVVT VPSSSLGTQT YICNVNHNKPS NTKVDRKRVEP KSCDKTHTCP

251
us-09-499-662-143 PCPAPPELLGG PSVFLFPPPKP KDTILMISRTPT EYTCVVVDVSDV HEDPEVKFNW 300
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us-09-499-662-117 PCPAPPELLGG PSVFLFPPPKP KDTILMISRTPT EYTCVVVDVSDV HEDPEVKFNW
us-09-499-662-147 PCPAPPELLGG PSVFLFPPPKP KDTILMISRTPT EYTCVVVDVSDV HEDPEVKFNW
us-09-499-662-89 PCPAPPELLGG PSVFLFPPPKP KDTILMISRTPT EYTCVVVDVSDV HEDPEVKFNW
us-09-499-662-157 PCPAPPELLGG PSVFLFPPPKP KDTILMISRTPT EYTCVVVDVSDV HEDPEVKFNW

301
us-09-499-662-143 YVDGVEVHNA KTKPREEQYN STYRVSVSLT VLHQDWLNGK EYKCKVSNKA 350
us-09-499-662-145 YVDGVEVHNA KTKPREEQYN STYRVSVSLT VLHQDWLNGK EYKCKVSNKA
us-09-499-662-117 YVDGVEVHNA KTKPREEQYN STYRVSVSLT VLHQDWLNGK EYKCKVSNKA
us-09-499-662-147 YVDGVEVHNA KTKPREEQYN STYRVSVSLT VLHQDWLNGK EYKCKVSNKA
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us-09-499-662-157 YVDGVEVHNA KTKPREEQYN STYRVSVSLT VLHQDWLNGK EYKCKVSNKA

us-09-499-662-157 YVDGVEVHNA KTKPREEQYN STYRVSVSLT VLHQDWLNGK EYKCKVSNKA 351
us-09-499-662-143 LPAPIEKTIS KAKGQPREPQ VYTLPPSREE MTKNQVSLTLC LVKGFYPSDI 400
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401
us-09-499-662-143 AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW OQGNVFCSCV 450
us-09-499-662-145 AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW OQGNVFCSCV
us-09-499-662-117 AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW OQGNVFCSCV
us-09-499-662-147 AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW OQGNVFCSCV
us-09-499-662-89 AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW OQGNVFCSCV
us-09-499-662-157 AVEWESNGQP ENNYKTTTPV LDSDGSFFLY SKLTVDKSRW OQGNVFCSCV

451
us-09-499-662-143 MHEALHNHYT QKSLSLSPGK 470
us-09-499-662-145 MHEALHNHYT QKSLSLSPGK
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:01:42 ; Search time 230.21 Seconds
(without alignments)
38.599 Million cell updates/sec

Title: 2_g_3_g_4

Perfect score: 246

Sequence: 1 SYWMOXXXXXXXXXXXXX.....XXXXXXXXXXNRDYSNNWYFDV 80

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /SIDSI/gcgdata/hold-geneseq/geneq-emb1/AA1985.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246	100.0	145	AAW83038	Anti-Fas humanised
2	246	100.0	145	AA14775	Fragment of humani
3	246	100.0	145	AAW90925	Humanised anti-Fas
4	246	100.0	464	AAW83041	Anti-Fas MAb HFE7A
5	246	100.0	464	AA14747	Mouse anti-Fas an
6	246	100.0	464	AAW90897	Murine anti-Fas an
7	246	100.0	470	AAW83036	Anti-Fas humanised
8	246	100.0	470	AAW83037	Anti-Fas humanised
9	246	100.0	470	AA14776	Humanised anti-Fas
10	246	100.0	470	AA14779	Humanised anti-Fas
11	246	100.0	470	AAW90926	Humanised HFE7A de

12	246	100.0	470	21	AAW90929	Humanised HFE7A de
13	246	100.0	470	21	AAW90933	Humanised anti-Fas
14	246	100.0	470	21	AAW90934	Humanised anti-Fas
15	246	100.0	470	21	AAW90935	Humanised anti-Fas
16	246	100.0	470	21	AAW90936	Humanised HFE7A de
17	176	71.5	119	16	AAW90937	Anti-EGFR antibody
18	176	71.5	119	16	AAW90938	Anti-EGFR antibody
19	164	66.7	111	18	AAW90939	Anti-DNA antibody
20	164	66.7	111	18	AAW90940	Anti-DNA antibody
21	164	66.7	111	18	AAW90941	Anti-DNA antibody
22	161	65.4	119	21	AAW90942	Murine 15B8 heavy
23	160	65.0	111	18	AAW90943	Anti-DNA antibody
24	158	64.2	309	22	AAW90944	SNV-env leader/hum
25	157.5	64.0	240	16	AAW90945	ScFv(FWP51). Synt
26	157.5	64.0	241	13	AAW90946	FWP51 fusion prote
27	157.5	64.0	637	13	AAW90947	(FRP51)-ETA fusion
28	157	63.8	111	18	AAW90948	Anti-DNA antibody
29	156	63.4	137	19	AAW90949	Protein sequence o
30	156	63.4	140	19	AAW90950	Murine Act-1 heavy
31	156	63.4	144	19	AAW90951	Consensus protein
32	156	63.4	180	19	AAW90952	Heavy chain of a h
33	155	63.0	117	20	AAW90953	Murine 6G425 heavy
34	155	63.0	117	20	AAW90954	Humanised 6G425 F(
35	155	63.0	117	21	AAW90955	Humanised murine 6
36	155	63.0	117	21	AAW90956	Murine 6G425 heavy
37	155	63.0	117	21	AAW90957	Humanised 6G425 F(
38	155	63.0	117	21	AAW90958	Single chain Fv an
39	154	62.6	262	22	AAW90959	Anti-gp54 MAb T16
40	153	62.2	119	19	AAW90960	Anti-gp54 MAb T16
41	153	62.2	245	19	AAW90961	Monoclonal antibod
42	148.5	60.4	125	20	AAW90962	Anti-IL-8 MAb 6G4
43	147.5	60.0	135	16	AAW90963	Anti IL-8 antibody
44	147.5	60.0	135	18	AAW90964	Anti IL-8 monoclon
45	147.5	60.0	135	18	AAW90965	Anti IL-8 monoclon

ALIGNMENTS

RESULT 1
AAW83038
ID AAW83038 standard; Protein; 145 AA.
XX AAW83038;
DT 15-MAR-1999 (first entry)
XX Anti-Fas humanised antibody HFE7A heavy chain variable region.

HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
systemic lupus erythematosus; graft versus host disease;
Sjogren syndrome; pernicious anaemia; Addison's disease;
scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
rheumatoid arthritis; autoimmune haemolytic anaemia;
myasthenia gravis; multiple sclerosis; Basedow's disease;
thrombopenia purpura; insulin-dependent diabetes; allergy;
atrophy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
transplant rejection; therapy.

XX	Homo sapiens.	OS
XX	Synthetic.	OS
XX	Key	Location/Qualifiers
XX	Peptide	1..19
XX	Protein	/label= Sig_peptide
XX	Region	20..145
XX	Region	/label= Mat_protein
XX	Region	50..54
XX	Region	/label= CDR_H1
XX	Region	/note= "Claim 9"
XX	Region	69..84

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FT FT /label= CDR_H2
FT FT /note= "claim 9"
FT FT 118..129
FT FT /label= CDR_H3
FT FT /note= "claim 9"
XX AU9859701-A.
XX 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX (SANY ) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
XX Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70104.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
XX Example 3; Page 207; 292pp; English.
XX This is the amino acid sequence of the VD type humanised heavy
XX chain variable region of murine anti-human Fas monoclonal antibody
XX HFE7A. It was utilised in a claimed humanised HFE7A heavy chain
XX (see AAV70079). The invention provides methods for producing humanised
XX antibodies by culturing host cells. Humanised versions of HFE7A (see
XX AAV83031-37) are capable of inducing apoptosis in abnormal cells
XX expressing Fas, and of inhibiting Fas-induced apoptosis in normal
XX cells. Humanised antibodies are used to evaluate, in animal models,
XX treatments of diseases that involve Fas/Fas ligand interactions, and
XX also to treat such diseases, including autoimmune disease (e.g.
XX systemic lupus erythematosus, Hashimoto's disease, graft versus host
XX disease, Sjogren syndrome, pernicious anaemia, Addison's disease,
XX scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
XX arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
XX gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
XX and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
XX myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
XX anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX SQ Sequence 145 AA;
Query Match 100.0%; Score 246; DB 19; Length 145;
Best Local Similarity 42.5%; Pred. NO. 1.4e-11;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 symqvwkqapqgrlwmgeidpsdystynqkfkgtkaltvdtstastaymelssrsd 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 tavyyccarnrdysnnwfydv 129
RESULT 2
ID AAB14775
XX AAB14775 standard; peptide; 145 AA.
XX AC AAB14775;
XX 24-NOV-2000 (first entry)
XX

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XX DE Fragment of humanised anti-Fas antibody heavy chain, SEQ ID NO:75.
XX DE Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX KW murine; humanised antibody; complementarity determining region; CDR;
XX KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX KW hepatitis; AIDS; graft rejection; heavy chain.
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX PN JP2000169393-A.
XX 20-JUN-2000.
XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX N-PSDB; AAV72146.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody.
XX Example 15; Page 88; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX of diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX SQ Sequence 145 AA;
Query Match 100.0%; Score 246; DB 21; Length 145;
Best Local Similarity 42.5%; Pred. NO. 1.4e-11;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 symqvwkqapqgrlwmgeidpsdystynqkfkgtkaltvdtstastaymelssrsd 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 tavyyccarnrdysnnwfydv 129
RESULT 3
ID AAW90925
XX AAW90925 standard; Protein; 145 AA.
XX AC AAW90925;
XX 08-AUG-2000 (first entry)
XX Humanised anti-Fas antibody HFE7A heavy chain protein.
XX

```

Db	50	sywmqvwkqapggqrlewmgeidspsdytnynqkfkgkatltvdsastaymelsslr	sd 109
Qy	61	XXXXXXXXXXNRDYSNNWYFDV 80	
		::::::::::::::::::::	
Db	110	tavyycarnrdysnnwyfdv 129	
RESULT 4			
AAW83041	ID	AAW83041 standard; Protein; 464 AA.	
XX	XX	AC	
XX	XX	AAW83041;	
DT	15-MAR-1999	(first entry)	
XX	XX	Anti-Fas MAb HFE7A heavy chain.	
DE	XX	HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;	
KW	KW	apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;	
KW	KW	systemic lupus erythematosus; graft versus host disease;	
KW	KW	Sjogren syndrome; pernicious anaemia; Addison's disease;	
KW	KW	scleroderma; Goodpasture syndrome; Crohn's disease; sterility;	
KW	KW	rheumatoid arthritis; autoimmune haemolytic anaemia;	
KW	KW	myasthenia gravis; multiple sclerosis; Basedow's disease;	
KW	KW	thrombopenia purpura; insulin-dependent diabetes; allergy;	
KW	KW	acopy; arteriosclerosis; myocarditis; cardiomyopathy;	
KW	KW	glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;	
KW	KW	transplant rejection; therapy; complementarity determining region;	
KW	KW	CDR.	

XX	
XX	Mus musculus.
XX	
FH	Key
FT	Location/Qualifiers
FT	Peptide
FT	1.19
FT	/label= Sig_peptide

FI	20..404	/label= Mat_protein
FT	20..140	/label= Variable
FT	141..464	/label= Constant
FT	50..54	CDR_H1
FT	/note= "claim 9"	
FT	69..84	CDR_H2
FT	/note= "claim 9"	
FT	118..128	CDR_H3
FT	/note= "claim 9"	
XX		
PN	AU9859701-A.	
XX		
PD	08-OCT-1998.	
XX		
PF	30-MAR-1998;	98AU-0059701.
XX		
PR	08-OCT-1997;	97JP-0276064.
PR	01-APR-1997;	97JP-0082953.
PR	25-JUN-1997;	97JP-0169088.
XX		
PA	(SANY) SANKYO CO LTD.	
XX		

PI AKIO S, HIGEYUKI H, HIIRO I, JUI O, KIMURA I,
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

DR WFL; 1998-343440/47.
DR N-PSDB; AAV71029.
XX XX

PT used to evaluate drugs in animal models and to treat rat-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS

XX PS Reference Example 4; Page 187-188; 292pp; English.
XX CC This is the amino acid of the heavy chain of murine anti-human Fas
CC monoclinal antibody HFE7A. CDNA (see AAV70129) encoding the heavy
CC chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828)
CC RNA by RT-PCR (see AAV70125-26). The invention provides humanised
CC HFE7A antibodies (see AAW83031-37) produced by CDR grafting. These
CC antibodies are capable of inducing apoptosis in abnormal cells
CC expressing Fas, and of inhibiting Fas-induced apoptosis in normal
CC cells. They are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to treat
CC such diseases, including autoimmune disease (e.g. systemic lupus
CC erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease,
CC scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
CC arthritis, autoimmune haemolytic anaemia, sterility, myasthenia
CC gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura
CC and insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX SQ Sequence 464 AA;

Query Match 100.0%; Score 246; DB 19; Length 464;
Best Local Similarity 42.5%; Pred. No. 3.9e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 50 symwqwkprpggglewgeidpsdsytnyqkfkgtlvtstssstymqlssltse 109

QY 61 XXXXXXXXNRDYSNNWYFDV 80
: : : : : | | | | | : : : : :
Db 110 savvycaarnrdysnnwyfdv 129

RESULT 5
AAB14747
ID AAB14747 standard; Protein; 464 AA.
XX AC AAB14747;
XX DT 24-NOV-2000 (first entry)
XX DE Mouse anti-Fas antibody HFE7A heavy chain.
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; complementarity determining region; CDR; human Fas;
KW Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX OS Mus musculus.
XX PN JP2000169393-A.
XX PD 20-JUN-2000.
XX PF 30-SEP-1999; 99JP-0278301.
XX PR 30-SEP-1998; 98JP-0276883.
XX PA (SANY) SANKYO CO LTD.
XX DR WPI; 2000-485645/43.
XX N-PSDB; AAA72108.
XX PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -

XX PS Example 4; Page 67-68; 139pp; Japanese.
XX CC The invention relates to compositions for the prevention or treatment
CC of diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. The present sequence represents the
CC heavy chain of the murine anti-human Fas monoclonal antibody HFE7A,
CC which is produced by hybridoma HFE7A (FERM-BP-5828).
XX SQ Sequence 464 AA;

Query Match 100.0%; Score 246; DB 21; Length 464;
Best Local Similarity 42.5%; Pred. No. 3.9e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 50 symwqwkprpggglewgeidpsdsytnyqkfkgtlvtstssstymqlssltse 109

QY 61 XXXXXXXXNRDYSNNWYFDV 80
: : : : : | | | | | : : : : :
Db 110 savvycaarnrdysnnwyfdv 129

RESULT 6
AAW90897
ID AAW90897 standard; Protein; 464 AA.
XX AC AAW90897;
XX DT 08-AUG-2000 (first entry)
XX DE Murine anti-Fas antibody HFE7A heavy chain protein.
XX KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antarteriosclerotic;
KW hepatotropic; apoptosis; systemic lupus erythematosus; HFE7A;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX OS Mus musculus.
XX PN EP990663-A2.
XX PD 05-APR-2000.
XX PF 29-SEP-1999; 99EP-0307711.
XX PR 30-SEP-1998; 98JP-0276881.
XX PR 30-SEP-1998; 98JP-0276882.
XX PA (SANY) SANKYO CO LTD.
XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
XX N-PSDB; AAA11546.

XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Example reference 4; Page 100-102; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thymoregimetic,
CC antirheumatic, nephrotropic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a murine anti-Fas monoclonal antibody HFE7A heavy chain described in the
CC method of the invention.
XX
SQ Sequence 464 AA;

Query Match 100.0%; Score 246; DB 21; Length 464;
Best Local Similarity 42.5%; Pred. NO. 3.9e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEDPSYTYNQKFGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMQVKGKPGGKLEIGEDPSYTYNQKFGKATLTVDTSSTAYMQLSLTSD 109
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 SAVYYCARNDYSNNWYFDV 129

RESULT 7
ID AAW83036 standard; Protein: 470 AA.
XX
AC AAW83036;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas humanised antibody HFE7A heavy chain.
XX
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX

OS Homo sapiens.
OS Synthetic.
XX
FH Key
FT Peptide
FT 1..19
FT /label= Sig_peptide
FT 20..470
FT /label= Mat_protein
FT 20..140
FT /label= Variable
FT 141..464
FT /label= Constant
FT 50..54
FT /label= CDR_H1
FT /note= "claim 9"
FT 69..84
FT /label= CDR_H2
FT /note= "claim 9"
FT 118..129
FT /label= CDR_H3
FT /note= "claim 9"
XX AU9859701-A.
PD 08-OCT-1998.
XX 30-MAR-1998; 99AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
XX 01-APR-1997; 97JP-0082953.
XX 25-JUN-1997; 97JP-0169088.
XX (SANY) SANKYO CO LTD.
XX
PI Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX
DR WPI: 1998-543440/47.
DR N-PSDB; AAV70079.
XX
PT New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX
PS Claim 22; Page 212-213; 292pp; English.
XX
CC This is the amino acid sequence of the VD type humanised heavy
CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
CC pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion
CC fragment of the humanised VD type HFE7A heavy chain and DNA
CC encoding human IgG1 constant region (see AAV70079), and is deposited
CC as FERM BP-6074 (claimed). The invention provides methods for
CC producing humanised antibodies by culturing host cells. Humanised
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
CC of inducing apoptosis in abnormal cells expressing Fas, and of
CC inhibiting Fas-induced apoptosis in normal cells. The humanised
CC antibodies are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to
CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 246; DB 19; Length 470;


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XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72159.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX Claim 21; Page 95-96; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX Sequence 470 AA;

Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. No. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXXXXDEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMQVKGAPGRLWNGEIDPSDSTYNQKFGKATLTVDTSASTAYMELSLRSED 109
Qy 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 TAVYYCARNRDSNNWYFDV 129

RESULT 10
AAB14779
ID AAB14779 standard; Protein; 470 AA.
XX AC AAB14779;
XX DT 24-NOV-2000 (first entry)
XX DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
XX KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
XX murine; humanised antibody; complementarity determining region; CDR;
XX human Fas; Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
XX hepatitis; AIDS; graft rejection; heavy chain.
XX OS Chimeric - Mus musculus.
XX OS Chimeric - Homo sapiens.
XX PN JP2000169393-A.
XX PD 20-JUN-2000.
XX PF 30-SEP-1999; 99JP-0278301.
XX PR 30-SEP-1998; 98JP-0276883.

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PA (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72184.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX Claim 21; Page 108-109; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX Sequence 470 AA;

Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. No. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXXXXDEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMQVKGAPGRLWNGEIDPSDSTYNQKFGKATLTVDTSASTAYMELSLRSED 109
Qy 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 TAVYYCARNRDSNNWYFDV 129

RESULT 11
AAW90926
ID AAW90926 standard; Protein; 470 AA.
XX AC AAW90926;
XX DT 08-AUG-2000 (first entry)
XX DE Humanised HFE7A designed heavy chain protein.
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjorgen's syndrome; anaemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX OS Synthetic.
XX PN EP990663-A2.
XX PD 05-APR-2000.
XX PF 29-SEP-1999; 99EP-0307711.
XX PR 30-SEP-1998; 98JP-0276881.

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PR 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR N-PSDB; AAA11597.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
XX Example reference 15; Page 134-136; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, cardiatic and hepatotropic activity. (I) induce
CC antiarteriosclerotic, cardiatic and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
CC the method described in the invention.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. NO. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXXXXFEIDPSDTYTNQKFGXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMQVVKQPGGRLWGMGEIDPSDSTYTNQKFGKATLTDTSASTAMELSSRSD 109

QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 TAVYYCARNDYSNNWYFDV 129

RESULT 12
AAW90929
ID AAW90929 standard; Protein; 470 AA.
XX
XX AAW90929;
XX
XX 08-AUG-2000 (first entry)
XX
XX Humanised HFE7A designed heavy chain protein #2.
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiatic;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW

hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX Synthetic.
XX EP990663-A2.
PN
XX 05-APR-2000.
PD
XX 29-SEP-1999; 99EP-0307711.
XX
XX 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
XX (SANY) SANKYO CO LTD.
PA
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI; 2000-258930/23.
XX N-PSDB; AAA11622.
DR
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
XX Example reference 22; Page 150-152; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiatic and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
CC the method described in the invention.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. NO. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXXXXFEIDPSDTYTNQKFGXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMQVVKQPGGRLWGMGEIDPSDSTYTNQKFGKATLTDTSASTAMELSSRSD 109

QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 TAVYYCARNDYSNNWYFDV 80

RESULT 12
AAW90929
ID AAW90929 standard; Protein; 470 AA.
XX
XX AAW90929;
XX
XX 08-AUG-2000 (first entry)
XX
XX Humanised HFE7A designed heavy chain protein #2.
XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiatic;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW

Db 110 tavyycarnrdysnnwyfdv 129

RESULT 13
AAW90933
ID AAW90933 standard; Protein: 470 AA.
XX AC AAW90933;
XX DT 08-AUG-2000 (first entry)
XX DE Humanised anti-Fas designed heavy chain Heu 1 protein.
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX OS Synthetic.
XX EP990663-A2.
XX PN 05-APR-2000.
XX PD 29-SEP-1999; 99EP-0307711.
XX PF 30-SEP-1998; 98JP-0276881.
XX PR 30-SEP-1998; 98JP-0276882.
XX PA (SANY) SANKYO CO LTD.
XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX N-PSDB; AAA11644.
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems -
XX Claim 2; Page 169-170; 263pp; English.
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,
XX antirheumatic, nephrotropic, antiinfertility, neuroprotective,
XX antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
XX apoptosis by binding to cell surface Fas or inhibit it by competitive
XX inhibition of ligand binding. (I) are used to treat and/or prevent
XX diseases associated with the Fas/Fas ligand system, especially systemic
XX lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
XX versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
XX anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
XX disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
XX multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
XX dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
XX cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
XX (B, C or D) or alcoholic), and transplant rejection. (I) selectively
XX inhibit apoptosis in normal cells but selectively induce it in abnormal
XX cells. They bind to both human and murine Fas, so can be evaluated in
XX murine disease models. (I) act on the active site of Fas, i.e. they mimic
XX the native ligand, do not induce liver disease, and have reduced risk of

CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
CC which is described in the method of the invention.
XX SQ Sequence 470 AA;
Query Match 100.0%; Score 246; DB 21; Length 470;
Best Local Similarity 42.5%; Pred. No. 4.1e-10;
Matches 34; Conservative 46; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYWMQXXXXXXXXXXXXXXXXXXEIDPSDSTYNKFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWMQVWKGPGGLWNGEIDPSDSTYNNGKFGKATLTVDSTSTAYMELSLRSD 109
Qy 61 XXXXXXXXNRDYSNNWYFDV 80
Db 110 tavyycarnrdysnnwyfdv 129
RESULT 14
AAW90934
ID AAW90934 standard; Protein: 470 AA.
XX AC AAW90934;
XX DT 08-AUG-2000 (first entry)
XX DE Humanised anti-Fas designed heavy chain Heu 2 protein.
XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX OS Synthetic.
XX EP990663-A2.
XX PN 05-APR-2000.
XX PD 29-SEP-1999; 99EP-0307711.
XX PF 30-SEP-1998; 98JP-0276881.
XX PR 30-SEP-1998; 98JP-0276882.
XX PA (SANY) SANKYO CO LTD.
XX PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-258930/23.
XX N-PSDB; AAA11645.
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
XX inflammatory or autoimmune disease, induces apoptosis selectively in
XX cells with abnormal Fas-Fas ligand systems -
XX Claim 2; Page 174-176; 263pp; English.
XX This invention describes a novel humanized anti-Fas antibody-like
XX molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
XX ligand system, by binding to Fas on the cell surface, and prevents
XX apoptosis in cells with a normal system, by inhibiting binding between
XX Fas and its ligand. The products of the invention have anti-inflammatory,
XX anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
XX immunomodulatory, dermatological, immunosuppressive, thyromimetic,

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Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	176	71.5	119	2	US-08-553-497A-8	Sequence 8, Appl	
2	176	71.5	119	2	US-08-553-497A-12	Sequence 12, Appl	
3	164	66.7	111	3	US-08-881-037-14	Sequence 14, Appl	
4	164	66.7	111	3	US-08-881-037-16	Sequence 16, Appl	
5	164	66.7	119	3	US-08-881-037-61	Sequence 61, Appl	
6	164	66.7	119	3	US-08-881-037-62	Sequence 62, Appl	
7	160	65.0	111	3	US-08-881-037-17	Sequence 17, Appl	
8	160	65.0	119	3	US-08-881-037-63	Sequence 63, Appl	
9	159	64.6	98	3	US-08-881-037-59	Sequence 59, Appl	
10	157.5	64.0	241	1	US-08-235-838-11	Sequence 11, Appl	
11	157.5	64.0	241	2	US-08-465-473B-11	Sequence 11, Appl	
12	157.5	64.0	637	1	US-08-235-838-16	Sequence 16, Appl	
13	157.5	64.0	637	2	US-08-465-473B-16	Sequence 16, Appl	
14	157	63.8	111	3	US-08-881-037-15	Sequence 15, Appl	
15	157	63.8	119	3	US-08-881-037-60	Sequence 60, Appl	
16	155	63.0	117	3	US-09-027-449-48	Sequence 48, Appl	
17	155	63.0	117	3	US-09-027-449-49	Sequence 49, Appl	
18	155	63.0	117	3	US-08-804-444A-48	Sequence 48, Appl	
19	155	63.0	117	3	US-08-804-444A-49	Sequence 49, Appl	
20	155	63.0	117	4	US-09-026-985-48	Sequence 48, Appl	
21	155	63.0	117	4	US-09-026-985-49	Sequence 49, Appl	
22	147.5	60.0	135	1	US-08-398-613A-50	Sequence 50, Appl	
23	147.5	60.0	135	1	US-08-398-612A-50	Sequence 50, Appl	
24	147.5	60.0	135	1	US-08-398-611A-50	Sequence 50, Appl	
25	147.5	60.0	135	2	US-08-491-334A-50	Sequence 50, Appl	
26	147.5	60.0	135	3	US-09-027-449-37	Sequence 37, Appl	
27	147.5	60.0	135	3	US-08-804-444A-37	Sequence 37, Appl	

```

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MERCK 1726
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
TELEFAX: 703-243-6410
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids

```

```
Qy      1 SYWQXXXXXXXXXXXXXIEDPSDSTYNQNKFXXXXXXXXXXXXXXXXXXXXX 60
        ||| : : : : : : : : | | | | | | | | : : : : : : : : : :
Db     23 SYNHWKVRPGGGLWEIGEDPSDSTYNNOKFGKATLVDKSSATYMOJSLTSED 82
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QY 61 XXXXXXXXNR 70
Db 83 SAVIYCAKGR 92

RESULT 4

US-08-881-037-16
Sequence 16, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-16

Query Match 66.7%; Score 164; DB 3; Length 111;
Best Local Similarity 30.0%; Pred. No. 7.7e-06;
Matches 21; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTNNQKFKGXXXXXXXXXXXXXXXXXXXX 60
Db 23 SYWHVVKRPGQGLEWIGEDPSDYTYNNQKFKGKATLTVDKSSSTAYMQLSLTSED 82

QY 61 XXXXXXXXNR 70
Db 83 SAVIYCAKGR 92

RESULT 5

US-08-881-037-61
Sequence 61, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-JUN-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 203442110710
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-881-037-61

Query Match 66.7%; Score 164; DB 3; Length 119;
Best Local Similarity 30.0%; Pred. No. 9.5e-06;
Matches 21; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTNNQKFKGXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYWHVVKRPGQGLEWIGEDPSDYTYNNQKFKGKATLTVDKSSSTAYMQLSLTSED 90

QY 61 XXXXXXXXNR 70
Db 91 SAVIYCAKGR 100

RESULT 6

US-08-881-037-62
Sequence 62, Application US/08881037
Patent No. 6080588
GENERAL INFORMATION:
APPLICANT: Glick, Gary D.
APPLICANT: Swanson, Patrick C.
TITLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/881,037

; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-62

Query Match 66.7%; Score 164; DB 3; Length 119;
Best Local Similarity 30.0%; Pred. No. 9.5e-06;
Matches 21; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXXXXXX 60
DB 31 SYWMHWKQPGGLEWIGEDPSDSTYNNQKFGKATLTVDKSSSTAYMQLSLTSED 90

QY 61 XXXXXXXXNR 70
DB 91 SAVYYCAKGR 100

RESULT 7
US-08-881-037-17
; Sequence 17, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:

; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-17

Query Match 65.0%; Score 160; DB 3; Length 111;
Best Local Similarity 29.0%; Pred. No. 1.7e-05;
Matches 20; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXXXXXX 61
DB 24 YWMHWKQPGGLEWIGEDPSDSTYNNQKFGKATLTVDKSSSTAYMQLSLTSED 83

QY 62 XXXXXXXXNR 70
DB 84 AVYYCAKGR 92

RESULT 8
US-08-881-037-63
; Sequence 63, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-881-037-63

Query Match 65.0%; Score 160; DB 3; Length 119;
Best Local Similarity 29.0%; Pred. No. 2.1e-05;
Matches 20; Conservative 46; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWMQXXXXXXXXXXEIDPSDSTYNNQKFGXXXXXXXXXXXXXXXXXXXXXXXXX 61

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Db 32 YMHVWVKRPGQGLEWIGEDPSDYTYNQKFKGKATLTVDKSTWYMQLSLTSRDS 91
QY 62 XXXXXXXXNR 70
Db 92 AVYYCAKGR 100

RESULT 9
US-08-881-037-59
; Sequence 59, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Click, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-59

Query Match 64.6%; Score 159; DB 3; Length 98;
Best Local Similarity 29.4%; Pred. No. 1.5e-05;
Matches 20; Conservative 46; Mismatches 2; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDYTYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYMHVWVKRPGQGLEWIGEDPSDYTYNQKFKGKATLTVDKSSSTWYMQLSLTSRDS 90
QY 61 XXXXXXXX 68
Db 91 SAVYYCAK 98

RESULT 10
US-08-235-838-11
; Sequence 11, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
```

```
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd
; APPLICANT: Hardman, No. 5571894man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,838
; FILING DATE: TBA
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,832
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91-810079.3
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-235-838-11

Query Match 64.0%; Score 157.5; DB 1; Length 241;
Best Local Similarity 27.5%; Pred. No. 0.00031;
Matches 22; Conservative 47; Mismatches 10; Indels 1; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPSDYTYNQKFKGXXXXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 32 SYMHVWVKRPGQGLEWIGEDPSDYTYNQKFKGKATLTVDKSSSTWYMQLSLTSRDS 91
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 92 SAVYYCAKG-GASGDWYFDV 110

RESULT 11
US-08-465-473B-11
; Sequence 11, Application US/08465473B
; Patent No. 5939531
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd
; APPLICANT: Hardman, No. 5939531man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 34
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Best Local Similarity 30.9%; Pred. No. 2e-05;

Matches 21; Conservative 47; Mismatches 0; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 31 NYWMQVVKQPGGLEWIGIEDPSDSTYNQKFGKATLTVDTSSTAYMQLSLTSED 90
QY 61 XXXXXXXX 68
Db 91 SAVVYCAR 98

RESULT 3
S26463
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26463
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26463
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <KAV>
A:Cross-references: EMBL:X59113; NID:g51922; PIDN:CAA41839.1; PID:g51923
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 68.1%; Score 167.5; DB 2; Length 111;
Best Local Similarity 28.8%; Pred. No. 3.2e-05;
Matches 23; Conservative 48; Mismatches 8; Indels 1; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 23 SYWINVVKQPGGLEWIGIENIPSDSTYNQKFK-DKATLTVDKSSSTAYMQLSPSTE 81
QY 61 XXXXXXXXNRDYSNNWYFDV 80
Db 82 DSAVYCTRYGYGYNWYFDV 101

RESULT 4
PH1162
Ig heavy chain V region (clone 10C.2A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1162
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545
A:Accession: PH1162
A:Molecule type: DNA
A:Residues: 1-87 <SCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;6-87/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 165; DB 2; Length 87;
Best Local Similarity 31.8%; Pred. No. 3.7e-05;
Matches 21; Conservative 44; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 22 SYWMQVVKQPGGLEWIGIEDPSDSTYNQKFGKATLTVDKSSSTAYMQLSLTSED 81

QY 61 XXXXXX 66

Db 82 SAVFYC 87

RESULT 5
PH1161
Ig heavy chain V region (clone 13B.2A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: PH1161
R:Schitteck, B.; Rajewsky, K.
J. Exp. Med. 176, 427-438, 1992
A:Title: Natural occurrence and origin of somatically mutated memory B cells in mice.
A:Reference number: PH1105; MUID:92364545
A:Accession: PH1161
A:Molecule type: DNA
A:Residues: 1-88 <SCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-88/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 163; DB 2; Length 88;
Best Local Similarity 31.8%; Pred. No. 5.6e-05;
Matches 21; Conservative 44; Mismatches 1; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 23 SYWMQVVKQPGGLEWIGIHFPSDSTYNQKFGKATLTVDKSSSTAYMQLSLTSED 82

QY 61 XXXXXX 66
Db 83 SAVFYC 88

RESULT 6
PL0089
Ig heavy chain V region (12S18-1) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
C:Accession: PL0089
R:Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.;
J. Exp. Med. 169, 519-533, 1989
A:Title: Structural characterization of antidiotypic antibodies; evidence that Ab25
A:Reference number: PL0080; MUID:89094248
A:Accession: PL0089
A:Molecule type: mRNA
A:Residues: 1-119 <MEE>
A:Cross-references: GB:X59580; GB:Y00794; NID:g51591; PIDN:CAA41456.1; PID:g930150
A:Note: the sequence shown here is from the VH region of an antidiotypic monoclonal
A:Note: sequences from two other clones (18S28-16 and 12S84-3) were almost identical
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 163; DB 2; Length 119;
Best Local Similarity 27.5%; Pred. No. 8.9e-05;
Matches 22; Conservative 47; Mismatches 9; Indels 2; Gaps 1;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
Db 31 NYWMQVVKQPGGLEWIGIENIPSDSTYNQKFGKATLTVDTSSTAYMQLSLTSED 90

QY 61 XXXXXXXXNRDYSNNWYFDV 80

Db 91 SAVYICARNEGVA--WYFDV 108

RESULT 7
B22769
Ig heavy chain V region (B1-8.V1/V2) - mouse (tentative sequence)
C:Species: Mus musculus (house mouse)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996

[illegible]

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:11:47 ; Search time 53.64 Seconds
(without alignments)
57.747 Million cell updates/sec

Title: 2_g_3_g_4
Perfect score: 246
Sequence: 1 SYWMQXXXXXXXXXXE.....XXXXXXXXXXRDYNNWYFDV 80

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	150	61.0	117	1	HV12_MOUSE
2	147.5	60.0	120	1	HV50_MOUSE
3	146	59.3	117	1	HV13_MOUSE
4	145	58.9	117	1	HV06_MOUSE
5	140	56.9	120	1	HV03_MOUSE
6	139.5	56.7	139	1	HV07_MOUSE
7	133.5	54.3	138	1	HV48_MOUSE
8	133	54.1	140	1	HV02_MOUSE
9	132	53.7	117	1	HV05_MOUSE
10	130	52.8	121	1	HV01_MOUSE
11	125.5	51.0	118	1	HV51_MOUSE
12	125	50.8	117	1	HV04_MOUSE
13	124	50.4	117	1	HV09_MOUSE
14	124	50.4	117	1	HV10_MOUSE
15	124	50.4	117	1	HV49_MOUSE
16	121	49.2	117	1	HV42_MOUSE
17	113.5	46.1	119	1	HV38_MOUSE
18	111	45.1	117	1	HV41_MOUSE
19	110	44.7	136	1	HV15_MOUSE
20	109.5	44.5	118	1	HV39_MOUSE
21	109.5	44.5	137	1	HV11_MOUSE
22	109	44.3	117	1	HV16_MOUSE
23	108.5	44.1	323	1	CO3_XENLA
24	108	43.9	117	1	HV18_MOUSE
25	107	43.5	119	1	HV40_MOUSE
26	105	42.7	117	1	HV52_MOUSE
27	105	42.7	119	1	HV37_MOUSE
28	104.5	42.5	123	1	HV24_MOUSE
29	104	42.3	114	1	HV00_MOUSE
30	103.5	42.1	123	1	HV18_MOUSE
31	103.5	42.1	142	1	HV01_RAT
32	103.5	42.1	144	1	HV26_MOUSE
33	103	41.9	116	1	HV36_MOUSE

34	103	41.9	122	1	HV20_MOUSE
35	103	41.9	275	1	EPI2_STAEP
36	102.5	41.7	657	1	CN16_HAEIN
37	101.5	41.3	123	1	HV19_MOUSE
38	100.5	40.9	123	1	HV22_MOUSE
39	99.5	40.4	123	1	HV23_MOUSE
40	99.5	40.4	740	1	KRB6_CANAL
41	99	40.2	552	1	API_SCHPO
42	99	40.2	1097	1	DPD0_YEAST
43	98	39.8	147	1	HVIC_HUMAN
44	97.5	39.6	652	1	CN16_YEREN
45	97.5	39.6	720	1	KRB6_YEAST

ALIGNMENTS

RESULT 1					
HV12_MOUSE					
ID	HV12_MOUSE	STANDARD;	PRT;	117 AA.	
AC	P01756;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V region MOPC 104E.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				P01789 mus musculus
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				P30193 staphylococ
OX	NCBI_TaxID=10090;				P44764 haemophilus
RN	[1]				P01788 mus musculus
RP	SEQUENCE.				P01791 mus musculus
RX	MEDLINE=83075344; PubMed=6816276;				P01792 mus musculus
RA	Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,				P87023 candida alb
RA	Hood L.E.;				Q001663 schizosacch
RT	"Complete amino acid sequence of a mouse mu chain: homology among				P15436 saccharomyc
RT	heavy chain constant region domains.";				P01744 homo sapien
RL	Biochemistry 21:5415-5424(1982).				P53052 versinia en
CC	- - MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA				P32486 saccharomyc
CC	PROTEIN HAS ALSO BEEN DETERMINED.				
CC	- - MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.				
DR	PIR; A02039; MHMS4E.				
DR	InterPro; IPR003006; Iq_MHC.				
DR	InterPro; IPR003596; Iq_v.				
DR	Pfam; PF00047; ig; 1.				
DR	SMART; SM00406; Igv; 1.				
KW	Immunoglobulin V region; Glycoprotein.				
FT	DISULFID 22 96				
FT	CARBOHYD 55 55				
FT	NON_TER 117 117				
SQ	SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;				
Query Match	61.0%;	Score	150;	DB 1;	Length 117;
Best Local Similarity	25.3%;	Pred. No.	0.00043;		
Matches	20;	Conservative	53;	Mismatches	2;
Indels	4;	Gaps	2;		
QY	2	YWMQXXXXXXXXXXEIDPSDSTNTYNQKFKGXXXXXXXXXXXXXXXXXXXXXXX 61			
Db	32	YWMQVVKQSGKSLWIGDINPNNGTSTYNQKFKGKATLTVDKSSSTAYVWQLNLTSEDS 91			
QY	62	XXXXXXXXXXRDYNNWYFDV 80			
Db	92	AVTYCA--RDY--DWYFDV 106			
RESULT 2					
HV50_MOUSE					
ID	HV50_MOUSE	STANDARD;	PRT;	120 AA.	
AC	P06329;				
DT	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Ig heavy chain V region AC38 15.3.				

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 105
FT DOMAIN 106 120
FT DISULFID 22 96
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 60.0%; Score 147.5; DB 1; Length 120;
Best Local Similarity 25.0%; Pred. No. 0.00073;
Matches 20; Conservative 50; Mismatches 9; Indels 1; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYMHWIRQPGGLEWIGGINSNGTNYNEKFKSKATLTVDKSSATYMLSTPSE 89
Qy 61 XXXXXXXXNRDYSNNWYFDV 80
Db 90 DSAVYICARWDYEGDRYFDV 109

RESULT 3
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;

Query Match 59.3%; Score 146; DB 1; Length 117;

Best Local Similarity 22.8%; Pred. No. 0.00094;
Matches 18; Conservative 54; Mismatches 3; Indels 4; Gaps 1;
Qy 2 YWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 61
Db 32 YMKVVKQSHGKSLWIGDINPNNGGTSYNQKFKGKATLTVDKSSATYMLSLTSDS 91
Qy 62 XXXXXXXXNRDYSNNWYFDV 80
Db 92 AVIYCARDR----YWFYFDV 106

RESULT 4
HV06_MOUSE
ID HV06_MOUSE STANDARD; PRT; 117 AA.
AC P01750;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 102 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Faskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; A02032; HVMS02.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 58.9%; Score 145; DB 1; Length 117;
Best Local Similarity 26.5%; Pred. No. 0.0011;
Matches 18; Conservative 46; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYMHWVKRPGGLEWIGRHPDSDTNYNEKFKGKATLTVDKSSATYMLSLTSED 109
Qy 61 XXXXXXXX 68
Db 110 SAVYICAI 117

RESULT 5
HV03_MOUSE
ID HV03_MOUSE STANDARD; PRT; 120 AA.
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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CC -----
DR EMBL: J00529; AAA38170.1; -.
DR PIR: A02034; MHMS18.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 56.7%; Score 139.5; DB 1; Length 139;
Best Local Similarity 22.8%; Pred. No. 0.0046;
Matches 18; Conservative 49; Mismatches 11; Indels 1; Gaps 1;

QY 1 SYNMQXXXXXXXXXXEIDPSDYNTNOKFKGXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYNMHWYKQPRGLEWIGRIDPNSGCTKYNEFK-SKATLTVDKPSSTAYMQLSLTSE 108
QY 61 XXXXXXXXXNRDYSNNWTFD 79
Db 109 DSAVYVCARYDYVGYSSYFD 127

RESULT 7
HV48_MOUSE STANDARD; PRT; 138 AA.
ID ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR: A02033; HVMST7.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138
FT DOMAIN 21 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 127
FT DOMAIN 128 130
FT DISULFID 41 115
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

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QY 2 YWQXXXXXXXXXXXXXETDPSVTNYNQKFGXXXXXXXXXXXXXXXXXXXXXXX 61
Db 32 YYNWKVKQSHGKLEWIGDINPNNGGTSYNQKFKGKATLTVDKSSSATYMLRSLTSEDS 91
QY 62 XXXXXXXXXXXRDYSNNWYFDV 80
Db 92 AVTYCARGYDYP---FDV 107

RESULT 12
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC *- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR FIR; A02030; HVMS23.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 50.8%; Score 125; DB 1; Length 117;
Best Local Similarity 19.1%; Pred. No. 0.06;
Matches 13; Conservative 49; Mismatches 6; Indels 0; Gaps

QY 1 SYWQXXXXXXXXXXXXXETDPSVTNYNQKFGXXXXXXXXXXXXXXXXXXXXXXX 61
Db 50 SYWNVKQPGGQLEWIGNPNNGGTSYNQKFKGKATLTVDKSSSATYMLRSLTSEDS 109
QY 61 XXXXXXXX 68
Db 110 SAVVYCAR 117

RESULT 13
HV09_MOUSE
ID HV09_MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 186-1 precursor.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
DR PIR; B02034; HVMS61.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 50.4%; Score 124; DB 1; Length 117;
Best Local Similarity 19.1%; Pred. No. 0.073; 7; Indels 0; Gaps 0;
Matches 13; Conservative 48; Mismatches 7; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWHVVKQPRGRLWIGRIDPNSGTYNEKFKSKATLTVDTSSSTAYMQLSLTSED 109
QY 61 XXXXXXXX 68
Db 110 SAVYYCAR 117

RESULT 14
HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 145 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies; somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
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CC or send an email to license@isb-sib.ch).
DR EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
```

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CC -----
DR EMBL; J00533; AAA38602.1; -.
DR PIR; C02034; HVMS45.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37DE8A3F543E996 CRC64;

Query Match 50.4%; Score 124; DB 1; Length 117;
Best Local Similarity 19.1%; Pred. No. 0.073; 7; Indels 0; Gaps 0;
Matches 13; Conservative 48; Mismatches 7; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNQKFGKXXXXXXXXXXXXXXXXXXXXX 60
Db 50 SYWHVVKQPRGRLWIGRIDPNSGTYNEKFKSKATLTVDKPSTAYMQLSLTSED 109
QY 61 XXXXXXXX 68
Db 110 SAVYYCAR 117

RESULT 15
HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC or send an email to license@isb-sib.ch).
DR EMBL; M13788; AAA38506.1; -.
DR PIR; A02035; MHMSB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 B4.
FT DOMAIN 20 49 FRAMEWORK-1.
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Search completed: August 14, 2002, 15:23:12
Job time: 685 sec

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Query Match          75.8%; Score 186.5; DB 1; Length 143;  
Best Local Similarity 32.5%; Pred. No. 1.8e-05;  
Matches 26; Conservative 47; Mismatches 4; Indels 3; Gaps 1;  
  
QY      1 SYMOMXXXXXXXXXXXXEIDPSDYTNYNQKFKGXXXXXXXXXXXXXXXXXX 60  
       |||| : ::::: : ||||||| ||||| : ::::: :  
Db      31 SYMHVVKRPGGLEWIGVIDPSDYTNYNQKFKGKATLVDTSSSTAYMLSLTSED 90  
  
QY      61 XXXXXXXXXXXNRDYSNNWFEDV 80  
       : ::::: | : ||||  
Db      91 SAVVYCPTVD---DWVFEDV 107
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RESULT 2
Q924P9 ID Q924P9 PRELIMINARY; PRT; 143 AA.
AC Q924P9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE V303-D-J-C MU PROTEIN (FRAGMENT).
GN V303-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069916; BAB63932.1; -.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; 43CD8C72D52134F6 CRC64;

Query Match 71.1%; Score 175; DB 11; Length 143;
Best Local Similarity 30.8%; Pred. No. 0.00014;
Matches 24; Conservative 50; Mismatches 4; Indels 0; Gaps 0;

QY 1 SYWMQXXXXXXXXXXEIDPSDSTYNNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 31 SYWMQVVKQPGQGWGEIDPSDIYDYNQEFKGAITLVDTSSTAYMQLSLTSED 90

QY 61 XXXXXXXXXNRDYSNNWYF 78
    ::::: || |
Db 91 SAVYTCAR-RYYGGDYW 107

RESULT 4
Q91WT3 ID Q91WT3 PRELIMINARY; PRT; 481 AA.
AC Q91WT3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013488; AAH13488.1; -.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4EB5C253038B718 CRC64;

Query Match 64.8%; Score 159.5; DB 11; Length 481;
Best Local Similarity 27.3%; Pred. No. 0.029;
Matches 21; Conservative 50; Mismatches 5; Indels 1; Gaps 1;

QY 2 YWQXXXXXXXXXXEIDPSDSTYNNQKFGKXXXXXXXXXXXXXXXXXXXXXXXXX 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 51 YWMVVKQPGQGWGEIDPSDSTYNNQKFGKTTLTVDTSSTAYMQLSLTSEDA 110

QY 62 XXXXXXXXXNRDYSNNWYF 78
    ::::: || |
Db 111 VYFCARGPRD-SSGYW 126

RESULT 5
Q924R3 ID Q924R3 PRELIMINARY; PRT; 145 AA.
AC Q924R3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE VHI86.2-D-J-C MU PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067787; BAB63272.1; -.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 15996 MW; 35B1A36E4280BA81 CRC64;

Query Match 64.4%; Score 158.5; DB 11; Length 145;
Best Local Similarity 25.0%; Pred. No. 0.003;
Matches 20; Conservative 48; Mismatches 11; Indels 1; Gaps 1;
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Qy	61	XXXXXXXXXXNRDYSNNWYFDV	80
Dd	91	SAVYYCARFYDYE---YFDV	107

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RESULT 9
Q9QXF0
ID Q9QXF0 PRELIMINARY; PRT; 117 AA.
AC Q9QXF0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
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DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE VJ186.2-D-J-C MU PROTEIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067793; BAB63278.1; -.
FT NON_TER 1
FT NON_TER 145
SQ SEQUENCE 145 AA; 16141 MW; 55A59A7908B2CD6A CRC64;

Query Match 56.7%; Score 139.5; DB 11; Length 145;
Best Local Similarity 22.8%; Pred. No. 0.094;
Matches 18; Conservative 49; Mismatches 11; Indels 1; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXEIDPDSYTNYNQKFGXXXXXXXXXXXXXXXXXXXXX 60
Db 31 SYWMHWKQPGQGLEWIGRIDPNPNSGGTKYNEKEK-SKATLTVDKPSSTAYMQLSSLTSE 89

Qy 61 XXXXXXXXNRDYSNNWYFD 79
Db 90 DSAVIYCARVDYGSYFD 108

RESULT 14
ID Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808 (2000).
DR EMBL; AF206029; AAF69327.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;

Query Match 55.5%; Score 136.5; DB 11; Length 110;
Best Local Similarity 20.5%; Pred. No. 0.092;
Matches 16; Conservative 54; Mismatches 7; Indels 1; Gaps 1;

Qy 1 SYWMQXXXXXXXXXXEIDPDSYTNYNQKFG-XXXXXXXXXXXXXXXXXXXXX 59
Db 23 SSMHWAKQPGQGLEWIGIHPNSGHTNYNEKFKGKATLTVDTSSTAYVDLSLTSED 82
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Qy 60 XXXXXXXXNRDYSNNWY 77
Db 83 SAVVYCARQRRNYAMDY 100

RESULT 15
ID Q924Q0 PRELIMINARY; PRT; 143 AA.
AC Q924Q0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE V165-D-J-C MU PROTEIN (FRAGMENT).
GN V165-D-J-C MU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069915; BAB63931.1; -.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 15704 MW; C99D2433F2BAD8A0 CRC64;
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Best Local Similarity 21.5%; Pred. No. 0.19;
Matches 17; Conservative 51; Mismatches 8; Indels 3; Gaps 1;

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Db 31 SYWITWVKQPGQGLEWIGDIYFGSGSTNYNEKFSKATLTVDKPSSTAYMQLSLTSED 90

Qy 61 XXXXXXXXNRDYSNNWYFD 79
Db 91 SAVIYCAPD---SNHLYFD 106
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Job time: 680 sec

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:35 ; Search time 230.21 Seconds
(without alignments)
226.770 Million cell updates/sec

Title: US-09-499-662-143
Perfect score: 2517
Sequence: 1 MGWSCIIIFLVATATGVHSQ.....MHEALHNYTKSLSLSPGK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1982.DAT.*
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14: /SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1993.DAT.*
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18: /SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA1998.DAT.*
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22: /SIDS1/gcgdata/hold-genseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	21	AAW90933 Humanised anti-Fas
2	2515	99.9	470	21	AAW90934 Humanised anti-Fas
3	2514	99.9	470	19	AAW83037 Anti-Fas humanised
4	2514	99.9	470	21	AAW14779 Humanised anti-Fas
5	2514	99.9	470	21	AAW90929 Humanised HFE7A de
6	2514	99.9	470	21	AAW90935 Humanised anti-Fas
7	2501	99.4	470	19	AAW83036 Anti-Fas humanised
8	2501	99.4	470	21	AAW14776 Humanised anti-Fas
9	2501	99.4	470	21	AAW90926 Humanised HFE7A de
10	2495	99.1	470	21	AAW90936 Humanised HFE7A de
11	2346.5	93.2	731	22	AAW52156 Humanised HMFg-1 h

12	2346.5	93.2	741	22	AAW52159 Humanised HMFg-1 h
13	2341.5	93.0	729	22	AAW52158 Humanised HMFg-1 h
14	2341.5	93.0	739	22	AAW52161 Humanised HMFg-1 h
15	2335.5	92.8	730	22	AAW52157 Humanised HMFg-1 h
16	2335.5	92.8	740	22	AAW52160 Humanised HMFg-1 h
17	2304	91.5	652	19	AAW48650 Heavy chain of hMA
18	2290.5	91.0	465	22	AAW72228 Humanised 323/A3 (
19	2287	90.9	470	21	AAW808026 A dimeric anti-CD2
20	2286	90.8	466	22	AAW03755 Chimeric 2403 IgG
21	2285.5	90.8	464	22	AAW72232 Humanised 323/A3 (
22	2255	89.6	476	20	AAW88464 Monoclonal antibody
23	2251.5	89.5	481	13	AAW24442 Sequence of antibody
24	2248	89.3	472	20	AAW50166 Human reshaped F19
25	2232	88.7	449	14	AAW43339 Completely humanis
26	2232	88.7	449	19	AAW49816 Amino acid sequenc
27	2230	88.6	476	14	AAW31023 Antibody D heavy c
28	2229.5	88.6	583	22	AAW83156 Ganglioside GM2 an
29	2202.5	87.5	467	22	AAW36210 Human immune syste
30	2200.5	87.4	452	20	AAW29458 Recombinant immuno
31	2200.5	87.4	452	21	AAW30322 Humanised anti-IL-
32	2200.5	87.4	452	21	AAW77766 Humanised anti-IL-
33	2200	87.4	472	20	AAW50157 Chimeric mouse/hum
34	2193	87.1	592	22	AAW83838 Amino acid sequenc
35	2191.5	87.1	452	19	AAW89316 Anti-IL-8 humanise
36	2190	87.0	595	20	AAW86003 Anti-5T4 single ch
37	2188.5	86.9	473	22	AAW64475 Human type antihum
38	2186	86.8	474	22	AAW14177 Human novel protei
39	2185.5	86.8	473	22	AAW64471 Human type antihum
40	2181.5	86.7	475	22	AAW63640 Amino acid sequenc
41	2180.5	86.6	473	22	AAW64469 Human type antihum
42	2177	86.5	468	20	AAW55689 D9D10 heavy chain
43	2177	86.5	711	20	AAW85692 MoAbII fusion pro
44	2173.5	86.4	473	22	AAW64473 Human type antihum
45	2162	85.9	470	13	AAW22757 Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1
AAW90933
ID AAW90933 standard; Protein; 470 AA.
AC AAW90933;
DT 08-AUG-2000 (first entry)
XX XX Humanised anti-Fas designed heavy chain Heu 1 protein.
DE DE
XX XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW KW Sjorgren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX XX
OS Synthetic.
XX XX
PN PN EP990663-A2.
XX XX
PD PD 05-APR-2000.
XX XX
PF PF 29-SEP-1999; 99EP-0307711.
XX XX
PR PR 30-SEP-1998; 98JP-0276881.
PR PR 30-SEP-1998; 98JP-0276882.
XX XX
PA PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR N-PSDB; AAA11644.
XX
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
PS
PS Claim 2; Page 169-170; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis, hepatitis; transplant rejection.
XX
XX Synthetic.
OS
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
PD
XX
XX 29-SEP-1999; 99EP-0307711.
PF
XX
XX 30-SEP-1998; 98JP-0276881.
PR
XX
XX 30-SEP-1998; 98JP-0276882.
PR
XX
XX (SANY) SANKYO CO LTD.
PA
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR N-PSDB; AAA11645.
DR
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
XX Claim 2 ; Page 174-176; 263pp; English.
PS
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis, hepatitis; transplant rejection. (I) selectively
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

Db 361 kakgqpreqvvtlppsreemtknqvslclvkqfypsdiavwesnggpnnykttppv 420
QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 421 lqsdgsfflyskltdvksrwqgnvfscsvmhealhnhytqkslspsgk 470
RESULT 2
AAW90934
ID AAW90934 standard; Protein; 470 AA.
XX
AC AAW90934;
XX
XX 08-AUG-2000 (first entry)
DT
XX Humanised anti-Fas designed heavy chain Heu 2 protein.
DE
XX
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
XX Synthetic.
OS
XX
XX EP990663-A2.
XX
XX 05-APR-2000.
PD
XX
XX 29-SEP-1999; 99EP-0307711.
PF
XX
XX 30-SEP-1998; 98JP-0276881.
PR
XX
XX 30-SEP-1998; 98JP-0276882.
PR
XX
XX (SANY) SANKYO CO LTD.
PA
XX
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI; 2000-258930/23.
DR N-PSDB; AAA11645.
DR
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems -
XX
XX Claim 2 ; Page 174-176; 263pp; English.
PS
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 2
CC which is described in the method of the invention.

XX
SQ Sequence 470 AA;

Query Match 99.9%; Score 2515; DB 21; Length 470;
Best Local Similarity 99.8%; Pred. No. 7e-143;
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSQVGVGAEVKKPGASVKYCKRSGSYTFTSYMMQWVKQAP 60

Db 1 mgwscililflvatatgvhsqvlvgsgaevkpgasvkysckasgytftsyymqwkqap 60

QY 61 GQGLEWMEIDPSDSYTNQKFKGKATLVDTSTSTAYMELSSLRSEDTAVYICARNRD 120

Db 61 gqglewmeidpsdsytnqkfkgkatitvdtststaymelsslrse dtavvyicarnrd 120

QY 121 YSNNNYFDWGGCTLVTVSSASTKPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVTS 180

Db 121 ysnnnfyfdwggctlvtvssastkpsvfplapsksts ggtaaigclvkd yfpepvtvs 180

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKDKRVEP 240

Db 181 wnsгалtsгvhtfpavlgssglyslssv tvpssslgtqtyicnvnhkpsntkdkrvep 240

QY 241 KSCDKTHRCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Db 241 kscdkthrcppcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360

Db 301 yvdgvevhnatkpreeqynstyrvvsvl tvl hqdwlngkeykckvsnkalpapiektis 360

QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYGSPDSIAVWESNGOPENNYKTTTPV 420

Db 361 kakgqprepqv ytlppsreemtknqvs ltc lvgfypsdiavwesngopennykttppv 420

QY 421 LDSGSEFLYSKLTVDKSRWQQGNVFCGVMHEALHNYTKQSLSLSPGK 470

Db 421 ldsdgsfflyskltvdksrwqqgnvfscvsmheal hnytkqslslspgk 470

RESULT 3

AAW83037

ID AAW83037 standard; Protein; 470 AA.

XX AC AAW83037;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-Fas humanised antibody HFE7A heavy chain.

XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;

KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;

KW systemic lupus erythematosus; graft versus host disease;

KW Sjogren syndrome; pernicious anaemia; Addison's disease;

KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;

KW rheumatoid arthritis; autoimmune haemolytic anaemia;

KW myasthenia gravis; multiple sclerosis; Basedow's disease;

KW thrombopenia purpura; insulin-dependent diabetes; allergy;

KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;

KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;

KW transplant rejection; therapy.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Peptide 1..19

FT Protein /label= Sig_peptide

FT /label= Mat_protein

FT Region 20..140

FT /label= Variable

FT Region 141..464

FT /label= Constant

FT Region 50..54

FT /label= CDR_H1

FT /note= "Claim 9"

FT Region 69..84

FT /label= CDR_H2

FT /note= "claim 9"

FT Region 118..129

FT /label= CDR_H3

FT /note= "Claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

PR 01-APR-1997; 97JP-0082953.

PR 25-JUN-1997; 97JP-0169088.

XX (SANY) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

PI Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

DR N-PSDB; AAV70080.

XX

PT New antibodies and proteins bind conserved epitope of Fas antigen -

PT used to evaluate drugs in animal models and to treat Fas-associated

PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,

PT myocarditis, hepatitis and AIDS

XX Claim 22; Page 225-227; 292pp; English.

XX

CC This is the amino acid sequence of the HV type humanised heavy

CC chain of murine anti-human Fas monoclonal antibody HFE7A. It

CC includes humanising R44G and A76T amino acid substitutions that are

CC are conserved in the human IgG heavy chain. Host Escherichia coli

CC pgHPDHV3 SANK 70298 harbors plasmid pgHPDHV3 carrying a fusion

CC fragment of the humanised HV type HFE7A heavy chain and DNA

CC encoding human IgG1 constant region (see AAV70080), and is deposited

CC as FERM BP-6273 (claimed). The invention provides methods for

CC producing humanised antibodies by culturing host cells. Humanised

CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable

CC of inducing apoptosis in abnormal cells expressing Fas, and of

CC inhibiting Fas-induced apoptosis in normal cells. The humanised

CC antibodies are used to evaluate, in animal models, treatments of

CC diseases that involve Fas/Fas ligand interactions, and also to

CC treat such diseases, including autoimmune disease (e.g. systemic

CC lupus erythematosus, Hashimoto's disease, graft versus host disease,

CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,

CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,

CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,

CC multiple scleritis, Basedow's disease, thrombopenia purpura and

CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,

CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic

CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).

XX Sequence 470 AA;

SQ

Query Match 99.9%; Score 2514; DB 19; Length 470;

Best Local Similarity 99.8%; Pred. No. 8.1e-143;

Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYFTSYMMQWVKQAP 60
Db 1 mgwsciilflvatatgvsqvlvqsgaevkpkgasvkscasgyftsywmqwkqap 60

Qy 61 GQGLEWNGEIDPSDSYTNYNQKFGKATLVDTSTAYMELSLRSEDVAVYYCARNRD 120
Db 61 gqglewngeidpsdsytnynqkfgkatltvdtststaymelslrseavyyccarnrd 120

Qy 121 YSNWNVFDVWGQGLTVVVSASRKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPTVVS 180
Db 121 ysnwnyfdvwegtclvtvssastkgspsvflpapskstsagtaalgclvkdyfpeptvs 180

Qy 181 WNSGALTSVGHVTHPFAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 181 wnsгалtsvghthfpavllqssglyslssvwtvpssslgtqtyicnvnhkpsntkvdkrvpe 240

Qy 241 KSCDKHTHTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccppapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

Qy 301 YVDGVEVHNAKTRPREQYNSTRYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaktprreeqynstryrvsvltvlhqdwlngkeyckvsknkalpapiektis 360

Qy 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
Db 361 kagqppepvytlppsreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420

Qy 421 LDSGGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqognvfscsvnmhealhnhytqkslsispkg 470

RESULT 4
AAB14779
ID AAB14779 standard; Protein; 470 AA.
XX AAB14779;
AC AAB14779;
XX AAB14779;
DT 24-NOV-2000 (first entry)
XX Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
DE Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region: CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX JP2000169393-A.
PN 20-JUN-2000.
XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY) SANKYO CO LTD.
PA WPI: 2000-485645/43.
XX N-PSDB; AAB72184.
DR Preventive or treating agent for the diseases caused by an abnormality
DR in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX Claim 21; Page 108-109; 139pp; Japanese.

XX The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementary determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.

XX Sequence 470 AA;
SQ

Query Match 99.9%; Score 2514; DB 21; Length 470;
Best Local Similarity 99.8%; Pred. No. 8.1e-143;
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYFTSYMMQWVKQAP 60
Db 1 mgwsciilflvatatgvsqvlvqsgaevkpkgasvkscasgyftsywmqwkqap 60

Qy 61 GQGLEWNGEIDPSDSYTNYNQKFGKATLVDTSTAYMELSLRSEDVAVYYCARNRD 120
Db 61 gqglewngeidpsdsytnynqkfgkatltvdtststaymelslrseavyyccarnrd 120

Qy 121 YSNWNVFDVWGQGLTVVVSASRKGPSVFLPAPSSKSTSGTAALGCLVKDYFPEPTVVS 180
Db 121 ysnwnyfdvwegtclvtvssastkgspsvflpapskstsagtaalgclvkdyfpeptvs 180

Qy 181 WNSGALTSVGHVTHPFAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 181 wnsгалtsvghthfpavllqssglyslssvwtvpssslgtqtyicnvnhkpsntkvdkrvpe 240

Qy 241 KSCDKHTHTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccppapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300

Qy 301 YVDGVEVHNAKTRPREQYNSTRYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaktprreeqynstryrvsvltvlhqdwlngkeyckvsknkalpapiektis 360

Qy 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
Db 361 kagqppepvytlppsreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420

Qy 421 LDSGGSFFLYSKLTVDKSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqognvfscsvnmhealhnhytqkslsispkg 470

RESULT 5
AAW90929
ID AAW90929 standard; Protein; 470 AA.
XX AAW90929;
AC AAW90929;
XX AAW90929;
DT 08-AUG-2000 (first entry)
XX Humanised HFE7A designed heavy chain protein #2.
DE Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;

CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, anti-diabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (II) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (II) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;
Best Local Similarity 99.8%; Pred. No. 8.1e-143;
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFVATATGVHSQVQLVQSGAEVKKPGASVKYSCASGYTFTSYWQWVKQAP 60
DB 1 mgwsciiilfvatatghvqlvqsgaevkpkpgasvkscasgytftsywmqvrqap 60
QY 61 GQGLEWMEIDPSDSTNTNQKFKGKATLTVDTSSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 ggglewmgeidpsdsytnyngkfkgkatltvdtststaymelsslrse dtavyyca rnr d 120
QY 121 YSNWYFDVWGQGTLLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
DB 121 ysnw yfdv w g g t l l v t v s s a s t k g p s v f l a p s s k s t s g g t a a l g c l v k d y f p e p t v t y s 180
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
DB 181 wns g a l t s g v h t f p a v l q s s g l y s l s s v v p s s s l g t q t y i c n v n h k p s n t k v d k r v e p 240
QY 241 KSCDKHTCTCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300
DB 241 k s c d k h t c t c p c p a p e l l g g p s v f l f p p p k d t l m i s r t p e v t c v v v d v s h e d p e v k f n m 300
QY 301 YVDGVEVHNAKTPRREQNSTRYVYVSLTVLHQDLNGLNGKCYKSNKALPAPIETKTS 360
DB 301 y v d g v e v h n a k t p r e e q n s t r y v y v s l t v l h q d l n g l n g k c y k s n k a l p a p i e t k t s 360
QY 361 KAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
DB 361 k a k g q p r e p v y t l p p s r e e m t k n q v s l t c l v k g f y p s d i a v e w e s n g q p e n n y k t p p v 420
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSPGK 470
DB 421 l q s d g s f f l y s k l t v d k s r w q q g n v f c s m v h e a l h n h y t q k s l s l s p g k 470

RESULT 7

AAW83036
ID AAW83036 standard; Protein; 470 AA.

XX AC AAW83036;

XX DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas humanised antibody HFE7A heavy chain.
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /label= Sig_peptide
FT Protein 20..470 /label= Mat_protein
FT Region 20..140 /label= Variable
FT Region 141..464 /label= Constant
FT Region 50..54 /label= CDR_H1
FT /note= "claim 9"
FT Region 69..84 /label= CDR_H2
FT /note= "claim 9"
FT Region 118..129 /label= CDR_H3
FT /note= "claim 9"
XX AU9859701-A.
PN
PD 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX (SANY) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI; 1998-543440/47.
DR N-PSDB; AAV70079.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
PT used to evaluate drugs in animal models and to treat Fas-associated
PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
PT myocarditis, hepatitis and AIDS
XX Claim 22; Page 212-213; 292pp; English.
PS
XX This is the amino acid sequence of the VD type humanised heavy
CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
CC pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion
CC fragment of the humanised VD type HFE7A heavy chain and DNA
CC encoding human IgG1 constant region (see AAV70079), and is deposited
CC as FERM BP-6074 (claimed). The invention provides methods for
CC producing humanised antibodies by culturing host cells. Humanised
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
CC of inducing apoptosis in abnormal cells expressing Fas, and of
CC inhibiting Fas-induced apoptosis in normal cells. The humanised
CC antibodies are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to

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CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;

Query Match 99.4%; Score 2501; DB 19; Length 470;
Best Local Similarity 99.4%; Pred. No. 4.8e-142;
Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSCIIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSKASGYTFTSYMMQWKQAP 60
Db 1 mgwsciiilflvatatgvhsgaelvqsgaevkkgpgasvkvsckasgytftsyymmqqwkqap 60

QY 61 GQGLEWMEIDPDSYSTNYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
Db 61 gqglewmgeidpdsystnyngkfkgkatltvdtstastaymelslrsedatvyyccarnrd 120

QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVS 180
Db 121 ysnwfyfdvwgqgltvvtvssastkgpsvflpapskstsrgtaalgclvkdyfpeptvs 180

QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKRVEP 240
Db 181 wnsгалtsgvhtfpavilqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvep 240

QY 241 KSCDKHTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpcpapellggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaaktkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 360

QY 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Db 361 kagqprepqvylppstreemtknqvsltclvkgyfypsdiavewesngqpennykttppv 420

QY 421 LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYTKQSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqognvfscsvmhrealhnytkqslslspgk 470

RESULT 8
AAB14776
ID AAB14776 standard; Protein; 470 AA.
XX
AC AAB14776;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5628;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
```

```
XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI: 2000-485645/43.
XX N-PSDB; AAA72159.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
PS Claim 21; Page 95-96; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;
```

```
Query Match 99.4%; Score 2501; DB 21; Length 470;
Best Local Similarity 99.4%; Pred. No. 4.8e-142;
Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGSCIIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSKASGYTFTSYMMQWKQAP 60
Db 1 mgwsciiilflvatatgvhsgaelvqsgaevkkgpgasvkvsckasgytftsyymmqqwkqap 60

QY 61 GQGLEWMEIDPDSYSTNYNQKFKGKATLVDTSTSTAYMELSLRSEDATVYYCARNRD 120
Db 61 gqglewmgeidpdsystnyngkfkgkatltvdtstastaymelslrsedatvyyccarnrd 120

QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAAALGCLVKDYFPEPTVS 180
Db 121 ysnwfyfdvwgqgltvvtvssastkgpsvflpapskstsrgtaalgclvkdyfpeptvs 180

QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKRVEP 240
Db 181 wnsгалtsgvhtfpavilqssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvep 240

QY 241 KSCDKHTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpcpapellggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 300

QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaaktkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 360

QY 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 420
Db 361 kagqprepqvylppstreemtknqvsltclvkgyfypsdiavewesngqpennykttppv 420

QY 421 LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHREALHNYTKQSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqognvfscsvmhrealhnytkqslslspgk 470

RESULT 9
AAB90926
```

AAW90926 standard; Protein; 470 AA.
 AAW90926;
 08-AUG-2000 (first entry)
 Humanised HFE7A designed heavy chain protein.
 Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;
 hepatotropic; apoptosis; systemic lupus erythematosus;
 Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 Synthetic.
 EP990663-A2.
 05-APR-2000.
 29-SEP-1999; 99EP-0307711.
 30-SEP-1998; 98JP-0276881.
 30-SEP-1998; 98JP-0276882.
 (SANY) SANKYO CO LTD.
 Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 WPI: 2000-258930/23.
 N-PSDB; AA11597.
 New humanized anti-Fas antibody, useful for treating or preventing e.g.
 inflammatory or autoimmune disease, induces apoptosis selectively in
 cells with abnormal Fas-Fas ligand systems -
 Example reference 15; Page 134-136; 263pp; English.
 This invention describes a novel humanized anti-Fas antibody-like
 molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 ligand system, by binding to Fas on the cell surface, and prevents
 apoptosis in cells with a normal system, by inhibiting binding between
 Fas and its ligand. The products of the invention have anti-inflammatory,
 anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 antirheumatic, nephrotropic, antinfertility, neuroprotective,
 antiartherosclerotic, cardiac and hepatropic activity. (I) induce
 apoptosis by binding to cell surface Fas or inhibit it by competitive
 inhibition of ligand binding. (I) are used to treat and/or prevent
 diseases associated with the Fas/Fas ligand system, especially systemic
 lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 inhibit apoptosis in normal cells but selectively induce it in abnormal
 cells. They bind to both human and murine Fas, so can be evaluated in
 murine disease models. (I) act on the active site of Fas, i.e. they mimic
 the native ligand, do not induce liver disease, and have reduced risk of
 inducing a human anti-murine antibody response. This sequence represents
 a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 the method described in the invention.

Sequence 470 AA;

Query Match 99.4%; Score 2501; DB 21; Length 470;
 Best Local Similarity 99.4%; Pred No. 4.8e-142;
 Matches 467; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSQVLQSGAEVKKPGASVKVSKASGVTFTSYWQWYKQAP 60
 DB 1 mgwsciilflvatatgvhsqvlvqsgaevkkpgasvkvsckasgytftsymmqwvkqap 60
 QY 61 GGLLEWMEIDSDSYNTNQNFKGKATLTVDSTSTAYWELSLRSEDATAYYICARNRD 120
 DB 61 ggllewmgeidpsdsytnynqkfkgkatltvdsastaymelsslrsestavyycarnrd 120
 QY 121 YNNNYFDVWGGTGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALCLVKDYFPEPTVYS 180
 DB 121 ynnnyfdvwwgegtltvtvssastkgpsvfplapsskstsggtaaalclvdyfpeptvys 180
 QY 181 WNSGALTSVGHFTFPAVLQSSGLYSLSVVTVPSSSISLTQTYICNVNHNKPSNTKVKRVEP 240
 DB 181 wnsгалtsvghtfpavlvqssglyslsvvtvpssslgtqtyicnvnhkpntkvdkrvep 240
 QY 241 KSCDKTHCTPCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDYSHEDPEVKFNW 300
 DB 241 kscdkthctpcpcpapellggpsvflfpppkkdtlmisrtpevtcvvvdvshedepevkfnw 300
 QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDLNGLKEYCKVSNKALPAPIEKTIS 360
 DB 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdlnglkeyckvsnkalpapiektis 360
 QY 361 KAKGPPEQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
 DB 361 kaggppeqvylppstreemtknqvsltclvkgyfypsdiavewesngqpennnykttppv 420
 QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 470
 DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhycqkslsispsgk 470

RESULT 10
 AAW90936
 ID AAW90936 standard; Protein; 470 AA.
 XX
 AC AAW90936;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised HFE7A designed heavy chain HHH type protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiartherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 XX
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-2589930/23.
 DR N-PSDB; AAA11655.
 XX
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Claim 2; Page 188-189; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type .
 XX which is described in the method of the invention.
 XX
 SQ Sequence 470 AA;

Query Match 99.1%; Score 2495; DB 21; Length 470;
 Best Local Similarity 98.7%; Pred. No. 1.1e-141;
 Matches 464; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSKCKASGYTFTSYMMQWVKQAP 60
 DB 1 mgwsciiilflvatatgvhsqvlvsgaevkpgasvkvsckasgytftsymbmqwvrrqp 60
 QY 61 GQGLEWMGEIDPSDYTNYNOKFKGKATLTVDSTSTAYMELSLRSDEDTAVYYCARNRD 120
 DB 61 gqglewmgeidpsdytnynokfkgrvtitrdtststaymelsslrseadtavyyccarnrd 120
 QY 121 YSNWNYFDVWQCGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 DB 121 ysnwnyfdvwdgctltvtsvssastkgpsvfplapskstsaggtaalgclvkdypfpvptvs 180
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240
 DB 181 wnsгалtsгvhtfpavlgssglyslssvttvtpssslgqtyicnvnhkpstnkvdkrvpe 240
 QY 241 KSCDKHTCCPCPAPELLIGGFSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
 DB 241 kscdkhtccpcpaeliggsfvflfpkpkdtlmisrtpevtcvvdrvshedpevkfnw 300
 QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 DB 301 yvdgvevhnatkpreedynstyrvvsvltvlhgdwlngkeykckvsnkalpapiektis 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
 DB 361 kakgqprepqvtytlpppreemtknqvsltclvkgfypsdiavewesngqpennnykttppv 420

Db 361 kakgqprepqvtytlpppreemtknqvsltclvkgfypsdiavewesngqpennnykttppv 420
 QY 421 LDSGCSFFLYSKLFTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 470
 DB 421 ldsdgsfflysklftvdksrwqgnvfscvsmhealhnhytqkslsislpak 470

RESULT 11

AAM52156
 ID AAM52156 standard; Protein; 731 AA.

XX AC AAM52156;

XX DT 05-FEB-2002 (first entry)

XX DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.

XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;

XX KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200174905-A1.

XX PD 11-OCT-2001.

XX PF 26-MAR-2001; 2001WO-GB01324.

XX PR 03-APR-2000; 2000GB-0008049.

XX PR 02-OCT-2000; 2000US-237159P.

XX PA (ANTI-) ANTISOMA RES LTD.

XX PI Young RJ;

XX DR WPI: 2001-662969/76.

XX PT Novel compound used to treat cancer has target cell-specific portion

XX PT comprising humanised monoclonal antibody having specificity for

XX PT polymorphic epithelial mucin, and cytotoxic portion having

XX PT endonucleolytic activity -

XX PS Claim 20; Figure 7; 176pp; English.

XX CC The invention relates to a compound which comprises a target

XX CC cell-specific portion, comprising an humanised monoclonal antibody,

XX CC having specificity for polymorphic epithelial mucin (PEM) or its antigen

XX CC binding fragment and a cytotoxic portion having endonucleolytic activity,

XX CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The

XX CC compound has cytostatic activity useful for treating cancer and acting as

XX CC a potential inducer of apoptosis.

XX SQ Sequence 731 AA;

Query Match 93.2%; Score 2346.5; DB 22; Length 731;
 Best Local Similarity 93.0%; Pred. No. 1.4e-132;
 Matches 437; Conservative 20; Mismatches 10; Indels 3; Gaps 1;

QY 1 MGWSCIIILFLVATATGVHSQVQLVSGAEVKKPGASVKVSKCKASGYTFTSYMMQWVKQAP 60

DB 1 mgwsciiilflvatatgvhsqvlvsgaevkpgasvkvsckasgytftsymbwvrrqp 60

QY 61 GQGLEWMGEIDPSDYTNYNOKFKGKATLTVDSTSTAYMELSLRSDEDTAVYYCARNRD 120

DB 61 gqglewmgeidpsdytnynokfkgrvtitrdtststaymelsslrseadtavyyccarsyd 120

QY 121 YSNWNYFDVWQCGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180

DB 121 fa---wfwywgqgtltvtsvssastkgpsvfplapskstsaggtaalgclvkdypfpvptvs 177

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240

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Db 178 wnsгалtsгvhtfpavlgssglsesvvtvpssstgtqtyicnvnkpsntkvdckvpe 237
QY 241 KSCDKHTHTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 238 kscdkhtcpcpapellggpsvflfppkpkdtlmsrtpevtcvcvvdvshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvдgvevhнаktпреeqynstyrvvsvlvtlвqdwlngkeykckvsnkalpapiеktis 357
QY 361 KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPV 420
Db 358 kakgqprepqvylppsrdeltnqvsltcclvkgyfypsdiavwesngqpennyykttppv 417
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 470
Db 418 ldsдsfflyskltvdksrwqgnvfscsvmhеalhnhytqkslsispgk 467

RESULT 12
AAM52159
ID AAM52159 standard; Protein; 741 AA.
XX
AC AAM52159;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
PS Claim 20; Figure 10; 176pp; English.
XX
CC The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 741 AA;

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Query Match          93.2%; Score 2346.5; DB 22; Length 741;
Best Local Similarity 93.0%; Pred. No. 1.4e-132;
Matches 437; Conservative 20; Mismatches 10; Indels 3; Gaps 1;

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QY 1 MGMSCIILFLVATATGTVHSQVLVQSGAEYKVPASVYKSCASGYTFTSYMMQWVQAP 60
Db 1 mgwscililflvatatgvtshsqvqlvqsgaevkvpasvksckasgytfsaywiewvqap 60
QY 61 GQGLEWNGEIDPSDSYTNQKPKGKATLIVDTSTSTAYMELSLRSEDYAVYICARNRD 120
Db 61 gglewngeidpsdsytnqkpkgatlivdtststaymelslsrsedyavyyicarsyd 120
QY 121 YSNWNVFDVMGQGTFLVTVSSASTKGPSPVFLPAPSSKSTSGTAAALGCLVKDYFPPEPTVS 180
Db 121 ysnwnvfdvmgqgtflvtvssastkgpsvflpapskstsгtаaalgclvkdyppeptvs 177
QY 181 WNSGALTSГVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRVPE 240
Db 178 wnsгалtsгvhtfpavlgssglsesvvtvpssstgtqtyicnvnkpsntkvdckvpe 237
QY 241 KSCDKHTHTCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 238 kscdkhtcpcpapellggpsvflfppkpkdtlmsrtpevtcvcvvdvshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvдgvevhнаktпреeqynstyrvvsvlvtlвqdwlngkeykckvsnkalpapiеktis 357
QY 361 KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPV 420
Db 358 kakgqprepqvylppsrdeltnqvsltcclvkgyfypsdiavwesngqpennyykttppv 417
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 470
Db 418 ldsдsfflyskltvdksrwqgnvfscsvmhеalhnhytqkslsispgk 467

RESULT 13
AAM52158
ID AAM52158 standard; Protein; 729 AA.
XX
AC AAM52158;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
PS Claim 20; Figure 9; 176pp; English.
XX
CC The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,

```

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 729 AA;

Query Match 93.0%; Score 2341.5; DB 22; Length 729;
Best Local Similarity 93.0%; Pred. No. 2.7e-132;
Matches 436; Conservative 20; Mismatches 10; Indels 3; Gaps 1;
QY 1 MGWSCIILFLVATGVSQVQLVQSGAEVKKPGASVKYSCKASGTYFTSYMQWVKQAP 60
Db 1 mgwscilflivatgvsqqlvqsgaevkpgasvkysckasgytfsaywiewvraq 60
QY 61 GQGLEWNGEIDPDSSTYNQKFGKATLVDTSTAYMELSLRSEDVAVYCARNRD 120
Db 61 gqglewngelidpsstynqkfgkavltdtstntaymelslsrsedtavyycarsyd 120
QY 121 YSNWYFDVMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
Db 121 fa---wfaywgqglvtvssastkgpsvflapsskstsggtaalgclvkdypcptvs 177
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 178 wnsгалtsгvhtfpavlqssglyslsvtvtpssslgtqtyicnvnhkpsntkvdkkvpe 237
QY 241 KSCDKHTCPCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 238 kscdkhtcpcpapellggpsvflppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvдgvevhнаktpreeqynstyrvvsvlvtlhbqdwlngkeyckvsnkalpapiektis 357
QY 361 KAKQPREPOVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db 358 kakqprepqvyltpprdeitknqvsltclvkgyfypsdiavwesngqpennnykttppv 417
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
Db 418 ldsгsefflyskltvdksrwqgnvfscsvmhеalhnhytqkslsispg 466

RESULT 14
AAM52161
ID AAM52161 standard; Protein; 739 AA.
XX
AC AAM52161;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMF-1 heavy chain/DNase I fusion protein 6.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN W0200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX

PI Young RJ;
DR WPI; 2001-662969/76.
XX
XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
PS Claim 20; Figure 12; 176pp; English.
XX
CC The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 739 AA;

Query Match 93.0%; Score 2341.5; DB 22; Length 739;
Best Local Similarity 93.0%; Pred. No. 2.8e-132;
Matches 436; Conservative 20; Mismatches 10; Indels 3; Gaps 1;
QY 1 MGWSCIILFLVATGVSQVQLVQSGAEVKKPGASVKYSCKASGTYFTSYMQWVKQAP 60
Db 1 mgwscilflivatgvsqqlvqsgaevkpgasvkysckasgytfsaywiewvraq 60
QY 61 GQGLEWNGEIDPDSSTYNQKFGKATLVDTSTAYMELSLRSEDVAVYCARNRD 120
Db 61 gqglewngelidpsstynqkfgkavltdtstntaymelslsrsedtavyycarsyd 120
QY 121 YSNWYFDVMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
Db 121 fa---wfaywgqglvtvssastkgpsvflapsskstsggtaalgclvkdypcptvs 177
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 178 wnsгалtsгvhtfpavlqssglyslsvtvtpssslgtqtyicnvnhkpsntkvdkkvpe 237
QY 241 KSCDKHTCPCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 238 kscdkhtcpcpapellggpsvflppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvдgvevhнаktpreeqynstyrvvsvlvtlhbqdwlngkeyckvsnkalpapiektis 357
QY 361 KAKQPREPOVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db 358 kakqprepqvyltpprdeitknqvsltclvkgyfypsdiavwesngqpennnykttppv 417
QY 421 LDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 469
Db 418 ldsгsefflyskltvdksrwqgnvfscsvmhеalhnhytqkslsispg 466

RESULT 15
AAM52157
ID AAM52157 standard; Protein; 730 AA.
XX
AC AAM52157;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMF-1 heavy chain/DNase I fusion protein 2.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.

Search completed: August 14, 2002, 15:15:37
Job time: 835 sec

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OS Synthetic.
XX WO200174905-A1.
XX
XX
PD 11-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX 03-APR-2000; 2000GB-0008049.
PR
PR 02-OCT-2000; 2000US-237159P.
XX
XX (ANTI-) ANTISOMA RES LTD.
PA
XX
XX Young RJ;
PI
XX
XX WPI; 2001-662969/76.
DR
XX
XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
XX Claim 20; Figure 8; 176pp; English.
PS
XX
XX The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
XX Sequence 730 AA;
SQ
Query Match 92.8%; Score 2335.5; DB 22; Length 730;
Best Local Similarity 92.9%; Pred. No. 6.3e-132;
Matches 435; Conservative 20; Mismatches 10; Indels 3; Gaps 1;
QY 1 MGWSCIILFLVATATGVSQVGVGAEVKKPGASVKVCKASGYTFTSYWMQWVKQAP 60
Db 1 mgwsciiilflvatatgvsqvlvgdvgeevkpgasvkvsckasgytftsawvwirgap 60
QY 61 GQGLEWMEIDPSDSTNYNQKFKGKALTVDTSSTAYMELSSLRSEDTAVYYCARNRD 120
Db 61 gqglewmeidpsdstnynkfkgrvtvtrdtstntaymelsslrse dtavyycarsyd 120
QY 121 YSNHHYFDWVGQGLTVYSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVS 180
Db 121 fa---wfaywgqgtlvtvssastkgpsvfplapsskstsggtaalgclvkd yfpeptvs 177
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKDKRVEP 240
Db 178 wnsгалtsгvhtfpavlgsglyslssvvtvpssslgtqtyicnvnhkpsntkdkkvep 237
QY 241 KSCDTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300.
Db 238 kscdthtcppcpapellggpsvfifppkpktlmsrtpevtcvv dvshedpevkfnw 297
QY 301 YVDGVEVHNAKTKPREOYNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTIS 360
Db 298 yvdgvevhnaktkpreedynstyrsvsvltvlhgdlngkeyckvsnkalpapiektis 357
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
Db 358 kagqprepqvytlppsrdeltknqsvltclvkgyfypsdiavewesngqpenn ykttppv 417
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTOKSLSLSP 468
Db 418 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslslsp 465
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:04 ; Search time 82.88 Seconds
(without alignments)
138.514 Million cell updates/sec

Title: US-09-499-662-143
Perfect score: 2517
Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALNHVTKSLSPGK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2232	88.7	449	1	US-08-458-516-13
2	2230	88.6	476	2	US-08-378-939-10
3	2202.5	87.5	467	4	US-09-049-672A-8
4	2200.5	87.4	452	3	US-09-027-449-71
5	2200.5	87.4	452	4	US-09-026-985-71
6	2177	86.5	468	4	US-09-485-737B-67
7	2177	86.5	711	4	US-09-485-737B-90
8	2161.5	85.9	454	2	US-07-934-373C-22
9	2161.5	85.9	454	3	US-08-437-642B-22
10	2161.5	85.9	454	5	PCT-US93-07832-22
11	2144	85.2	472	4	US-08-793-450-8
12	2124	84.4	451	2	US-08-887-352B-14
13	2124	84.4	451	2	US-08-887-352B-16
14	2124	84.4	451	3	US-08-466-151-65
15	2124	84.4	451	4	US-09-109-207C-14
16	2124	84.4	451	4	US-09-109-207C-16
17	2124	84.4	451	4	US-09-296-005-14
18	2124	84.4	451	4	US-09-296-005-16
19	2121	84.3	478	3	US-08-487-550-8
20	2116	84.1	451	2	US-08-887-352B-18
21	2116	84.1	451	4	US-09-109-207C-18
22	2116	84.1	451	4	US-09-282-505-2
23	2116	84.1	451	4	US-09-054-255-2
24	2116	84.1	451	4	US-09-296-005-18
25	2105	83.6	453	3	US-08-466-151-8
26	2105	83.6	453	4	US-08-466-163B-8
27	2103.5	83.6	467	2	US-07-916-098A-45

28	2102.5	83.5	449	4	US-09-679-397-2	Sequence 2, Appl
29	2099.5	83.4	552	5	PCT-US93-07832-23	Sequence 23, Appl
30	2096.5	83.3	469	2	US-07-934-373C-23	Sequence 23, Appl
31	2096.5	83.3	469	3	US-08-437-642B-23	Sequence 23, Appl
32	2096	83.3	451	4	US-09-247-352-3	Sequence 3, Appl
33	2090.5	83.1	459	1	US-08-157-101A-7	Sequence 7, Appl
34	2072.5	82.3	467	1	US-08-704-744-81	Sequence 81, Appl
35	2070.5	82.3	473	4	US-09-049-672A-4	Sequence 4, Appl
36	2060.5	81.9	445	4	US-08-341-560B-17	Sequence 17, Appl
37	2054.5	81.6	446	3	US-08-397-411-7	Sequence 7, Appl
38	2054	81.6	476	3	US-08-487-550-12	Sequence 12, Appl
39	2022	80.3	442	5	PCT-US96-10043-9	Sequence 9, Appl
40	2022	80.3	476	3	US-08-487-550-4	Sequence 4, Appl
41	2010	79.9	442	1	US-08-461-968A-5	Sequence 5, Appl
42	2010	79.9	442	2	US-08-462-571-5	Sequence 5, Appl
43	1995.5	79.3	450	2	US-08-788-800-12	Sequence 12, Appl
44	1986	78.9	442	1	US-08-480-036-2	Sequence 2, Appl
45	1986	78.9	442	1	US-08-461-968A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 577085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: TSO, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

Query Match 88.7%; Score 2232; DB 1; Length 449;
Best Local Similarity 93.1%; Pred. No. 2.8e-158;
Matches 420; Conservative 14; Mismatches 15; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNQWVKQAPGQGLEWMGVIDPSDSVTNY 79
Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGYAFNYLIETWVRQAPGQGLEWIGVYIPGSGGTNY 60
QY 80 NQKFKKATLTDTSSTAYWELSSLRSEDTAVYICARNRDYNNWYFDYWGQGLTVTVS 139
Db 61 NEKFGKVTITVDESTNTAYWELSSLRSEDTAVYFCAR-RDGYGW-FAYWGQGLTVTVS 118
QY 140 SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 199
Db 119 SASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 178
QY 200 SGLYSLSVVTVTPSSSLGTQYICNVNHNKPSNTKVDKRPKSCDKTHTPCPCPAPELLG 259
Db 179 SGLYSLSVVTVTPSSSLGTQYICNVNHNKPSNTKVDKRPKSCDKTHTPCPCPAPELLG 238
QY 260 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKTKPREEQY 319
Db 239 GPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVEVHNKTKPREEQY 298
QY 320 NSTYRVSVLTVLHQDLWLNKEYCKKVSNNKALPAPIETKISKAKGQPREQVYTLPPSRE 379
Db 299 NSTYRVSVLTVLHQDLWLNKEYCKKVSNNKALPAPIETKISKAKGQPREQVYTLPPSRE 358
QY 380 EMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPNENYKTPTPVLDSGDSFFLYSKLTVDKSR 439
Db 359 ELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPNENYKTPTPVLDSGDSFFLYSKLTVDKSR 418
QY 440 WOQGNVFCSCVMHEALHNHYTQKSLSLSPCK 470
Db 419 WOQGNVFCSCVMHEALHNHYTQKSLSLSPCK 449

RESULT 2
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-378-939-10
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Best Local Similarity 88.4%; Pred. No. 4.3e-158;
Matches 421; Conservative 21; Mismatches 28; Indels 6; Gaps 1:
QY 1 MGSCIIILFLVATATGVHISOVLQVQSGAEVKKPGASVKVSCKASGYTFTSYNQWVKQAP 60
Db 1 MDWTWFLFVVAATGVQSQMQLVQVQSGAEVKKPGSSVTVSCKASGGTFSNATISWVRQAP 60
QY 61 GQGLEWMEIDPSDSYTNYNQKFKKATLFDVDTSTSTAYWELSSLRSEDTAVYICARNR- 119
Db 61 GQGLEWMEIDPSDSYTNYNQKFKKATLFDVDTSTSTAYWELSSLRSEDTAVYICARNR- 120
QY 120 -----DYSNNWYFDVWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 174
Db 121 RQANFRARVGVDFPMQGGTLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 175 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKV 234
Db 181 EPTVTSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKV 240
QY 235 DKRVEPKSCDKTHTPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
Db 241 DKRVEPKSCDKTHTPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 295 EVKFNWYDGVVEVHNKTKPREEQYNSTYRVSVLTVLHQDLWLNKEYCKKVSNNKALPAP 354
Db 301 EVKFNWYDGVVEVHNKTKPREEQYNSTYRVSVLTVLHQDLWLNKEYCKKVSNNKALPAP 360
QY 355 IEKTISKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPNENY 414
Db 361 IEKTISKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPNENY 420
QY 415 KTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 421 KTTTPVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 476
RESULT 3
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTU11
CLONE: 2747531
US-09-049-672A-8

Query Match 87.5%; Score 2202.5; DB 4; Length 467;
Best Local Similarity 89.28; Pred. No. 4.6e-156;
Matches 414; Conservative 19; Mismatches 28; Indels 3; Gaps 1;
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Qy 67 MGEIDPSDSTYNNQKFGKATLVDTSTAYMELSLRSEDYAVYYCARNRYSNNWY 126
Db 67 MGLAPENGAEVAYAKFLGRLTSEDTSADTAYMFLNNGSDESAIYYCARQH---YDF 123
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Db 124 FDFWGQGTMTVTVSSASVKGPSVFLPAPSSKSTSGTAAALGCLVKDYRPEPTVTSWNSGAL 183
Qy 187 TSGVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKYDKRVEPKSCDKT 246
Db 184 TSGVHTTFAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKYDKRVEPKSCDKT 243
Qy 247 HTCPCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNKYVDGVE 306
Db 244 HTCPCPAPPELLGSPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNKYVDGVE 303
Qy 307 VHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQP 366
Db 304 VHNKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQP 363
Qy 367 REPQVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGS 426
Db 364 REPQVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGS 423
Qy 427 FFLYSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 424 FFLYSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-09-027-449-71
Sequence 71, Application US/09027449
Patent No. 6025158
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA way

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: PI085R3-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-027-449-71

Query Match 87.4%; Score 2200.5; DB 3; Length 452;
Best Local Similarity 90.08; Pred. No. 6.2e-156;
Matches 407; Conservative 27; Mismatches 17; Indels 1; Gaps 1;
Qy 20 QVQLVQSGAEYKPKGASVYKSKASGYTFTSYMMQWVQAPQGGLEWGEIDPSDSTYNY 79
Db 1 EVQLVQSGGLVQPGSLRLSCAASGYSFSSHYHWHVRQAPGKLEWVGYYIDPSNGETTY 60
Qy 80 NQKFKGKATLVDTSTAYMELSLRSEDYAVYYCAR-NRDYSNNWTFDVGQGLTVTV 138
Db 61 NQKFKGRTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDFDVGQGLTVTV 120
Qy 139 SSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYRPEPTVTSWNSGALTSGVHTTFAVLQ 198
Db 121 SSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYRPEPTVTSWNSGALTSGVHTTFAVLQ 180
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKYDKRVEPKSCDKHTCPCPAPELL 258
Db 181 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKYDKRVEPKSCDKHTCPCPAPELL 240
Qy 259 GGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNKYVDGVEVHNKAKTTPREEQ 318
Db 241 GGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVFNKYVDGVEVHNKAKTTPREEQ 300
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSR 378
Db 301 YNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPSR 360
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 420
Qy 439 RWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 RWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 452
RESULT 5
US-09-026-985-71

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: Sequence 71, Application US/09026985
: Patent No. 6139426
: GENERAL INFORMATION:
: APPLICANT: Gonzalez, Tania R.
: APPLICANT: Leong, Steven R.
: APPLICANT: presta, Leonard G.
: TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
: TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
: NUMBER OF SEQUENCES: 72
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/026,985
: FILING DATE: 20-Feb-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Love, Richard B.
: REGISTRATION NUMBER: 34,659
: REFERENCE/DOCKET NUMBER: P1085R3-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650/225-5530
: TELEFAX: 650/953-9881
: INFORMATION FOR SEQ ID NO: 71:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 452 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
: US-09-026-985-71

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Query Match	87.4%	Score	2200.5	DB	4	Length	452		
Best Local Similarity	90.0%	Pred.	No. 6.2e-156						
Matches	407	Conservative	27	Mismatches	17	Indels	1	Gaps	1
QY	20	QVQLVQSGAEVKVPGASVKSCAKSGYTFYSYMQWVKQAPQGQGLEWNGEIDPSDSVTNY	79						
DB	1	EVQLVQSGGGLVPGGSLRLSCAASGYSFSSHYMHVRQAPGKGLEWVGVIDPSNGETTY	60						
QY	80	NQKPKGKATITVDTSTSTAYMELSSLSRSDTAVYIYCAR-NRDYSNNYVFDVWGQGLTVTV	138						
DB	61	NQKPKGKFTLSRDNKNTAYLQMNLSRAEDTAVYICARGDYRYNGDFFDVWGQGLTVTV	120						
QY	139	SSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWSGALTSGVHFTPAVLQ	198						
DB	121	SSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNWSGALTSGVHFTPAVLQ	180						
QY	199	SSGLYSLSSVTVTPSSSLGQTQYTCNNVNHKPSNTKYDKRVEPKSCDKTHTCTCPCPAPELL	258						
DB	181	SSGLYSLSSVTVTPSSSLGQTQYTCNNVNHKPSNTKYDKRVEPKSCDKTHTCTCPCPAPELL	240						
QY	259	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ	318						
DB	241	GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ	300						
QY	319	YNSTYRVVSVLTVHLQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSR	378						
DB	301	YNSTYRVVSVLTVHLQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTLPPSR	360						
QY	379	EEMTKNOVSLTCLVKGPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS	438						
DB	361	EEMTKNOVSLTCLVKGPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS	420						
QY	439	RWQQGNVFCSSVMHEALHNHYTQKSLSLSPGK	470						

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|||||
Db 421 RMOQGVNFSVCWMEALHNHYTKRSLSPK 452
|||||
RESULT 6
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEA
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

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Query Match	86.5%	Score 2177;	DB 4;	Length 468;
Best Local Similarity	88.2%;	Pred. No. 3.6e-154;		
Matches 410;	Conservative 20;	Mismatches 31;	Indels 4;	Gaps 1;

Qy	6	IILFLVATATGVHSQVOLVOSGAEVKKPGASVKSCAKSGYTFTSTWQWVQKAPQGGL	65
Db	7	IFSLFLTASVILSVQVOLVOSGSELKKPGASVISKSGYTFDTGMMNVQKAPQGGLK	66
Qy	66	WMGEIPDSDSYTNVYNKFKGKATLVTDSTSTAYMELSSLSRSEDTAIVYCARNDYSNNW	125
Db	67	WMGWINTYTGESTYVDDFGKRFVFLDTSVSAAYLOISLKAEDTATYFCARGFYA---	123
Qy	126	YFDWVGQGLTVTVSSASTKGPSVFELAPSSKTSGGTAAALGCLVLKDYFPEPVTVSNWSGA	185
Db	124	-MDYWGQGTIVTVSSASTKGPSVFELAPSSKTSGGTAAALGCLVLKDYFPEPVTVSNWSGA	182
Qy	186	LTSGVHTFPVAVLOSSGLYLSLSSVTVVPSSSLGQTQYICNVNHHKPSNTKVDKRVPEKSCDK	245
Db	183	LTSGVHTFPVAVLOSSGLYLSLSSVTVVPSSSLGQTQYICNVNHHKPSNTKVDKRVPEKSCDK	242
Qy	246	THTCPPCPAPPELLGGPSVFLFPPPKPDKDTLMISTRPEVTICVVDVSHEDPEVKFNWYVDGV	305
Db	243	THTCPPCPAPPELLGGPSVFLFPPPKPDKDTLMISTRPEVTICVVDVSHEDPEVKFNWYVDGV	302
Qy	306	EVHNATKPREEQYNSTYRVVSVLTVLHDQDLNGKEYCKVSNKALPAPTEKITSKAKGQ	365
Db	303	EVHNATKPREEQYNSTYRVVSVLTVLHDQDLNGKEYCKVSNKALPAPTEKITSKAKGQ	362
Qy	366	PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDG	425
Db	363	PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVPLDSDG	422
Qy	426	SFELYSKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK	470
Db	423	SFELYSKLTVDKSRWQGNVFCSCVMHEALHNHYTOKSLSLSPGK	467

RESULT 7
US-09-485-737B-90
: Sequence 90, Application US/09485737B

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; Patent No. 5350860
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS-015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

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Query Match	86.5%	Score 2177;	DB 4;	Length 711;
Best Local Similarity	88.2%;	Pred. NO. 6.3e-154;		
Matches 410;	Conservative 20;	Mismatches 31;	Indels 4;	Gaps 1;

Qy	6	IILFLVATGVHUSVOLVOSGAENVKKPGASVKVSCASGYTFTSYVMQWVKQAPQGGLQ	65
Db	7	IFSEFLTASVILSOLVQVOSGSELKKPGASKIKASGYTFTDYGMMWVKQAPQGGLK	66
Qy	66	WMGEIDPDSSTYTNQKFKGKATLVDTSTSTAYMELSLRSDETAIVYVCARNRDYSNNW	125
Db	67	WMGWINTYTCESYVDFDKGRFVSLDTSVSAAYLQISLKAEDTATYFCARGFYA---	123
Qy	126	YFDVWGOGTLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVTSWNSGA	185
Db	124	-MDYWGOGTTLTVTSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVTSWNSGA	182
Qy	186	LTSGVHTFPVAVLOSSGLYSLSSVVTVPSSSLGTQYICNVNKHPSNTKVDKRVKPSCDK	245
Db	183	LTSGVHTFPVAVLOSSGLYSLSSVVTVPSSSLGTQYICNVNKHPSNTKVDKRVKPSCDK	242
Qy	246	THTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGV	305
Db	243	THTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGV	302
Qy	306	EVHNAKTKPREEOYNSTYRVVSVLTVLHDWNLNGKEYCKVSNKALPAPIEKTISKAKGQ	365
Db	303	EVHNAKTKPREEOYNSTYRVVSVLTVLHDWNLNGKEYCKVSNKALPAPIEKTISKAKGQ	362
Qy	366	PREPQVYTLPPSREEMTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDG	425
Db	363	PREPQVYTLPPSREEMTKNOVSLTCLVKGFPSDIAVWESNGQPENNYKTPPVLDSDG	422
Qy	426	SFFLYSKLTVDKRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK	470
Db	423	SFFLYSKLTVDKRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK	467

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RESULT      8
US-07-934-373C-22
; Sequence 22, Application US/079344373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-AUG-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1194
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-22

Query Match	85.9%;	Score 2161.5;	DB 2;	Length 454;
Best Local Similarity	89.4%;	Pred. No. 4.9e-153;		
Matches 406;	Conservative	17;	Mismatches 28;	Indels 3; Gaps

QY	20	QVQLVQSGAEVKKPGASVKSCASGVFTSYVMQVKAQPGOGLEWMGEIDPDSDSYTNK	79
DB	1	QVQLQQSGPELVKPGASVKISCKTSGTFTFYTHMMWQSHGKSLIEWIGFKNPKNGSSH	60
QY	80	NQRFKGKATLTVDITSTSTAYMELSSLRSEDYAYIYCARNRDYSNNW--YFYDVMGQGTIV	136
DB	61	NQRFMDKATLAVDKSTSTAYMELRSLTSEDSGIYICARWRGLNYGDFVYFDVMGAGTTV	120
QY	137	TVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPPPTVSVWNSGALTSGVHTFPAP	196
DB	121	TVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSVWNSGALTSGVHTFPAP	180
QY	197	LQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRVPEPKSCDTHHTCCPCPAP	256
DB	181	LQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRVPEPKSCDTHHTCCPCPAP	240
QY	257	LLGGPSVFLPPPKDFTLMSRPEVTCVVDVYSHEDPEVKRNNYVDGVEVHNNAKTKPE	316
DB	241	LLGGPSVFLPPPKDFTLMSRPEVTCVVDVYSHEDPEVKFNNYVDGVEVHNNAKTKPE	300
QY	317	EQYNSTYRVYSLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPP	376
DB	301	EQYNSTYRVYSLTVLHODWLNKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPP	360
QY	377	SREEMTKNQVSLTCLVKGFYPYSIDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVD	436
DB	361	SREEMTKNQVSLTCLVKGFYPYSIDIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVD	420
QY	437	KSRWQGNVPSCSVMHEALHNHYTQKSLSLSPGK	470
DB	421	KSRWQGNVPSCSVMHEALHNHYTQKSLSLSPGK	454

Db 61 NORFMDKATLAVDKSTAYMELRSLTSEDGSIYYCARWGLNYGFDVRYFDVWGAGTV 120
Qy 137 TVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAY 196
Db 121 TVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAY 180
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKYDKRVEPKSCDKHTCTPCPCPAPE 256
Db 181 LQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKYDKRVEPKSCDKHTCTPCPCPAPE 240
Qy 257 LLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFENFNVDCGVEVHNATKPRE 316
Db 241 LLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVFENFNVDCGVEVHNATKPRE 300
Qy 317 EYNSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
Db 301 EYNSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
Qy 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTV 436
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTV 420
Qy 437 KSRWQOQGVFSCSVNHEALHNNHYTKQKSLSPGK 470
Db 421 KSRWQOQGVFSCSVNHEALHNNHYTKQKSLSPGK 454

RESULT 11
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABRIH, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-793-450-8

Query Match 85.2%; Score 2144; DB 4; Length 472;
Best Local Similarity 84.8%; Pred. No. 1e-151;
Matches 403; Conservative 27; Mismatches 37; Indels 8; Gaps 3;
Qy 1 MGWSCIILFLVATATGVHSGVQVLQSGAEVKKPGASVKVSCKASGYTFTSYNMWQWQAP 60
Db 1 MGWSCIILFLVATATGVHSGVQVLQSGAEVKKPGSETLSLTCTVYGSGFSGYVMSWRQPP 60
Qy 61 GQGLEWMEIDPSDSTYKNQKFKGKATLTVDTSSTAYMELSSLRSEDTAVYTCARNRD 120
Db 61 GQGLEWMEIDPSDSTYKNQKFKGKATLTVDTSSTAYMELSSLRSEDTAVYTCARPE 119
Qy 121 YSNWN-----YFDVWQGTGLTVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPE 175
Db 120 Y--KKYHCDWDFPWCQGTTVTVSSASTKGPSPVFLAPSSKSTSGGTAALGCLVKDYFPE 177
Qy 176 PVTVSNNSGALTSGVHTFPAYLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVD 235
Db 178 PVTVSNNSGALTSGVHTFPAYLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNKTKVD 237
Qy 236 KVEPKSCDKHTCTPCPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPE 295
Db 238 KAEPKSCDKHTCTPCPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPE 297
Qy 296 VKFNMYVDGVEVHNATKPREPQYNTSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPI 355
Db 298 VKFNMYVDGVEVHNATKPREPQYNTSTYRVSVSLTVLHODWLNKREYKCKVSNKALPAPI 357
Qy 356 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
Db 358 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 417
Qy 416 TTPPVLDSDGSGFFLYSKLTVDKSRWQOQGVFSCSVNHEALHNNHYTKQKSLSPGK 470
Db 418 TTPPVLDSDGSGFFLYSKLTVDKSRWQOQGVFSCSVNHEALHNNHYTKQKSLSPGK 472

RESULT 12
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:

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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-14

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Query Match 84.4%; Score 2124; DB 2; Length 451;
Best Local Similarity 87.6%; Pred. No. 3e-150;
Matches 396; Conservative 24; Mismatches 30; Indels 2; Gaps 2;

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RESULT 13
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123

```

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-16

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Query Match	84.4%	Score 2124;	DB 2;	Length 451;
Best Local Similarity	87.6%	Pred. No. 3e-150;		
Matches 396; Conservative 24; Mismatches 30; Indels 2; Gaps				
Qy	20	QVQLVQSGAEVKKPGASVKSCRASGYTFYS-YMMQVVKQAPGGQLEWMCIEDPSDYN 78		
Db	1	EVQLVESGGGLVPGGSLRLSCAASGYSITSGYSWNIRQAPGKLEWVASI-TYDGSIN 59		
Qy	79	YNQKFKGKALTVDTSTSTAYMELSSLRSEDTAVYVYCARNDYSNNKYFDWGQGLTVV 138		
Db	60	YNPSVKGRITISRDDSKNTFYLOMNSLRAREDYAVYVYCARSHYFGHWHFAVWGQGLTVV 119		
Qy	139	SSASTKGPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQ 198		
Db	120	SSASTKGPSVFPPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNNSGALTSGVHTFPAVLQ 179		
Qy	199	SSGLYSLSVVTVVPSSSLTGTQTYICNVNHRKPSNTKVDKRVKPEKSCDKTHTPCPAPPELL 258		
Db	180	SSGLYSLSVVTVVPSSSLTGTQTYICNVNHRKPSNTKVDKRVKPEKSCDKTHTPCPAPPELL 239		
Qy	259	GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATKPREQ 318		
Db	240	GGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATKPREQ 299		
Qy	319	YNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 378		
Db	300	YNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 359		
Qy	379	EEMTKNOVSLTCLVKGPYPDSIAVWESNGQPNNTKTPPVLDSDGSRFLYSKLTVDKS 438		
Db	360	EEMTKNOVSLTCLVKGPYPDSIAVWESNGQPNNTKTPPVLDSDGSRFLYSKLTVDKS 419		
Qy	439	RWQGNVYFSCSVKHEALHNHYTKQSLSPGK 470		
Db	420	RWQGNVYFSCSVKHEALHNHYTKQSLSPGK 451		

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RESULT 14
US-08-4666151-65
: Sequence 65, Application US/08466151
: Patent No. 6037453
: GENERAL INFORMATION:
: APPLICANT: Jardieu, Paula M.
: APPLICANT: Presta, Leonard G.
: TITLE OF INVENTION: Immunoglobulin Variants
: NUMBER OF SEQUENCES: 65
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 1 DNA Way
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,151
: FILING DATE:
: CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39, 044
; REFERENCE/DOCKET NUMBER: P0718P2CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-65

Query Match 84.4%; Score 2124; DB 3; Length 451;
Best Local Similarity 87.6%; Pred. No. 3e-150;
Matches 396; Conservative 24; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQWVKQAPGOGLEWNGEIDPDSVTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSNNWIRQAPGKLEWVASI-TYDGSIN 59
Qy 79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWGQGLTVV 138
Db 60 YNPVKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVV 119
Qy 139 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYPEPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYPEPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPCDKTHTCCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPCDKTHTCCPCPAPELL 239
Qy 259 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 240 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
Qy 439 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-109-207C-14
; Sequence 14, Application us/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
US-09-109-207C-14

Query Match 84.4%; Score 2124; DB 4; Length 451;
Best Local Similarity 87.6%; Pred. No. 3e-150;
Matches 396; Conservative 24; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQWVKQAPGOGLEWNGEIDPDSVTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYISITSGYSNNWIRQAPGKLEWVASI-TYDGSIN 59
Qy 79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYNNWYFDVWGQGLTVV 138
Db 60 YNPVKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGLTVV 119
Qy 139 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYPEPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVPFLAPSSKSTSGGTAALGCLVKDYPEPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPCDKTHTCCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKRVKPCDKTHTCCPCPAPELL 239
Qy 259 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
Db 240 GGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 419
Qy 439 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSVMHHEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:05
Job time: 688 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:18:59 ; Search time 108.64 Seconds
(without alignments)
415.703 Million cell updates/sec

Title: US-09-499-662-143

Perfect score: 2517

Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALHNHYTKSLSLSPGK 470

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1613.5	64.1	469	2 S37483	Ig gamma-2a chain
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1549	61.5	474	1 G2MS11	Ig gamma-2b chain
8	1547	61.5	446	2 S40295	Ig gamma-2a chain
9	1504.5	59.8	475	2 S01321	Ig gamma-2b chain
10	1474	58.6	470	2 S22080	Ig heavy chain pre
11	1467	58.3	472	2 S31459	Ig gamma-1 chain -
12	1432	56.9	374	2 S69339	Ig heavy chain v r
13	1426.5	56.7	444	2 PC4436	monoclonal antibod
14	1267	50.3	328	2 PC47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain c
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain c
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3HWU	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain c
25	1150	45.7	329	1 G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain C
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

30 1129 44.9 330 1 G2MSA
31 1127.5 44.8 329 2 S00847
32 1126.5 44.8 335 1 G2MSAB
33 1124 44.7 399 1 G2MSAM
34 1115 44.3 322 2 PS0019
35 1093.5 43.4 327 2 S06611
36 1080 42.9 405 1 G2MSBM
37 1070 42.5 277 2 I47162
38 996 39.6 548 2 S38864
39 943 37.5 627 2 S14683
40 925.5 36.8 549 2 S04845
41 867.5 34.5 241 2 S69131
42 854 33.9 246 2 S38950
43 798 31.7 220 2 A49444
44 762.5 30.3 249 2 S69340
45 759.5 30.2 572 2 B46529

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A;Reference number: A93433; MUID:82274238

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: Implications for evolution of

A;Reference number: S33887; MUID:83001943

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A;Reference number: A90563; MUID:71064024

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <CUN>

A;Note: this sequence has the G1m(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A;Reference number: A90564; MUID:71064025

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R;Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein NI

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A>Note: this sequence has the GIm(1f) and GIm(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A>Note: this sequence has the GIm(3) and GIm(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
endromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
A:Genetics:
C:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 9/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <Im1>
F:137-206/Domain: immunoglobulin homology <Im2>
F:243-310/Domain: immunoglobulin homology <Im3>
F:27-93,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.8%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 3.6e-93;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSISLTQTYICNVNHKPSNTKVDKRVKTPDLGDTTTCPCPAPPELLGG 260
Db 61 GLYSLSSVTVPSSSISLTQTYICNVNHKPSNTKVDKRVKTPDLGDTTTCPCPAPPELLGG 120

QY 261 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 320
Db 121 PSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 180

QY 321 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREE 380
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 381 MTKNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440
Db 241 LTRNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 441 QGQNFVCSVMHEALHNHYTQKSLSLSPCK 470
Db 301 QGQNFVCSVMHEALHNHYTQKSLSLSPCK 330

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.
A:Reference number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1639.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 2.3e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSSVTVPSSSISLTQTYICNVNHKPSNTKVDKRV----- 238
Db 61 GLYSLSSVTVPSSSISLTQTYICNVNHKPSNTKVDKRVKTPDLGDTTTCPCPAPPKSC 120

QY 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDT 273
Db 121 DTPPC 180

QY 274 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVHL 333
Db 181 LMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSVLTVHL 240

QY 334 QDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 393
Db 241 QDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300

QY 394 GFYPDSIAVEWESNGQPNENYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVME 453
Db 301 GFYPDSIAVEWESNGQPNENYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNFSCSVME 360

QY 454 ALHNHYTQKSLSLSPCK 470
Db 361 ALHNHYTQKSLSLSPCK 377

RESULT 3
A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 3e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPPEVTVSNNSGALTSGVHTFPAVLQSS 200

Db 1 ASTKGPSVFPPLAPCSRSTSGTAAALGCLVKDYFPPEVTVSNNSGALTSGVHTFPAVLQSS 60

QY 201 GLXLSVVTVVPSSSLGTQYICNVNHNKPSNTKVKRY----- 238

Db 61 GLXLSVVTVVPSSSLGTQYTCNVNHNKPSNTKVKRYELKTPLGTDTHTCPRCPKPKSC 120

QY 239 -----EPKSCDKTHTCCPCPAPELLGSPSVFLFPKPKDT 273

Db 121 DTPPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPAPELLGSPSVFLFPKPKDT 180

QY 274 LMISRTPEVTCVVVDVSHEDPEVKFNRYVDGVEVHNNAKTPREQYNSTYRVVSVLTVLH 333

Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNNAKTPREQYNSTYRVVSVLTVLH 240

QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 393

Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVK 300

QY 394 GFYPDSIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSLKLTVDKSRWQOGNVFSCVWHE 453

Db 301 GFYPDSIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSLKLTVDKSRWQOGNVFSCVWHE 360

QY 454 ALHNHYTQKSLSLSPGK 470

Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 4

S37483 Ig gamma-2a chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C;Accession: S37483

R;Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A;Reference number: S37483

A;Accession: S37483

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-469 <DUC>

A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 1613.5; DB 2; Length 469;
Best Local Similarity 64.6%; Pred. No. 9e-85;
Matches 305; Conservative 59; Mismatches 103; Indels 5; Gaps 4;

QY 1 MGWSCIIFLVATATGVHSGVOLVQSGAEVKKPGASVKASKASGYFTTYSWMQWVKQAP 60

Db 1 MGWSWIFLLISGTAGVHCQIQLOQSGPELVKPGASVKISKASGYFTTIDYIYNKQKP 60

QY 61 GQGLEWGEIDPSDYSYNYNOKFKGKATLVDTSTAYMELSLRSDTAVYFCARNRD 120

Db 61 GQGLUKWTGIYIPASGNTKYENEFKGAATLVDTSSSTAYMQLSLTSDTAVYFCARAMG 120

QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTS 180

Db 121 -ATATLIDYWGQGTTLTVSSAKTAPSVYPLAPVCGDGTSSVTGLGCLVKGYFPEPTLT 179

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVKDRVPE 240

Db 180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSWPSQSITCNVAHPASSTKVDDKIEP 238

QY 241 KSCDKTHTCPP-CPAPELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298

Db 239 RG-PTIKPCPCPKCAPNLLGGPSVFIPPPAKIKDVLMLSLSPIVTCVVVDVSEDDPDVQI 297

QY 299 NWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358

Db 298 SWEVNNVEVHTAQTOTHREDYNSLTRVVVSALPIQDQWMSGKEFKCKVNNKDLPAPIERT 357

QY 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTP 418

Db 358 ISKPKGSRAPQVYTLPPPEEMTKQVTLTCMTVDFMPEDYVVEWTNNGKTELNYKNT 417

QY 419 PVLDSGDSFFLYSLKLTVDKSRWQOGNVFSCVWHEALHNHYTQKSLSLSPGK 470

Db 418 PVLDSGDSGYFYMKLVKVEKKWVERNSYSCSVVHEGLNHHHTKSFSTPCK 469

RESULT 5

G2HU

Ig gamma-2 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000

C;Accession: A93906; A92809; A90752; A93132; A02148

R;Ellison, J.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982

A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain

A;Reference number: A93906; MUID:82197621

A;Accession: A93906

A;Molecule type: DNA

A;Residues: 1-326 <ELL>

A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056

A;Note: Lys-326 is probably removed posttranslationally

R;Wang, A.C.; Tung, E.; Fudenberg, H.H.

J. Immunol. 125, 1048-1054, 1980

A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, an

A;Reference number: A92809; MUID:81007873

A;Contents: myeloma protein T11

A;Accession: A92809

A;Molecule type: protein

A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>

A;Note: Trp-156 is at or near the complement-binding site

R;Connell, G.E.; Parr, D.M.; Hofmann, T.

Can. J. Biochem. 57, 758-767, 1979

A;Title: The amino acid sequences of the three heavy chain constant region domains of

A;Reference number: A90752; MUID:80001357

A;Contents: myeloma protein Z1e

A;Accession: A90752

A;Molecule type: protein

A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1

R;Hofmann, T.; Parr, D.M.

Mol. Immunol. 16, 923-925, 1979

A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobul-

A;Reference number: A93132; MUID:80114419

A;Contents: Z1e

A;Accession: A93132

A;Molecule type: protein

A;Residues: 238-275 <HOF>

R;Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A;Reference number: A94591

A;Contents: annotation; Z1e, revisions to residues 25, 59, 60, and 264-268

A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid

ned

R;Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A;Reference number: A90253; MUID:72033500

A;Contents: annotation; myeloma protein Sa, disulfide bonds

R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation; Sa, disulfide bonds
C:Genes: IGHG2
A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18

C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:103-109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:133-202/Domain: immunoglobulin homology <IM1>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 9.4e-85;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 200
DB 1 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 60

QY 201 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKRRVEPKSCDKHTHTCPPCPAPPELLGG 260
DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKRRVEPKSCDKHTHTCPPCPAPPELLGG 116

QY 261 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
DB 117 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176

QY 321 STYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRREE 380
DB 177 STYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRREE 236

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440
DB 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 296

QY 441 QGQNVFSCSVMHSEALHNHYTQKSLSLSPGK 470
DB 297 QGQNVFSCSVMHSEALHNHYTQKSLSLSPGK 326

RESULT 6
G4HU

Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104

A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A:Reference number: A90249; MUID:70207560
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics: IGHG4
A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 6

C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 3.7e-84;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 200
DB 1 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSVHTFPVAVLQSS 60

QY 201 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKRRVEPKSCDKHTHTCPPCPAPPELLGG 260
DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNKVDKRRVEPKSCDKHTHTCPPCPAPPELLGG 117

QY 261 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
DB 118 PSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 177

QY 321 STYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRREE 380
DB 178 STYRVVSVLTVTHQDMLNGKEYCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRREE 237

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440
DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 297

QY 441 QGQNVFSCSVMHSEALHNHYTQKSLSLSPGK 470
DB 298 QGQNVFSCSVMHSEALHNHYTQKSLSLSPGK 327

RESULT 7
G2WSLI

Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A02157; A26235; A26233; A53598

R:Fischer, R.; Voss, A.; Miersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific
A:Reference number: S25057
A:Accession: S25057

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fr

A:Reference number: A02157; MUID:80120716
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'Fp', 193-474 <YAM>

A:Cross-references: GB:J00461
A:Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain
 A:Reference number: A26235; MUID:80081501
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'PP', 193-376, 'T', 378-474 <TU1>
 A:Note: Lys-474 is probably removed posttranslationally.
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain
 A:Reference number: A26232; MUID:80081502
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'PP', 193-376, 'T', 378-474 <TU2>
 R:Ollo, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain genes
 A:Reference number: A26233; MUID:82173203
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
 A:Cross-references: GB:J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
 J. Biol. Chem. 269, 12345-12350, 1994
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID:94216359
 A:Accession: A53598
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 C:Comment: The a allele sequence is shown.
 C:Genetics:
 A:Introns: 138/1; 236/1; 258/1; 368/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) and two heavy (heavy) chains. In some cases, such as IgA and IgM, the subunits associate into larger multimers.
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin
 F:157-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>
 F:387-454/Domain: immunoglobulin homology <IM3>
 F:152/Disulfide bonds: interchain (to light chain) #status predicted
 F:164-220,288-348,394-452/Disulfide bonds: #status predicted
 F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.58; Score 1549; DB 1; Length 474;
 Best Local Similarity 61.4%; Pred. No. 4.2e-81;
 Matches 293; Conservative 66; Mismatches 108; Indels 10; Gaps 3;

Qy 1 MGWSCILFLVATATGVHSGVQVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAP 60
 Db 1 MEWSWIFLFLSGTAGVHSEVQVQSGPELVNPGASVKMSCKASGYTFTSYMMHWKRP 60
 Qy 61 GQLEWMGEIDPSYTNYNKFKGKAPLTVDTSSTAYMELSSRLSDTAVYYCARNR 120
 Db 61 GQLEWIGYINPNKDGKFKNEKFKGKATLTSDKSNATYMESSLTSDSAVYICARDYD 120
 Qy 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYPPEPTVS 180
 Db 121 YD---WFAYWGQGLTVTVSSAAKTPPSVYPLAPGCGDTGSSVTSGLVKGYFPESVTVT 177
 Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKDKRVEP 240
 Db 178 WNSGSLSSSVHTLFOALLQSLGLYTMSSSVTVTPSSVTSQVTCVAHPASSTTVDDKLEP 237
 Qy 241 KSCDKT-HTCPK-----CPAPELGGVFLFPKPKDLMISRTPEVTCTVVDVSHED 293
 Db 238 SGPSTINCPCKECKPCAPNLEGGPSVFIFPNKIDVLMISLTTPKVTCTVVDVSEDD 297
 Qy 294 PEVKFNWYVGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPA 353

Db 298 PDVQISWPNVNEVHTAQTHREDYNTIRVSVTLPIQHODWMSGKEFKCKVNNKDLPS 357
 Qy 354 PIKTIKAGKOPREPQVYITLPPSREEMTKNOVSLTCLVKGYPSDIAVWESNQPENN 413
 Db 358 PIKTIKIKGLVRAPQVYILPPPAEQLSRKRDVSLTCLVGNPGDISVWTSNGHTEEN 417
 Qy 414 YKTPPVLDSGSPFLYSKLVDSRWQOQNVFSCVMHEALHNHYTKSLSPGK 470
 Db 418 YKDTAPVLDSGSPFIYSKLNKTKWEKTSFSCNVRHGLKKNYLYLAKTKISRSPEGK 474

RESULT

8
 Ig gamma-2a chain (mAb735) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
 C:Accession: S40295
 R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.
 submitted to the EMBL Data Library, January 1993
 A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
 A:Reference number: S40295
 A:Accession: S40295
 A:Molecule type: protein
 A:Residues: 1-446 <KLE>
 C:Genetics:
 A:Map position: 12
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid
 F:1-446/Product: Ig gamma-2a chain #status experimental <KAT>
 F:1-117/Domain: V-D-J region <VDJ>
 F:118-446/Domain: C region <CHR>
 F:118-214/Domain: C1 region <CH1>
 F:215-230/Region: hinge
 F:231-340/Domain: C2 region <CH2>
 F:341-446/Domain: C3 region <CH3>
 F:360-427/Domain: immunoglobulin homology <IM>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
 F:132/Disulfide bonds: interchain (to light chain) #status predicted
 F:224, 227, 229/Disulfide bonds: interchain #status predicted
 F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.5%; Score 1547; DB 2; Length 446;
 Best Local Similarity 64.6%; Pred. No. 5.1e-81;
 Matches 292; Conservative 58; Mismatches 94; Indels 8; Gaps 4;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAPQGGLEWMGEIDPSYTN 79
 Db 1 QIQLQSGPELVNPGASVKISCKASGYTFTDYIIHWKQRPGEGLWIGIYPSGNTKY 60
 Qy 80 NQKFKGKATLVDTSTAYMELSSRLSDTAVYYCARNRDYNNWYFDVWGQGLTVTVS 139
 Db 61 NEKFKGKATLVDTSSSTAYMQLSSLTSDSAVYFCARGKFA---MDYWGQGSYTVTS 116
 Qy 140 SASYKGPSVFLAPSSKSTSGGTAALGCLVKDYPPEPTVSWNAGALTSGVHTFPAVLQS 199
 Db 117 SAKTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVLTWNSSLSGSGVHTFPAVLQS 176
 Qy 200 SGLXSLSSVTVTPSSSLGTQTYICNVNHPKSNTKDKRVEPKSCDKHTCPP--CPAPEL 257
 Db 177 D-LYTLSSSVTVSTWFPQSITCNVAHPASSTKVDDKIEPRG-PTIKPCPKCKPAPNL 234
 Qy 258 LGGPSVFLFPKPKDLMISRTPEVTCTVVDVSHEDPEVKFNWYVGVEVHNATKPREE 317
 Db 235 LGGPSVFIFPKPKIDVLMISLSPVTCVVDVSEDDPDVQISWPNVNEVHTAQTHRE 294
 Qy 318 QYNSTYRVSVLTVLHODWLNKGKEYCKVSNKALPAPTEKTSKAKGPREQVYTLPPS 377
 Db 295 DYNSTLRVVSALPIQHODWMSGKEFKCKVNNKDLPAPIERTISKPKGSRAPQVYVLP 354
 Qy 378 REEMTKNOVSLTCLVKGYPSDIAVWESNQPENNKTTPPVLDSGSGFFLYSKLTVDK 437

Db. 355 EEEMTKQVTLTCMTDFMPEDIVYVNTNGKTELNYKNTPEVLDSGSEYFMYSLRVEK 414
 QY 438 SRWQGVNFCSCVMHEALHNHYTKQSLSLSPG 469
 Db 415 KNWERNISYSCSVVHEGLNHHHTKSFSTRPG 446

RESULT 9
 S01321
 Ig gamma-2b chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
 C:Accession: S01321
 R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 Eur. J. Biochem. 176, 287-295, 1988
 A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed a
 A:Reference number: S01320; MUID:88329081
 A:Accession: S01321
 A:Molecule type: mRNA
 A:Residues: 1-475 <DE1>
 A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
 A:Note: this sequence was determined from the differentiated gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 1504.5; DB 2; Length 475;
 Best Local Similarity 60.8%; Pred. No. 1.4e-78;
 Matches 290; Conservative 65; Mismatches 113; Indels 9; Gaps 4;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWQWVKQAP 60
 Db 1 MEWIFLFLSTAGVQSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWQWVKQRT 60
 QY 61 GQLEWMGEIDPSDSTNYNOKFKGKATLTVDSTSTAYMELSLRSEDSTAVYICARNRD 120
 Db 61 GQLEWIGEITPGSGNSYFNEKFKGKATLTVDKSSSTAYLHLSLTSSEDSAVYFCAGPRQ 120
 QY 121 YSNWTFDVMGQGLTLTVSSASTKGFSPVPLAPSSKTSSTGGTAALGCLVKDYDPEPTVVS 180
 Db 121 V-GLLPFGYWGQGLTLTVSSAAKTPPSVPLAPCGDITGSSVTGLCLVKGYDPEPTVVT 179
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLTGTQYICNVNHNKPSNTKVDKRVPE 240
 Db 180 WNSGSLSSSVHTFPALLO-SGLTMSSTVTPSSVTPSPQVTCVSAHPASSTVVDKCLEP 238
 QY 241 KSCDKT-HTCPP-----CPAPELLGGPSVFLPPPKDITLMSRTPEVTTCVVVDYSHED 293
 Db 239 SGFTSTINCPCKECKPCAPNLEGPSVFIPPNIKDVLMSLTPKVTCTVVVDYSEDD 298
 QY 294 PEVKFMYDGVVHNAKTPREEQYNSTYRVVSVLTVHLQDWLNKGEYCKVSNKALPA 353
 Db 299 PDVQISWFNNVNLVAQTQTHREDYNSTIRVVSALPIQHDWMSGKEFKCKVNNKDLPA 358
 QY 354 PIEKTIKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYDPSDIAVEWESNGOPENN 413
 Db 359 PIERTISKIGIVRAQVILSPPPQSLSKKVDLSLTCLAVGSPEDISVETWSNGHTEEN 418
 QY 414 YKTPPVLDSGSEFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 470
 Db 419 YKDTAPVLDSGSEFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 475

RESULT 10
 S22080
 Ig heavy chain precursor (B/WT.4A.17.H5.A5) - bovine
 N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S22080; S06610; A31303
 R:Sanders, P.G.
 submitted to the EMBL Data Library, November 1991
 A:Reference number: S22080
 A:Accession: S22080
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-470 <SAN>
 A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
 Mol. Immunol. 26, 841-850, 1989
 A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g
 A:Reference number: S06610; MUID:90097956
 A:Accession: S06610
 A:Molecule type: DNA
 A:Residues: 142-470 <SYM>
 A:Cross-references: EMBL:X16701
 A:Note: the sequence was determined from the germline gene
 C:Genetics:
 A:Gene: Ig CH gamma-1
 A:Introns: 98/1; 111/1; 221/1
 A:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
 F:161-225/Domain: immunoglobulin homology <IMM>
 F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.6%; Score 1474; DB 2; Length 470;
 Best Local Similarity 60.2%; Pred. No. 7.8e-77;
 Matches 284; Conservative 63; Mismatches 115; Indels 10; Gaps 7;

QY 3 WSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWQWVKQAPGQ 62
 Db 5 WT--LLFVLSPAPIGVLSQVQLRESGSLVKPSQTLSTCTVSGFSLSSYALTWVRQAPGK 62
 QY 63 GLEWMGEIDPSDSTNYNOKFKGKATLTVDSTSTAYMELSLRSEDSTAVYICARNR--D 120
 Db 63 ALEWVGGI-TSGGTYTINPALKSRLSITKENSKQSVLSVSVTPEDTATYICARSTYGE 121
 QY 121 YSNWTFDVMGQGLTLTVSSASTKGFSPVPLAPSSKTSSTGGTAALGCLVKDYDPEPTVVS 180
 Db 122 VGDGATADAGQGLTLTVSSASTAPKVPYPLSCCGDKSSSTVTGLCLVSSYMPETVVT 181
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLTGTQYICNVNHNKPSNTKVDKRVPE 240
 Db 182 WNSGALKSGVHTFPAVLQSSGLYSLSSVTVPGSTSG-QTFTCNVAHPASSTKVDKRAVP 240
 QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLPPPKDITLMSRTPEVTTCVVVDVSHEDPEVKFNW 300
 Db 241 -TC-KPSPCDCCCPPELPGPSVFIPPPKDKTLTISGTPETVTCVVVDVGHDDPEVAFSW 298
 QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVHLQDWLNKGEYCKVSNKALPAPIEKTIS 360
 Db 299 FVDDVEVNTATKPREEQYNSTYRVVVSALRIQHDWTKGKEFKCKVHNEGLPAPIVRTIS 358
 QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGYDPSDIAVEWESNGQP--ENNKTTP 418
 Db 359 RTKGAPAREQVYVLAAPPQBELSKSTSLTCMTVSFYPDYIAVEWQRNGQPESEDKYGTTP 418
 QY 419 PVLDSGSEFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSLSPGK 470
 Db 419 PQLDADSSYFLYSKLRVDRNSWQEGDITYTCVVMHEALHNHYTKQSKSAGK 470

RESULT 11
 S31459
 Ig gamma-1 chain - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
 C:Accession: S31459
 R:Patric, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A:Reference number: S31459


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QY 196 VLOSSGLYSSVVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPCSCDKHTHTCPP--CP 253
Db 176 VLQSD--LYTLSSSVTPSSSWPSETVTCNVAHPASSTWKKKIVPRDQG---CKPCICT 230
QY 254 APELLGSPSVFLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 313
Db 231 VPEV---SSVFIPLPKPKDVTLLTPKVTVCVVVDISKDDPEVQFSWFDVDDVEVHTAQIQ 287
QY 314 PREEQNSTYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTT 373
Db 288 PREEQNSYRSVSELPIMHODWLNKKEFKCRVNSAFAPIETKISKGRPKAFQVYT 347
QY 374 LPSREEMTKNOVSLCLVKGYFSPDAVFNESNGOPENNNKPTTPVLDSDGSFFLYSKL 433
Db 348 IPPPKQEMAKDKVSLTCMITDFPEDITVEQWNGQPAENYKNTQIPMDTDGSIYFYSKL 407
QY 434 TVDKSRWQGNVFPSCSVMEALHNHYTOKLSLSLSPCK 470
Db 408 NVQKSNWEAGNTFTCSVLHLEGLHNHTKLSLSHSPGK 444

RESULT 14
I47159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAAS2217.1; PID:g433124
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAAS2217.1; PID:g433124
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 50.3%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 3.1e-65;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 APTKAPSVFLAPCSRDTSGPNVALGCLASSYFPEPTVTWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPCSCDKHTHTCPPAPPELLGG 260
Db 61 GLYSSSVTVTPASSLSKSKSYCNVNHPTTKVDKRVGCTKKPPCPCIPACESP---G 116
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 117 PSVFIPLPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTRPKKEQFN 176
QY 321 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLPIQHODWLNKKEFKCVNNKDLPAITRIISKAKGQTRPEQVYTLPPHAE 236
QY 381 MTKNOVSLTCLVKGYFSPDAVFNESNGQ--PENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LSRSKVSITCLVIGFYPPDPDIDVEWQNGQPEPEGNRYTRTPPOQVDGTYFLYSKFSVDKA 296

Query Match 50.3%; Score 1267; DB 2; Length 328;
Best Local Similarity 69.9%; Pred. No. 3.1e-65;
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps 2;

QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 APTKAPSVFLAPCSRDTSGPNVALGCLASSYFPEPTVTWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPCSCDKHTHTCPPAPPELLGG 260
Db 61 GLYSSSVTVTPASSLSKSKSYCNVNHPTTKVDKRVGCTKKPPCPCIPACESP---G 116
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 117 PSVFIPLPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTRPKKEQFN 176
QY 321 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLPIQHODWLNKKEFKCVNNKDLPAITRIISKAKGQTRPEQVYTLPPHAE 236
QY 381 MTKNOVSLTCLVKGYFSPDAVFNESNGQ--PENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LSRSKVSITCLVIGFYPPDPDIDVEWQNGQPEPEGNRYTRTPPOQVDGTYFLYSKFSVDKA 296

QY 439 RMOQGNVFPSCSVMEALHNHYTOKLSLSLSPGK 470
Db 297 SNQGGGIFQCAVMEALHNHYTOKLSISKTPGK 328
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RESULT 15
I47160

```
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
A:Reference number: I47158; MUID:95015845
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAAS2218.1; PID:g433126
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-references: EMBL:U03780; NID:g433125; PIDN:AAAS2218.1; PID:g433126
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IM>

Query Match 50.1%; Score 1261; DB 2; Length 328;
Best Local Similarity 69.6%; Pred. No. 6.8e-65;
Matches 231; Conservative 41; Mismatches 54; Indels 6; Gaps 2;

QY 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 APTKAPSVFLAPCSRDTSGPNVALGCLASSYFPEPTVTWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPCSCDKHTHTCPPAPPELLGG 260
Db 61 GLYSSSVTVTPASSLSKSKSYCNVNHPTTKVDKRVGCTKKPPCPCIPACESP---G 116
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 117 PSVFIPLPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHTAQTRPKKEQFN 176
QY 321 STYRVSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
Db 177 STYRVSVLPIQHODWLNKKEFKCVNNKDLPAITRIISKAKGQTRPEQVYTLPPHAE 236
QY 381 MTKNOVSLTCLVKGYFSPDAVFNESNGQ--PENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438
Db 237 LSRSKVSITCLVIGFYPPDPDIDVEWQNGQPEPEGNRYTRTPPOQVDGTYFLYSKFSVDKA 296

QY 439 RMOQGNVFPSCSVMEALHNHYTOKLSLSLSPGK 470
Db 297 SNQGGGIFQCAVMEALHNHYTOKLSISKTPGK 328

Search completed: August 14, 2002, 15:19:00
Job time: 688 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:13 ; Search time 53.64 seconds
(without alignments)
339.265 Million cell updates/sec

Title: US-09-499-662-143
Perfect score: 2517
Sequence: 1 MGWSCIILFLVATAGVHSQ.....MHEALHNHYTKSLSLSPGK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GCL_HUMAN	P01857 homo sapien
2	1610	64.0	326	1 GC2_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1 GC4_HUMAN	P01861 homo sapien
4	1331.5	48.9	323	1 GC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	46.2	290	1 GC3_HUMAN	P01860 homo sapien
7	1155	45.9	326	1 GCL_RAT	P20759 rattus norv
8	1150	45.7	329	1 GC1_MOUSE	P22436 mus musculu
9	1145	45.5	324	1 GCL_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1 GCB_RAT	P20761 rattus norv
11	1140	45.3	393	1 GCIM_MOUSE	P01869 mus musculu
12	1139	45.3	398	1 GC3M_MOUSE	P03987 mus musculu
13	1129	44.9	330	1 GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1 GCC_RAT	P20762 rattus norv
15	1126.5	44.8	335	1 GCAE_MOUSE	P01864 mus musculu
16	1124	44.7	399	1 GCAM_MOUSE	P01865 mus musculu
17	1115	44.3	322	1 GCA_RAT	P20760 rattus norv
18	1085	43.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1 GCBM_MOUSE	P01867 mus musculu
20	562.5	22.3	139	1 HV07_MOUSE	P01751 mus musculu
21	528	21.0	117	1 HV06_MOUSE	P01750 mus musculu
22	524.5	20.8	137	1 HV11_MOUSE	P01755 mus musculu
23	524	20.8	138	1 HV48_MOUSE	P03980 mus musculu
24	516	20.5	117	1 HV05_MOUSE	P01749 mus musculu
25	510	20.3	140	1 HV02_MOUSE	P01746 mus musculu
26	504	20.0	117	1 HV09_MOUSE	P01753 mus musculu
27	491	19.5	117	1 HV04_MOUSE	P01748 mus musculu
28	488	19.4	117	1 HV49_MOUSE	P06328 mus musculu
29	486.5	19.3	429	1 EPC_RAT	P01855 rattus norv
30	486	19.3	428	1 EPC_HUMAN	P01854 homo sapien
31	482	19.1	117	1 HV10_MOUSE	P01754 mus musculu
32	482	19.1	136	1 HV15_MOUSE	P01759 mus musculu
33	477	19.0	117	1 HV1G_HUMAN	P23093 homo sapien

RESULT_1	GCL_HUMAN	STANDARD:	PRT:	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
[2]				
RN	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RP	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
[3]				
RN	SEQUENCE OF 136-329 (EU).			
RP	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RL	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
[4]				
RN	SEQUENCE (MYELOMA PROTEIN NIE).			
RP	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
[5]				
RN	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RP	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
[6]				
RN	DISULFIDE BONDS			
RP	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P06336 mus musculu
P01743 homo sapien
P01756 mus musculu
P01757 mus musculu
P06329 mus musculu
P01747 mus musculu
P01744 homo sapien
P01872 mus musculu
P01871 homo sapien
P01745 mus musculu
P03988 oryctolagus
P01873 mus musculu

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
[7]
RP DISULFIDE BONDS.
RX MEDLINE-77070267; PubMed-1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE-81208100; PubMed-7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
CC MARKER & THE GLM (NON-1) MARKERS.
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.

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DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 223
FT DOMAIN 224 330
FT DISULFID 27 83
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FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134
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REMOVED POST-TRANSLATIONALLY.
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/FTTd=VAR_003886.
D -> E (IN GLM(NON-1) MARKER).
/FTTd=VAR_003887.
L -> M (IN GLM(NON-1) MARKER).
/FTTd=VAR_003888.

FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
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FT STRAND 274 276
FT STRAND 280 281
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FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 3770EEL06C2FA33D CRC64;

Query Match 69.8%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 1.le-113;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 201 GLYSLSVVVTPSSSLGTQTYICNVNHNKPSNTKVDKRPKSCDKTHTCCPCPAPPELLGG 260
Db 61 GLYSLSVVVTPSSSLGTQTYICNVNHNKPSNTKVDKRPKSCDKTHTCCPCPAPPELLGG 120

QY 261 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 121 PSVFLFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180

QY 321 STYRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380
Db 181 STYRVVSVLTVLHQDLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240

QY 381 MTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE IG gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
TL heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
[2]
RN SEQUENCE OF 88-115 FROM N.A.
RP TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: Implications for
TL evolution of a gene family.";
RL Cell 29:671-679(1982).
[3]
RN SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RP TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
TL heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407(1982).
[4]
RN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RP MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
TL evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
[5]
RN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RP MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
TL domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
[6]
RN SEQUENCE OF 238-275 (ZIE).
RP MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
TL immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
[7]
RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RP Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
[8]
RN SEQUENCE OF 1-121 (DOT).
RP MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
TL immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
[9]
RN DISULFIDE BONDS.
RP MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
[10]
RN DISULFIDE BONDS.
RP MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).

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EMBL: J00230; AAB59393.1; -;
PIR: A02148; G2HU.
HSSP: P01857; IFC1.
MIN: 147110; -;
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003600; Ig_Like.
Pfam: PF00047; Ig; 3;
SMART: SM00410; Ig_Like; 1.
SMART: SM00407; IGC1; 2.
PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 98
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
SQ
Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 1.5e-103;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
Oy 141 ASTGSPVFPPLAPSKSTSGGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
Dy 1 ASTGSPVFPPLAPSKSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
Oy 201 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKRPKSCDKTHTCPCPAPPELLGG 260
Dy 61 GLYSLSVVTVPSNFGTQTYTCNVDRKPSNTKVDKTKVERKCCVE---CPPCPAPP-VAG 116
Oy 261 PSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Dy 117 PSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176
Oy 321 STYRVVSVLTVHQDWLNGKEYCKVKSNKALPAPIEKTSKAKGQPRPQVYTLPPSREE 380
Dy 177 STYRVVSVLTVHQDWLNGKEYCKVKSNKGLPAPIEKTSKAKGQPRPQVYTLPPSREE 236
Oy 381 MTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 440
Dy 237 MTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 296
Oy 441 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 470
Dy 297 QQGNVFCSSVMHEALHNHYTQKSLSLSPGK 326
RESULT 3
ID4_HUMAN STANDARD; PRT; 327 AA.
AC P01861.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
CC -----
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DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSP; P01842; 7FAB.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 220
FT DOMAIN 221 327
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 8e-103;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
DB 1 ASTKGPSVEPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNPKVDKRVKPKSCDKTHTCTCPCPAPELGG 260
DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKSNPKVDKRVKPKSCDKTHTCTCPCPAPELGG 117
QY 261 PSVLFPPPKPKDTLMISRTPEVTCVVVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
DB 118 PSVLFPPPKPKDTLMISRTPEVTCVVVDSHEDPEVKFNWYVDGVEVHNAKTKPREEQFN 177
QY 321 STYRVSVLTVLHQLDNLGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSREE 380
DB 1 STYRVSVLTVLHQLDNLGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSREE 380

Db 178 STYRVSVLTVLHQLDNLGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSREE 237
QY 381 MTKNOVSLTCLVKGYFYPDSIAVEWESNGQPENNYKTPPVLDSDGFFLYSKLTVDKSRW 440
Db 238 MTKNOVSLTCLVKGYFYPDSIAVEWESNGQPENNYKTPPVLDSDGFFLYSKLTVDKSRW 297
QY 441 QGQNVFSCSVMHHEALHNHYTQKSLSLSPGK 470
Db 298 QGQNVFSCSVMHHEALHNHYTQKSLSLSPGK 327
RESULT 4
GC_RABIT ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-1 haplotype";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS; REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
CC -----
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CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.

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DR InterPro: IPR003597; Ig_cl.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00407; IG1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 104 104 T -> M (IN D11 MARKER).
FT VARIANT 104 104 104 T -> A (IN E15 MARKER).
FT VARIANT 185 185 185 T -> E (IN REF. 2).
FT CONFLICT 48 48 48 V -> V (IN REF. 2).
FT CONFLICT 71 71 71 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 144 144 144 N -> D (IN REF. 5).
FT CONFLICT 173 173 173 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 187 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 246 E -> G (IN REF. 5).
FT CONFLICT 256 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 266 Y -> W (IN REF. 5).
FT CONFLICT 280 280 280 Y -> S (IN REF. 5).
FT CONFLICT 284 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 1.4e-77;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVFELPAPSSKSTSGTAAALGLVKDYFPEPTVTVSWNSGALTSVYHTTPAVLQSSGLY 203
DB 4 KAPSVFELPACCGTPSTVTGLCLVKGVLPEPTVTVWNSGTLNGVTRTPFSVRQSSGLY 63

QY 204 SLSSVWVTPSSSLGTQYICNVNHKPSNTKVDKRVKPSKCDKTHCPCPAPELLGSPSV 263
DB 64 SLSSVSVTSSS---QPVTGNVAHPAINTKVDKTVASTCSK-----PTCPPPELLGSPSV 116

QY 264 FLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREQYNSTY 323
DB 117 FLPPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPREQYNSTY 176

QY 324 RVSVLVTLHQDWLNGREYKCYKSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTK 383
DB 177 RVSTLPIHQDWLNGREYKCYKSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTK 236

QY 384 NQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQG 443
DB 237 RSVSLTCMNGFYPSDISVEWERNKAEDNYKTTPPAVLDSGYSFLYKLSVPTSEWQRG 296

QY 444 NVFSCSYMHEALHNHYTKLSLSPGK 470
DB 297 DVFTCSYMHEALHNHYTKLSRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
```

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RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:19-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2rB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IG1; 2.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1 1 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 16 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 202 N-LINKED (GLCNAC. . .).
FT CARBOHYD 178 178 178
FT DISULFID 248 308 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
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Query Match 48.1%; Score 1210.5; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 3.9e-76;
Matches 233; Conservative 30; Mismatches 62; Indels 9; Gaps 4;

QY 140 SASTKGSVPFPLAPSSKSTSGTAAALGLVKDYFPEPTVTVSWNSGALTSVYHTTPAVLQ 199
DB 1 SARTTAPSVFPLAASCVDTSGMTLGLVKGYFPEPTVTVKWSGALTSVYHTTPAVLQ- 59

QY 200 SGLYSLSSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVKPSKCDKTH--TCPPCPAPEL 257
DB 60 SGLYSLTSMVTVSPSQKAT----CNVAPASSTKVDKTVETPRTZPBPCPTCKPCPPEN 115

QY 258 LGGPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVGVHNAKTKPRE 317
DB 116 LGGPSVFIFPPKPKDMLMISLTPRVTCVVVDVSDQPEVEVQTFWFDNKPVGNAKTKPRVE 175
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Db 179 ISKTGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
QY 419 PVLDSGDSFFLYSKLTVDKSRWQQGNFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 239 PMLDSGDSFFLYSKLTVDKSRWQQGNFSCSVMHEALHNHYTQKSLSLSPGK 290

RESULT 7
GC1_RAT
ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017;
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 2.4e-72;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVFPLAPSSKSTGTAALGLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQSS 200
Db 1 AETAPSYVPLAPGTALKSNWMTGLCLVKGYFPEPTVTSNWSGALTSGVHTFPAVLQ-S 59

QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVKRPEKSCDKTHTCPCPAPELLG 260
Db 60 GLYTLTSSVTVPSSTWPSQTVCNVHPASSTKVDDKIVPRNCG--GDCRPEC---ICTG 113

QY 261 ---PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREE 317
Db 114 SEVSSVFIFPPKPKDVLITITLTKVTCVVDVSHEDPEVHFSWFDVDEVHTAQTREPEE 173

QY 318 QYNSTYRVSVLTVLDHDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377
Db 174 QFNSTFRSVSELPILHDHDLNGRFRCKVTSAAFPSPLEKTIKPEPTQVPHVITMSPT 233

QY 378 REEMTKNQVSLTCLVKGFYPSDIAVEWESGQPENNYKTTTPPVLDSDGSFFLYSKLVADK 437
Db 234 KEEMTQNEVSICTCVKGYFPDIIYVEWQMGPQENYKNTPTPTMDTDSGFFLYSKLVNKK 293
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QY 438 SRWQQGNFVSCVMHEALHNHYTQKSLSLSPGK 470
Db 294 EKWQQGNFTCTSVLHEGLHNHHTKSLSHSPGK 326

RESULT 8
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
Best Local Similarity 65.0%; Pred. No. 5.5e-72;
Matches 213; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

QY 142 STKGPSVFPLAPSSKSTGTAALGLVKDYFPEPTVTSNWSGALTSGVHTFPAVLQSSG 201
Db 1 TTTAPSYVPLPGGSDITSGSSVTLGLCLVKGYFPEPTVKWNGALSSGVRVSSVLIQ-SG 59

QY 202 LYSLSVVTVTPSSSLGTQTYICNVNHPKNTKVKRPEKSCDKTHTCP--PCPAPELLG 259
Db 60 FYSLSLVTVPSSTWPSQTVCNVHPASSTKVDDKIVPRNCG--GDCRPEC---ICTG 118

QY 260 GPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREEQY 319
Db 119 GPSVFIFFPKPKDLMISLTLPKVTCCVVVDVSHEDPDVHVSFVNDKVEHTAWTQPREAQY 178

QY 320 NSTYRVSVLTVLDHDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRE 379
Db 179 NSTYRVSVLSALPIQHDHMRGKEFKCKVNNKALPAPIERTISKPKGKRAQTPOVYTIPTPRE 238
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RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 45.5%; Score 1144.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 1.3e-71;
Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;

QY 141 ASYKGPSPVPLAPSSKSTSGTAALGCLVDYRPPVTVSNNGALTSVGHVTPAVLQSS 200
DB 1 AQTAPSVYPLAPCGDTTSTVTLGCLVKGYPPEVTVTVNSGALSDVHTFFAVLIQ-S 59

QY 201 GLXSLSSVTVTPSSLSGTQYICNVNHNKPSNTKVDKRVPKS-----CDKTHTCPPCPA 254
DB 60 GLYTLTSVT--SSTWPSQVTCNVAPASSTKVDKVRERRNGGIGHKPCPTCHKCPV 117

QY 255 PELLGGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVFNKYVDGVEVINATKP 314
DB 118 PELLGGSVFIFPPKPKDILLISQNAKVCVVDVSEEDPDVQFSWFNVNVEVHTAQTP 177

QY 315 REEQYNSTYRVSVLTVHODWLNKGKVKCVSNKALPAPEKTIKAKGQPREPVVTL 374
DB 178 REEQYNSTFRVSLPQHODWMSGKEFKCVNNKALPSIEKTIISPKGLVLRPQVVM 237

QY 375 PPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLT 434
DB 238 GPPEQLTEQVSLTCLTSGFLPNDIGVWTSNGHIEKNYKNTPEVMDSDGSFFMYSKLN 297

QY 435 VDKSRWQGNVFCSSVWHEALHNNHYTQKLSLSPGK 470
DB 298 VERSRWDSRAPVGVSVVHGLNHHVKEISIRPPGK 333

RESULT 11
GC1N_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
```

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RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
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DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR PIR; B02159; GINSM.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357
FT DOMAIN 358 393 POTENTIAL.
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;

Query Match 45.3%; Score 1140; DB 1; Length 393;
Best Local Similarity 62.2%; Pred. No. 3.3e-71;
Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
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KW	Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;					
KW	Transmembrane; Alternative splicing.					
FT	NON_TER	1	97	CHI.		
FT	DOMAIN	1	97	HINGE.		
FT	DOMAIN	98	113	CH2.		
FT	DOMAIN	114	223	CH3.		
FT	DOMAIN	224	327	POTENTIAL..		
FT	TRANSMEM	346	362	CYTOPLASMIC (POTENTIAL).		
FT	DOMAIN	363	398	E -> G (IN REF. 2).		
FT	CONFLICT	333	333	E -> Q (IN REF. 2).		
FT	CONFLICT	342	382	E -> F (IN REF. 2).		
FT	CONFLICT	388	388	P -> F (IN REF. 2).		
SQ	SEQUENCE	398 AA;	CF7F264B50A41B95 CRC64;			
Query Match 45.3%; Score 1139; DB 1; Length 398;						
Best Local Similarity 64.7%; Pred. No. 4e-71;						
Matches 213; Conservative 44; Mismatches 68; Indels 4; Gaps						
QY	142	STKGPSVFPEPLAPSSKSGTGAALGCLVKDYFPPEPTVSNWGALTSGVHTFFAVLQSSG	201	:	:	:
Db	1	TTTPAPSIVLPVGSDTSGSVILGKGYFPPEPTVKNYGALSGGVRTVSVLIQ-SG	59	:	:	:
QY	202	LYLSVVTVTPSSSLGTQTTCINVNHHKPSNTKYDKRVEPKSCDTHITCP--PCPAPELLG	259	:	:	:
Db	60	FYSLSLVTFPSSTWPSQTVCINVAHPASKTLIKRIEPR-IPKPSTPPGSSCPPGNILG	118	:	:	:
QY	260	GPSVFLFPFKPKDTLMISRTPEVTCCVVDVSHEDPEVKFNWYVDGEVHNAKTKPREEQY	319	:	:	:
Db	119	GPSVFIFPPPKDALMTSLTPKVCVVVDVSEDDPDVHVSWFDNKEVHTAMTQPREAQY	178	:	:	:
QY	320	NSTRVRSVLTVLHQDWLNGKEYKCKSKNKALKPAIEKTISKAKGQPREPOVYITLPPSRE	379	:	:	:
Db	179	NSIFRVVSALPIQHODWMRKEFKCKVNKKALPAIERTISKPKGRAQTPQVYTIPPRE	238	:	:	:
QY	380	EMTKNQVSLTCLVKGFVPSDIAVEHESNGPENNYKTPPVLDSDGSFFLYSKLTVDKSR	439	:	:	:
Db	239	QMSKKVKSLSLCTVNFTEFAISIEWERNGLEQDKNTPPILDSDGTFLYSLKLTVDTS	298	:	:	:
QY	440	WOOGNPFCSVMHEALNNHYTKQSLSLSP 468		:	:	:
Db	299	WLQGEIFTCSVVHEALNNHHTQNLSRSP 327		:	:	:
RESULT	13					
ID	GC_AA_MOUSE	STANDARD;	PRT;	330 AA.		
AC	P01863;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					
DE	30-MAY-2000 (Rel. 39, Last annotation update)					
DE	Ig gamma-2A chain C region, A allele.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RX	[1]					
RX	SEQUENCE FROM N.A.					
RP	MEDLINE=81076554; PubMed=6777755;					
RA	Sikorav J.-L., Auffray C., Rougeon F.;					
RT	"Structure of the constant and 3' untranslated regions of the murine					
RL	Balb/c gamma 2a heavy chain messenger RNA.";					
RL	Nucleic Acids Res. 8:3143-3155(1980).					
RX	[2]					
RP	SEQUENCE FROM N.A.					
RP	MEDLINE=81198976; PubMed=6262729;					
RA	Yamawaki-Kataoka Y., Miyata T., Honjo T.;					
RT	"The complete nucleotide sequence of mouse immunogloblin gamma 2a gene					
RL	and evolution of heavy chain genes: further evidence for intervening					
RL	sequence-mediated domain transfer.";					
RL	Nucleic Acids Res. 9:1365-1381(1981).					
RX	[3]					
RP	SEQUENCE FROM N.A.					

RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Auffray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
RN -----
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RN -----
RX EMBL; V00798; CAA24178.1; -;
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 44.98; Score 1129; DB 1; Length 330;
Best Local Similarity 63.98; Pred. No. 1.5e-70;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

Qy 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGLVTHFPAVLQSS 200
Db 1 AKTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVTHFPAVLQSD 60

Qy 201 GLYSLSSVTVPPSSSLGQTQYICNVNHPKSTKVDKRVKPKSCDKTHTCPP--CPAPEL 258
Db 61 -LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKKIEPRG-PTIKPCPCCKCPAPNLL 118

Qy 259 GGPSVFLPPPKPKDTLMISRPETVCVVYVDSHEDPEVKFNNYVDGVVHNAKTKPREQ 318
Db 119 GGPSVFIIPPKIKDVLMSLSPITVCVVYDVEDPDQVQISWFVNNVEVHTAQQTTHRED 178

Qy 319 YNSTYRVSVLTVLHDLNLSKCKVSKNALKAPLIEKTIISKAGQPREPQVQVTLPPSR 378
Db 179 YNSTLRVVVALPIQHQDWSKKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPE 238

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPTPPVLDSGGSEFLYSKLTVDKS 438
Db 239 EEMTKKQVTLKMTVDFMPEDIYVEWTNNGKTELNYKTEPVLDSGGSYFMYSKLRVEKK 298
Qy 439 RWQOGNVFSCSVMHLEAHNHYTKQSLSLSPGK 470
Db 299 NWVERNSYSCSVVHGLEHNNHTTKSFSTRPGK 330

RESULT 14
GCC_RAT
ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
RN -----
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RN -----
RX EMBL; X07189; CAA30169.1; -;
DR PIR; S00847; S00847.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 1.9e-70;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

Qy 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWNSGALTSGLVTHFPAVLQSS 200
Db 1 ARTTAPSVYPLVPGSGTSGSLVTLGCLVKGYFPEPTVTKNSGALSSGVTHFPAVLQ-S 59

Qy 201 GLYSLSSVTVPPSSSLGQTQYICNVNHPKSTKVDKRVKPKSCDKTHTCPP--CPAPEL 257
Db 60 GLYTLSSSVTVPPSSVTSSTWSSQITVCSVAHPATKSNLIKRIEPR---RPKRPPTDTCSDDN 116

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QY 258 LGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
  |||||:||||| |||: |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 117 LGRPSVFIFPPPKDILMITLPKVTCCVVVDVSEEDPDQFSWFVDNVRVFTAQTPHEE 176
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 318 QYNSTRVRSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPS 377
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 177 QLNGTRVRSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPOVYTLPPS 236
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 378 REEMTKNOVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 437
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 237 REQMSKNKVSITCMTVTSFTPASISVSWERNGELEQDKNTLPVLDSDSEYFELYSKLSDVT 296
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 438 SRWQGNVFSVCSVMHEALHNHYTKQSLSPGK 470
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 297 DSMRGRDIIVTCVVVHEALHNHYTKQSLSPGK 329
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse.;
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT Multiple amino acid substitutions between murine gamma 2a heavy
RT chain Fc regions of Ig1a and Ig1b allotypic forms.;
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; ; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 2.3e-70;

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Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;
QY 141 ASFKGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 200
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 1 AKTAFSVPLVPVCGTGTGSSVTGLCLVKGYPPEPVTLTWNSGSLSSGVTTFPALLQ-S 59
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 201 GLYSLSVVTVPSSSSLGTQTYICNVNHPKSNKALPAPIETKISKAKGQPREPOVYTL 254
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 60 GLYTLSSSVTVTSNTWPSQITTCNVAHPASSTKVKKIEPRVPIITQNPCPPHQRPVPCAA 119
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 255 PELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 314
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 120 PDLGSPSVFIFPPPKDILMITLPKVTCCVVVDVSEEDPDQFSWFVDNVRVFTAQTPHEE 179
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 315 REQYNSTRVRSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPOVYTL 374
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 180 HREDYNSTRVRSVLTVLHODWLNKKEYCKVSNKALPAPIETKISKAKGQPREPOVYTL 239
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 375 PPSREEMTKNOVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLT 434
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 240 PPAEEMTKKEFSLTCTMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLR 299
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
QY 435 VDKSRWQGNVFSVCSVMHEALHNHYTKQSLSPGK 470
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||
Db 300 VOKSTWERSLFACSVVHEVLYLHNHLTKTISRSLGK 335
  |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:||||| |||||:|||||

Search completed: August 14, 2002, 15:23:14
Job time: 687 sec
```


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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:15 ; Search time 187.61 Seconds
(without alignments)
433.386 Million cell updates/sec

Title: US-09-499-662-143

Perfect score: 2517

Sequence: 1 MGWSCIIILFNATATGVHSQ.....MHEALHNHYTKSLSPCK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	1639.5	65.1	473	11 Q9D8L4	Q9d8l4 mus musculu
2	1628.5	64.7	463	11 Q91LC4	Q91lc4 mus musculu
3	1588.5	63.1	473	11 Q98L25	Q99125 mus musculu
4	1562	62.1	468	11 Q99L31	Q99131 mus musculu
5	1433.5	57.0	437	11 Q98L44	Q991a4 mus musculu
6	1420.5	56.4	473	11 Q91Z05	Q91z05 mus musculu
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus cabal
8	1257	49.9	701	4 Q96P08	Q96pc8 homo sapien
9	986	39.2	278	11 Q921K1	Q921k1 mus musculu
10	927.5	36.8	614	4 Q96GA6	Q96ga6 homo sapien
11	890.5	35.4	481	11 Q91WT3	Q91wt3 mus musculu
12	859	34.1	500	4 Q9BRV0	Q9brv0 homo sapien
13	836.5	33.2	481	11 Q91WT1	Q91wt1 mus musculu
14	820	32.6	488	11 Q91WR1	Q91wr1 mus musculu
15	812.5	32.3	597	4 Q96BD9	Q96bd9 homo sapien
16	804	31.9	496	4 Q96DK0	Q96dk0 homo sapien

ALIGNMENTS

RESULT 1

ID	Q9D8L4	PRELIMINARY;	PRT;	473 AA.
AC	Q9D8L4;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	1810060009RIK PROTEIN.			
GN	IGH-1 OR 1810060009RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikola I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,			
RT	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK007916; BAB25349.1; -.			
DR	HSSP; P01842; 7FAB.			

Q9bu10 homo sapien
Q9bqb8 homo sapien
Q91la6 mus musculu
Q96aa6 homo sapien
Q96k68 homo sapien
Q96ey0 homo sapien
Q99ka4 mus musculu
Q91wp5 mus musculu
Q91z07 mus musculu
Q91xe1 mus musculu
Q91x2 mus musculu
Q99m22 mus musculu
Q96kx8 homo sapien
Q9dcd9 mus musculu
Q9pp6 homo sapien
Q91v67 mus musculu
Q924p9 mus musculu
Q9y298 homo sapien
Q924q2 mus musculu
Q924r3 mus musculu
Q95978 homo sapien
Q924q5 mus musculu
Q924r8 mus musculu
Q96qs0 homo sapien
Q924p5 mus musculu
Q924q7 mus musculu
Q924r4 mus musculu
Q924q0 mus musculu
Q924p8 mus musculu

```
DR MGD; MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig.
DR SMART: SM00407; IGc1; 2.
DR SMART: SM00406; IGv; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match      65.1%; Score 1639.5; DB 11; Length 473;
Best Local Similarity 63.9%; Pred. No. 8.2e-129;
Matches 304; Conservative 69; Mismatches 94; Indels 9; Gaps 4;

QY 1 MGWSCILFLVATATGVSQVLQVSGAEVKKPGKASGYTFTSYMHWVKQAP 60
DB 1 MENSWFLELLSVTAGVHCQVLQKSGAELVKPGASVKISCKASGYTFTDYINWVKQP 60

QY 61 GQGLEWMEIDPSDSTNTNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLSSEDSAVYFCARS-G 119

QY 121 YSNNWYFDVWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 120 YDYDW-FATWGQGLTVVSAAKTATFSVPLAPVCGGTGSSVTLGCLVKGYFPEPTVIT 178

QY 181 WNSGALTSGVHTFPFPAVLQSSGLYSLSSVTVPSSSISLGTQTYICNVNHNKPSNTKVDKRVPP 240
DB 179 WNSGSLSSGVHTFPFALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASSIKVDKKIEP 237

QY 241 K-----SCDKHTCPCPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDDP 294
DB 238 RVPIITQNCPPLKECPCCAAPDLLGGPSVFIFPPKIKDVLMISSLSPMVTQVVDVSEDDP 297

QY 295 EVKFNMYDGVGVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
DB 298 DQVISHFVNNEVHTAQTQTHREDYNSTLRVYSALPIQHQDWMSGKEFKCKVNNRALPSP 357

QY 355 IEKTSKAGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 414
DB 358 IEKTIISKRGPRAPQVYVLPPEAEEMTKKEFSLTCMITGFLPAETAVDWTSNGRTEQNY 417

QY 415 KTTPPVLDSDGSFFLYSKLTVDKSRMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 418 KNTATVLDSDGSFYMYSKLRVQKSTWERSGLFACSVVHGLNHLTKTISRSLGK 473
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```
RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003435; AA03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
```

```
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig.
DR SMART: SM00409; Ig.
DR SMART: SM00407; IGc1; 2.
DR SMART: SM00406; IGv; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match      64.7%; Score 1628.5; DB 11; Length 463;
Best Local Similarity 63.8%; Pred. No. 6.6e-128;
Matches 301; Conservative 71; Mismatches 89; Indels 11; Gaps 5;

QY 1 MGWSCILFLVATATGVSQVLQVSGAEVKKPGKASGYTFTSYMHWVKQAP 60
DB 1 MEWITFLIFLISGTAGVHSQVLQKSGAELRPGASVRLSCASGYTFTGIGVSWVKQRT 60

QY 61 GQGLEWMEIDPSDSTNTNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRD 120
DB 61 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAVYFCARSS 120

QY 121 YSNNWYFDVWGQGLTVTVSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 121 YSYD-LFAYWGQGLTVVSAAKTTPPSVPLAPGSAAQTNMSWVTLGCLVKGYFPEPTVT 179

QY 181 WNSGALTSGVHTFPFPAVLQSSGLYSLSSVTVPSSSISLGTQTYICNVNHNKPSNTKVDKRVPP 240
DB 180 WNSGSLSSGVHTFPFPAVLQSD-LYTLSSSVTVPSSTWPSSETVTCNVAHPASSIKVDKKIIV 238

QY 241 KSDKHTHTCPP--CPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298
DB 239 RDCG-----CKPCICTYPEV---SSVFIFPPKPKDVLITLTPKVTCVVVDISKDDPEVQF 291

QY 299 NMYVDGVGVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358
DB 292 SFWFDDVEVHTAQTQPREQFNSTFRSVSELPTIMHODWLNKGKEFKCRVNSAAPPAPIEKT 351

QY 359 ISKAGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTT 418
DB 352 ISKTGRPRAPQVYTLPPPEQMAKDKVSLTCMITDFFEDITVEHWQNGQPAENYKNTQ 411

QY 419 PVLDSGDSFFLYSKLTVDKSRMQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 412 PIMDTDGSFYIYKLVNQSNEAGNFTFCVSLHGLNHNHTEKLSLSPGK 463

RESULT 3
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam: PF00047; Ig.
DR SMART; SM00409; Ig.
DR SMART; SM00407; Ig.
```


Qy	395	FYSDIAVAVESNGQ--PENNYKTTTPPVL-DSDG--SFFLYSKLTVDKSRWQQGNVFSCS	449
		: : : : : :	
Db	402	ESPDKLVLRWLOGSQELPREKYLTWASROEPSQGITTFATVTSILRYAAEDWKKGDFSCM	461
		: : : : : :	
Qy	450	VMHEALHNHYTKQSLSLSPOK	470
		: :	
Db	462	VGHEALPLAFTQTETIDRLAGK	482
		: :	
 RESULT 13			
	Q91WT1	PRELIMINARY;	PRT; 481 AA.
ID	Q91WT1	AC	
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	HYPOTHETICAL 52.1 KDA PROTEIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata;		
OX	Nmblat; Eutheria; Rodentia;		
CC	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
PT	TISSUE=COLON;		
RA	Straussberg R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.		
DR	ENBL; BC013490; AAH13490.1; -.		
KW	Hypothetical protein.		
SK	SEQUENCE 481 AA; 52105 MW;		
			97DF68D159463F65 CRC64;

RESULT 14

Q91WRI PRELIMINARY; PRT; 488 AA.

ID Q91WRI;
AC AC
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 53.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[...]
RN SEQUENCE FROM N.A.
RP RP
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC013539; AH13539.1; -.
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 32.6%; Score 820; DB 11; Length 488;
Best Local Similarity 39.4%; Pred. No. 3.1e-60;
Matches 192; Conservative 84; Mismatches 177; Indels 34; Gaps 16;

QY 1 MGWNWIFLVATATGTVHSSQVLVQSQAEGVKPKGASVKVCASKGYFTSYVMOWKQAP 60
DB 1 MGWNWIFLLSAGTAGIYSEVLOOQGPELVKPGASVKLSCKASGYITDYVNWKQSH 60
QY 61 GGQLEWGEIDPDSYNYNOKFKGATLTVDSTSTAYMELSSLRSEDATAVYYCARNRD 120
DB 61 GKSLWTGDINPYNGGTYSYNOKFKGATLTVDKSSSIAYMQLNLTSDDSAVYYCARGPV 120
QY 121 YSNWWEI----DVWGOGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPE 175
DB 121 YYS--YFSYRGDIYWGOGTLVTSAEPAREPTIYPLT-FPQALSSDPVIIGCLLHDYFPS 177
QY 176 -PVRVSNNSGALTSGVHTFPVQLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHKPSNTK 233
DB 178 GTMNVTGWKSKDITTYNFPPALASGGRYTMSSQLTLPAVECPGESVKCSQH--DSNPV 236
QY 234 VDKRVKPSCDKTHTCPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHED 293
DB 237 QELNVNCGPICSPPTTPPPSCQ-----PSLSLORPALED-LILGSDASITCTLNLG--RD 289
QY 294 PE-VKFNNYVDGVEVHNAKTKPREEQNST---YRVSVSLTVLHQDWLNGKEYKCKVSNK 349
DB 290 PEGAVFTW-----EPSTGKDVAQKAVONCGCYSSVSLPGCAERNWSASFCTVTHP 344
QY 350 ALPAPIEKTISKAGQPREPOVYTLPPSRREMTKNQ-VSLTCLVKGPYPDIAEVNESNG 408
DB 345 ESOT-LTGTTAKVTYVTFPQVHLPPPSELALNELVSLTCLVRAENPKVELVYRWLHGN 403
QY 409 Q----PENNYKITPPVLDSGD--GFFLYSKLTVDKSRQQGVNSFYSCSYHEALHNHYTQKS 463
DB 404 EELSPELYLFEPLKEGEGATTVLVTSVRVSAEIWKQGDQYSCWVGHEALPMNFTQKT 463
QY 464 LSLSPGK 470
DB 464 IDRLSGK 470

RESULT 15

Q96BB9 PRELIMINARY; PRT; 597 AA.

ID Q96BB9;
AC AC
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:37 ; Search time 230.21 seconds
(without alignments)
226.770 Million cell updates/sec

Title: US-09-499-662-145

Perfect score: 2517

Sequence: 1 MWGSCILFLVATATGVHSQ.....MHEALHNYTKSLSPCK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5.

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
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16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
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18: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	21	AAW90934 Humanised anti-Fas
2	2515	99.9	470	21	AAW90933 Humanised anti-Fas
3	2512	99.8	470	19	AAW83037 Anti-Fas humanised
4	2512	99.8	470	21	AAW14779 Humanised anti-Fas
5	2512	99.8	470	21	AAW50929 Humanised HFE7A de
6	2512	99.8	470	21	AAW90935 Humanised anti-Fas
7	2499	99.3	470	19	AAW83036 Anti-Fas humanised
8	2499	99.3	470	21	AAW14776 Humanised anti-Fas
9	2499	99.3	470	21	AAW90926 Humanised HFE7A de
10	2497	99.2	470	21	AAW90936 Humanised HFE7A de
11	2348.5	93.3	731	22	AAW52156 Humanised HMF6-1 h

12	2348.5	93.3	741	22	AAW52159 Humanised HMF6-1 h
13	2343.5	93.1	729	22	AAW52158 Humanised HMF6-1 h
14	2343.5	93.1	739	22	AAW52161 Humanised HMF6-1 h
15	2337.5	92.9	730	22	AAW52157 Humanised HMF6-1 h
16	2337.5	92.9	740	22	AAW52160 Humanised HMF6-1 h
17	2303	91.5	652	19	AAW48650 Heavy chain of hma
18	2290.5	91.0	465	22	AAW72228 Humanised 323/A3 (
19	2285.5	90.8	464	22	AAW72232 Humanised 323/A3 (
20	2285	90.8	470	21	AAW808026 A dimeric anti-CD2
21	2284	90.7	466	22	AAE03755 Chimeric 2403 IgG
22	2254	89.6	476	20	AAW98464 Monoclonal antibody
23	2253.5	89.5	481	13	AAW44442 Sequence of antibody
24	2246	89.2	472	20	AAW50166 Human reshaped Flg
25	2232	88.7	476	14	AAW31023 Antibody D heavy c
26	2231.5	88.7	583	22	AAW83156 Ganglioside GM2 an
27	2230	88.6	449	14	AAW43339 Completely humanis
28	2230	88.6	449	19	AAW49816 Amino acid sequenc
29	2200.5	87.4	467	22	AAW36210 Human immune syste
30	2198.5	87.3	452	20	AAW29458 Recombinant immuno
31	2198.5	87.3	452	21	AAW30322 Humanised anti-IL-
32	2198.5	87.3	452	21	AAW77766 Humanised anti-IL-
33	2198	87.3	472	20	AAW50157 Chimeric mouse/hum
34	2191	87.0	592	22	AAW83838 Amino acid sequenc
35	2189.5	87.0	452	19	AAW89316 Anti-IL-8 humanise
36	2188	86.9	474	22	AAW14177 Human novel protei
37	2188	86.9	595	20	AAW86003 Anti-5T4 single ch
38	2186.5	86.9	473	22	AAW64475 Human type antihum
39	2183.5	86.8	473	22	AAW64471 Human type antihum
40	2183.5	86.8	475	22	AAW63640 Amino acid sequenc
41	2178.5	86.6	473	22	AAW64469 Human type antihum
42	2177	86.5	468	20	AAW5689 D9D10 heavy chain
43	2177	86.5	711	20	AAW85692 MoTabii fusion pro
44	2171.5	86.3	473	22	AAW64473 Human type antihum
45	2161	85.9	470	13	AAW22757 Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1

AAW90934

ID AAW90934 standard; Protein; 470 AA.

AC AAW90934;

DT 08-AUG-2000 (first entry)

XX Humanised anti-Fas designed heavy chain Heu 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
XX dermatologic; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;
XX multiple sclerosis; Basedow's disease; myasthenia gravis;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX Synthetic.

XX EP990663-A2.

PD 05-APR-2000.

XX 29-SEP-1999; 99EP-0307711.

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI: 2000-258930/23.
DR N-PSDB; AAA11645.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Claim 2 : Page 174-176; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 2
CC which is described in the method of the invention.
XX
SQ Sequence 470 AA;

Query Match 100.0%; Score 2517; DB 21; Length 470;
Best Local Similarity 100.0%; Pred. No. 4.4e-143;
Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVKSCASGVTFTSYMMQWVKQAP 60
DB 1 mgwscililflvatatgvhsgvqlvqsgaevkpgasvkvsckasgytftsywmqwkqap 60
QY 61 GCGLEWNGEIDPSDSTNTNOKFKGKATITVDTSTAYMELSSLSRSEDVAVYCARNRD 120
DB 61 gggiewngeidpsdstyntnqkfkgkatitvdtststaymelslsrsedtavycarnrd 120
QY 121 YSNWNYFDVWGGTTLTVTSASSTKGPSVFLAPSSKTSGGTAALGCLVKDFPPEVTYS 180
DB 121 ysnwnyfdvwwgttlvtvsastkgsfvflapsskstsggtaalgclvkdyfpeptyvs 180
QY 181 WNSGALTSVGHVFPVQLQSGSLYSLSVTVPSSSLGCTQTYICNVNWKPSNTKVDKRVPEP 240
DB 181 wnsгалtsvghvfpvqlqsgslsylvstvpssslgctqtyicnvnhkpsnktkvdkrvpep 240
QY 241 KSCDKHTHTCCPAPPELLGGPSVFLFPPPKDITLSTRTPEVTCVVVDVSHEDPEVKFNW 300
DB 241 kscdkhtcpcpapellggpsvflfpppkdltlstrtpevtcvvvdvshedepevkfnw 300
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
DB 301 yvdgvevhnaktprreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360
QY 361 KAGQPREPQVYTLPPSREMTKNQVSLCIVKGFPYSDIAVEWESNGQPENNYKTTTPV 420
DB 361 kagqprepqvtytlppsremtnqnqslclvkgfpydsdiavewesngqpennykttppv 420

DB 361 kagqprepqvtytlppsremtnqnqslclvkgfpydsdiavewesngqpennykttppv 420
QY 421 LDSGSGFFLYSKLTVDKSRWQOGNVPSCSYMHEALHNHYTKQSLSLSPGK 470
DB 421 ldsdgsfflyskltvdksrwqgnvfscsymhealhnhytcqkslsispgk 470
RESULT 2
AAW90933
ID AAW90933 standard; Protein; 470 AA.
XX
AC AAW90933;
XX
DT 08-AUG-2000 (first entry)
DE Humanised anti-Fas designed heavy chain Heu 1 protein.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.
XX
PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX
DR WPI: 2000-258930/23.
DR N-PSDB; AAA11644.
XX
PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
PS Claim 2; Page 169-170; 263pp; English.
XX
CC This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (1) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.98; Score 2515; DB 21; Length 470;
Best Local Similarity 99.88; Pred. No. 5.8e-143;
Matches 469; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCILFLVATATGVHSGVQVLSGAEVKKPGASVKVSKASGYTFTSYWMQWVKQAP 60
Db 1 mgwscilflvatatgvhsqvlvgsgaevkkpgasvkvsckasgytftsywmqwkqap 60
QY 61 GQGLEWGEIDPSISYNYNOKFKGKATITVDTSTSTAYMELSLRSEDVAYVYCARNRD 120
Db 61 gqglewgeidpsdsytnyngdkfgkatitvdtststaymelslrseadvayycarnrd 120
QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVLDKDYFEPPTVTS 180
Db 121 ysnwnyfdvwwgqglvtvssastkgpsvfplapssksts gtaalgclvldkyfpepvtvs 180
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSNTKVDKRVPE 240
Db 181 wnsгалtsgvhtfpavlgssglyslssvstvtpssslgqtqyicnvnhpkpsntkvdkrvpe 240
QY 241 KSCDKTHCTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthctcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNATKPREQYNTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnatkpreeqyntyrvvsvltvlhodwlnkgeyckvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
Db 361 kagqprepqvytlppsreemtknqvsltclvkgfypsdiavewesngqpennnykttppv 420
QY 421 LDSGSEFLYSLKLVADKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK 470
Db 421 ldsgefflyskltvdksrwqgnvfscsvmh ealhnhytgkslsispgk 470

RESULT 3

ID AAW83037 standard; Protein; 470 AA.

XX AC AAW83037;

XX DT 15-MAR-1999 (first entry)

XX DE Anti-Fas humanised antibody HFE7A heavy chain.

KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT 20..470
FT /label= Mat_protein
FT Region 20..140
FT /label= Variable
FT Region 141..464
FT /label= Constant
FT Region 50..54
FT /label= CDR_H1
FT /note= "Claim 9"
FT Region 69..84
FT /label= CDR_H2
FT /note= "claim 9"
FT Region 118..129
FT /label= CDR_H3
FT /note= "claim 9"

XX AU9859701-A.

XX 08-OCT-1998.

XX 30-MAR-1998; 98AU-0059701.

XX 08-OCT-1997; 97JP-0276064.

XX 01-APR-1997; 97JP-0082953.

XX 25-JUN-1997; 97JP-0169088.

XX (SANY) SANKYO CO LTD.

XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;

XX Masahiko O, Nobufusa S, Shin Y, Tohru T;

XX WPI; 1998-543440/47.

XX N-PSDB; AAV70080.

DR New antibodies and proteins bind conserved epitope of Fas antigen -
DR used to evaluate drugs in animal models and to treat Fas-associated
DR diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
DR myocarditis, hepatitis and AIDS

PS Claim 22; Page 225-227; 292pp; English.

XX This is the amino acid sequence of the HV type humanised heavy
CC chain of murine anti-human Fas monoclonal antibody HFE7A. It
CC includes humanising R44G and A76T amino acid substitutions that are
CC conserved in the human IgG heavy chain. Host Escherichia coli
CC pgRPHV3 SANK 70298 harbors plasmid pgRPHV3 carrying a fusion
CC fragment of the humanised HV type HFE7A heavy chain and DNA
CC encoding human IgG1 constant region (see AAV70080), and is deposited
CC as FERM BP-6273 (Claimed). The invention provides methods for
CC producing humanised antibodies by culturing host cells. Humanised
CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
CC of inducing apoptosis in abnormal cells expressing Fas, and of
CC inhibiting Fas-induced apoptosis in normal cells. The humanised
CC antibodies are used to evaluate, in animal models, treatments of
CC diseases that involve Fas/Fas ligand interactions, and also to
CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple scleritis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).

SQ Sequence 470 AA;

Query Match 99.8%; Score 2512; DB 19; Length 470;

Best Local Similarity 99.6%; Pred. No. 8.8e-143;

Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYWQWVKQAP 60
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkpgasvkvsckasgyftftsywmqwkqap 60
QY 61 GQGLEWNGEIDPSDSYNNQKFKGKATITVDNSTAYMELSSLRSEDFAVYYCARNRD 120
Db 61 gqglewmgeidpsdsytnynqkfkgtltdtststaymelslsrsedcavyyccarnrd 120
QY 121 YSNWNYFDVWGQGLTVNTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVS 180
Db 121 ysnwnyfdvwgqgltvntvssastkgpsvflpapskstsrgtaalgclvkdypcptvs 180
QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
Db 181 wnsгалtsvghtfpavllqsgslyslssvstvppssslgtqtyicnvnhkpsntkvdkrvp 240
QY 241 KSCDKHTCPCPAPPELLGGPSVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 kscdkhtcpcpapellggpsvflpppkdtlmsrtpevtcvvdvshedpevkfnw 300
QY 301 YVDGVEVHNAKTKPREQYNTSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdnlngkeyckvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 361 kagqprepqvylppstreemtknqvsllclvkgfypsdiavewesngqpennyykttppv 420
QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqkslspsgk 470
```

RESULT 4

AA014779 standard; Protein; 470 AA.

AA014779;

24-NOV-2000 (first entry)

Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.

Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
murine; humanised antibody; complementarity determining region; CDR;
human Fas; Fas ligand; apoptosis modulator; programmed cell death;
autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
hepatitis; AIDS; graft rejection; heavy chain.

Chimeric - Mus musculus.

Chimeric - Homo sapiens.

JP2000169393-A.

20-JUN-2000.

30-SEP-1999; 99JP-0278301.

30-SEP-1998; 98JP-0276883.

(SANY) SANKYO CO LTD.

WPI: 2000-485645/43.

N-PSDB; AA072184.

Preventive or treating agent for the diseases caused by an abnormality
in the Fas/Fas ligand system e.g. autoimmune diseases, contains
anti-Fas antibody -

Claim 21; Page 108-109; 139pp; Japanese.

XX

CC The invention relates to compositions for the prevention or treatment
of diseases caused by an abnormality in the Fas/Fas ligand system
containing an anti-Fas antibody as the active component. The anti-Fas
antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
or a humanised version of HFE7A containing identical CDRs
(complementarity determining regions) to antibody HFE7A. Via its
interaction with Fas, the antibody of the invention acts as a modulator
of apoptosis. The composition of the invention may therefore be used in
the treatment or prevention of conditions such as autoimmune diseases,
allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
represent the heavy chains (or fragments thereof) of various humanised
HFE7A-derived anti-Fas antibodies.

Sequence 470 AA;

Query Match 99.8%; Score 2512; DB 21; Length 470;
Best Local Similarity 99.6%; Pred. No. 8.8e-143;
Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYWQWVKQAP 60

Db 1 mgwsciiilflvatatgvsqvlvqsgaevkpgasvkvsckasgyftftsywmqwkqap 60

QY 61 GQGLEWNGEIDPSDSYNNQKFKGKATITVDNSTAYMELSSLRSEDFAVYYCARNRD 120

Db 61 gqglewmgeidpsdsytnynqkfkgtltdtststaymelslsrsedcavyyccarnrd 120

QY 121 YSNWNYFDVWGQGLTVNTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVS 180

Db 121 ysnwnyfdvwgqgltvntvssastkgpsvflpapskstsrgtaalgclvkdypcptvs 180

QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240

Db 181 wnsгалtsvghtfpavllqsgslyslssvstvppssslgtqtyicnvnhkpsntkvdkrvp 240

QY 241 KSCDKHTCPCPAPPELLGGPSVFLPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300

Db 241 kscdkhtcpcpapellggpsvflpppkdtlmsrtpevtcvvdvshedpevkfnw 300

QY 301 YVDGVEVHNAKTKPREQYNTSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTIS 360

Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdnlngkeyckvsnkalpapiektis 360

QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420

Db 361 kagqprepqvylppstreemtknqvsllclvkgfypsdiavewesngqpennyykttppv 420

QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470

Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqkslspsgk 470

RESULT 5

AA090929

ID AA090929 standard; Protein; 470 AA.

AA090929;

08-AUG-2000 (first entry)

Humanised HFE7A designed heavy chain protein #2.

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
neurotropic; antifertility; neuroprotective; antiarteriosclerotic;
hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
Hashimoto disease; rheumatoid arthritis; graft versus host disease;
Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;

CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
CC antiarteriosclerotic, cardiant and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
CC which is described in the method of the invention.

XX Sequence 470 AA;

Query Match 99.8%; Score 2512; DB 21; Length 470;
Best Local Similarity 99.6%; Pred No. 8.8e-143;
Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFVATGVHQSQVLQSGAEVKKPGASVKYSCASGYTFTSYMMQWYKQAP 60
Db 1 mgwscililfvatgvhsqvlvqsgaeavkpgasvkyscasgytftsymwqvrqap 60
QY 61 GQGLEWMEIDPSDSTNTNQKFKGKATITVDSTSTAYMELSLRSEDATVYICARNRD 120
Db 61 gqglewmgeidpsdstyntnqkfkgkatitvdststaymelsslrse dtavvycarnrd 120
QY 121 YSNWYFDVWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
Db 121 ysnw yfdwgggltv tvssastk gpsvflapssk stsggtaalgclvkdyfpeptvys 180
QY 181 WNSGALTSGVHTFPPAVLYQSSGLYSLSVVTVFSSSLGTQTYICNVNHPKSNTKVDKRVEP 240
Db 181 wnsгалtsгvhtfpavlyqsglyslsvvtvpssslgtqtyicnvnhkpsntkvdkrvep 240
QY 241 KSCDKTHCTCPCPAPPELLCGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300
Db 241 kscdkthctcpapellcgpsvflfpppkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLDHQMNGKEYCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvldhqwngkeyckvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
Db 361 kagqprepqv ytlppsreemtknq vsltclvk gfypsdiavewesngqpennyktppv 420
QY 421 LSDSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 470
Db 421 ldsdgsfflyslkltvdksrwqgnvfscvsmhealhnhytqkslspsgk 470

RESULT 7

ID AAW83036 standard; Protein; 470 AA.

XX AAW83036;

AC AAW83036;

XX 15-MAR-1999 (first entry)

DT 15-MAR-1999 (first entry)

XX

DE Anti-Fas humanised antibody HFE7A heavy chain.
XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; AIDS;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
OS Homo sapiens.
OS Synthetic.
Key Location/Qualifiers
FT Peptide 1..19 /label= sig_peptide
FT Protein 20..470 /label= Mat_protein
FT Region 20..140 /label= Variable
FT Region 141..464 /label= Constant
FT Region 50..54 /label= CDR_H1
FT Region 69..84 /note= "claim 9"
FT Region /label= CDR_H2
FT Region 118..129 /note= "claim 9"
FT Region /label= CDR_H3
FT Region /note= "claim 9"
XX AU9859701-A.
XX 08-OCT-1998.
XX 30-MAR-1998; 98AU-0059701.
XX 08-OCT-1997; 97JP-0276064.
PR 01-APR-1997; 97JP-0082953.
PR 25-JUN-1997; 97JP-0169088.
XX (SANY) SANKYO CO LTD.
XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
XX WPI; 1998-543440/47.
XX N-PSDB; AAV70079.
XX New antibodies and proteins bind conserved epitope of Fas antigen -
XX used to evaluate drugs in animal models and to treat Fas-associated
XX diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
XX myocarditis, hepatitis and AIDS
PS Claim 22; Page 212-213; 292pp; English.
XX This is the amino acid sequence of the VD type humanised heavy
XX chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
XX pgHSL7A62 SANK 73397 harbors plasmid pgHSL7A62 carrying a fusion
XX fragment of the humanised VD type HFE7A heavy chain and DNA
XX encoding human IgG1 constant region (see AAV70079), and is deposited
XX as FERM BP-6074 (claimed). The invention provides methods for
XX producing humanised antibodies by culturing host cells. Humanised
XX versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
XX of inducing apoptosis in abnormal cells expressing Fas, and of
XX inhibiting Fas-induced apoptosis in normal cells. The humanised
XX antibodies are used to evaluate, in animal models, treatments of
XX diseases that involve Fas/Fas ligand interactions, and also to

```
CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;

Query Match 99.3%; Score 2499; DB 19; Length 470;
Best Local Similarity 99.1%; Pred. No. 5.3e-142;
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSTYMWQVVKQAP 60
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftstymwqvkqap 60
QY 61 GQGLEWMEIDPSDSTNYNKKFKGKATITVDTSSTAYMELSLRSEDATVYYCARNRD 120
DB 61 gqglewmeidpsdstnyndkfkgkatitvdtstastaymelslrse dtavyyccarnrd 120
QY 121 YSNNNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 121 ysnnnwyfdvwgqgl tvtvssastkgpsvfplapsskstsggtaalgclvkd yfpeptvts 180
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
DB 181 wnsгалтsgvhtfpav lqssglys lssv tvtpssslgtqt yicnvnhnkp sntkvdkrv 240
QY 241 KSCDKTHTCPPCPAPELLGGSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccpccp apellggsvflfpkpkdtlmisrtpevtcvv dshdpevkfnw 300
QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKIS 360
DB 301 yvdgvevhnatkpre eqynstyrvvsvl tvlhodwlngkeyckvsnkalpapietkis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV 420
DB 361 kakgqprepqvytl ppsreemtknqvs ltc lvkgfypsdiave wesngopennykttppv 420
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 421 ldsdgsfflyskltv dksrwqgnvfscsvmh ealhnhytqksls lspgk 470

RESULT 8
AAB14776
ID AAB14776 standard; Protein: 470 AA.
XX
AC AAB14776;
XX
XX
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
```

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XX 30-SEP-1999; 99JP-0278301.
XX 30-SEP-1998; 98JP-0276883.
XX (SANY ) SANKYO CO LTD.
XX WPI; 2000-485645/43.
XX N-PSDB; AAA72159.
XX Preventive or treating agent for the diseases caused by an abnormality
XX in the Fas/Fas ligand system e.g. autoimmune diseases, contains
XX anti-Fas antibody -
XX Claim 21; Page 95-96; 139pp; Japanese.
XX The invention relates to compositions for the prevention or treatment
XX or diseases caused by an abnormality in the Fas/Fas ligand system
XX containing an anti-Fas antibody as the active component. The anti-Fas
XX antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
XX or a humanised version of HFE7A containing identical CDRs
XX (complementarity determining regions) to antibody HFE7A. Via its
XX interaction with Fas, the antibody of the invention acts as a modulator
XX of apoptosis. The compositions of the invention may therefore be used in
XX the treatment or prevention of conditions such as autoimmune diseases,
XX allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
XX glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
XX and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
XX represent the heavy chains (or fragments thereof) of various humanised
XX HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;

Query Match 99.3%; Score 2499; DB 21; Length 470;
Best Local Similarity 99.1%; Pred. No. 5.3e-142;
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSTYMWQVVKQAP 60
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftstymwqvkqap 60
QY 61 GQGLEWMEIDPSDSTNYNKKFKGKATITVDTSSTAYMELSLRSEDATVYYCARNRD 120
DB 61 gqglewmeidpsdstnyndkfkgkatitvdtstastaymelslrse dtavyyccarnrd 120
QY 121 YSNNNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 121 ysnnnwyfdvwgqgl tvtvssastkgpsvfplapsskstsggtaalgclvkd yfpeptvts 180
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
DB 181 wnsгалтsgvhtfpav lqssglys lssv tvtpssslgtqt yicnvnhnkp sntkvdkrv 240
QY 241 KSCDKTHTCPPCPAPELLGGSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNW 300
DB 241 kscdkthtccpccp apellggsvflfpkpkdtlmisrtpevtcvv dshdpevkfnw 300
QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKIS 360
DB 301 yvdgvevhnatkpre eqynstyrvvsvl tvlhodwlngkeyckvsnkalpapietkis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV 420
DB 361 kakgqprepqvytl ppsreemtknqvs ltc lvkgfypsdiave wesngopennykttppv 420
QY 421 LDSGGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 421 ldsdgsfflyskltv dksrwqgnvfscsvmh ealhnhytqksls lspgk 470

RESULT 9
AAW90926
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AAW90926 standard; Protein; 470 AA.
AAW90926;
08-AUG-2000 (first entry)
Humanised HFE7A designed heavy chain protein.
Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
Hashimoto disease; rheumatoid arthritis; graft versus host disease;
Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;
multiple sclerosis; Basedow's disease; arteriosclerosis; myocarditis;
insulin dependent diabetes mellitus; hepatitis; transplant rejection.
cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
Synthetic.
EP990663-A2.
05-APR-2000.
29-SEP-1999; 99EP-0307711.
30-SEP-1998; 98JP-0276881.
30-SEP-1998; 98JP-0276882.
(SANY) SANKYO CO LTD.
Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
WPI: 2000-258930/23.
N-PSDB; AA11597.
New humanized anti-Fas antibody, useful for treating or preventing e.g.
inflammatory or autoimmune disease, induces apoptosis selectively in
cells with abnormal Fas-Fas ligand systems
Example reference 15; Page 134-136; 263pp; English.
This invention describes a novel humanized anti-Fas antibody-like
molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by binding to Fas on the cell surface, and prevents
apoptosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
immunomodulatory, dermatological, immunosuppressive, thyromimetic,
antirheumatic, nephrotropic, antiinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
apoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
(B, C or D) or alcoholic), and transplant rejection. (I) selectively
inhibit apoptosis in normal cells but selectively induce it in abnormal
cells. They bind to both human and murine Fas, so can be evaluated in
murine disease models. (I) act on the active site of Fas, i.e. they mimic
the native ligand, do not induce liver disease, and have reduced risk of
inducing a human anti-murine antibody response. This sequence represents
a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
the method described in the invention.

Sequence 470 AA;

Query Match 99.3%; Score 2499; DB 21; Length 470;
Best Local Similarity 99.1%; Pred. No. 5.3e-142;
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MGWSCIILFLVATATGVHSQVLVQSGAEVKKPGCASVKVSKASGYTFTSYWMQVVKQAP 60
Db 1 mgwsciilflvatatgvhsqvlvqsgaevkkpgcasvkvsckasgytftsywmqvwkqap 60
QY 61 GCGLEWNGETDPSDSTYNQKPKGKATINVDSTSTPAYMELSLRSEDFAVYVCARNRD 120
Db 61 gqrlwmgelidpsdsytnyngkfkgkatilvtdtsastaymelslrseidcavvyccarnrd 120
QY 121 YSNWTFDVMGQCTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
Db 121 ysnwtfdvmgqctlvtvssastkgpsvfplapssksts gtaalgclvkdypcptvts 180
QY 181 WNSGALTSVGHVTPPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHPKNTKVDRKREP 240
Db 181 wnsгалtsvghtfpavllqssglsylssvstvpssslgtqtyicnvnhpkntkvdkrrep 240
QY 241 KSCDKHTCTPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkhtctpcpapel lggpsvflppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTTIS 360
Db 301 yvdgvevhnaaktprreeqynstyrvvsvltv l hqdwlngkeykckvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPV 420
Db 361 kakgqprepqvylppsreemtknqvsl tclvkgyfypsdiavwesngqpennykttppv 420
QY 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSVYHMEALHNHYTQKSLSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqqgnvfscsvymhealhnhytcqkslsispgk 470

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RESULT 10

AAW90936

ID AAW90936 standard; Protein; 470 AA.

XX AC

AAW90936;

XX DT

08-AUG-2000 (first entry)

XX DE

Humanised HFE7A designed heavy chain HHH type protein.

XX KW

Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
Hashimoto disease; rheumatoid arthritis; graft versus host disease;
Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
Goodpasture syndrome; Crohn's disease; thrombopenia purpura; allergy;
multiple sclerosis; Basedow's disease; arteriosclerosis; myocarditis;
insulin dependent diabetes mellitus; hepatitis; transplant rejection.
cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX OS

Synthetic.

XX PN

EP990663-A2.

XX PD

05-APR-2000.

XX PF

29-SEP-1999; 99EP-0307711.

XX PR

30-SEP-1998; 98JP-0276881.

XX PR

30-SEP-1998; 98JP-0276882.

XX PA

(SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 DR N-PSDB; AAA11655.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX Claim 2; Page 188-189; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antiarthrosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
 CC which is described in the method of the invention.
 XX
 SQ Sequence 470 AA;

Query Match 99.2%; Score 2497; DB 21; Length 470;
 Best Local Similarity 98.9%; Pred. No. 7e-142;
 Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPGASVKVSCKASGYFTSTYMWQVVKQAP 60
 DB 1 mgwsciiilflvatatgshsqvqlvqsgaevkpgasvkvsckasgyftstymwqvrvqap 60
 QY 61 GQGLEWNGEIDPSDSTNYNOKFKGKATITVDTSSTAYMELSLRSDEDTAVYYCARNRD 120
 DB 61 gqglewngeidpsdstnyynokfkgkatitvdtststaymelslrsedtdavyyccarnrd 120
 QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 DB 121 ysnwnyfdvwgqglvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 180
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNFKVDKRVPE 240
 DB 181 wnsгалtsгvhtfpavlqssglyslssvttvtpssslgtqtyicnvnhnkpsnftkvdkrvpe 240
 QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
 DB 241 kscdkthtccpccpapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 300
 QY 301 YVDGVEVHNAKTPREEQYNSTYRWVSVLTVLHQDLWLNKGKEYCKVSNKALPAPIETIS 360
 DB 301 yvdgvevhnaktprreeqynstyrwvsylvtlvhlqdlwlnkgkeyckvsnkalpapiektis 360
 QY 361 KAKQCPREPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
 DB 361 kakqcprepqvyyitlppsreemtknqvsltclvkgfyfypsdiavewesngqpennyykttppv 420

DB 361 kakgqprepqvyyitlppsreemtknqvsltclvkgfyfypsdiavewesngqpennyykttppv 420
 QY 421 LDSGSEFLYSLKLTVDKSRWQGGNVFSCSYNHEALHNHYTOKSLSLSPCK 470
 DB 421 ldsgsseflyslkltvdksrwqggnvfscsynhealhnhytokslslspgk 470
 RESULT 11
 AAM52156
 ID AAM52156 standard; Protein: 731 AA.
 XX
 AC AAM52156;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
 XX
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200174905-A1.
 XX
 PD 11-OCT-2001.
 XX
 PF 26-MAR-2001; 2001WO-GB01324.
 XX
 PR 03-APR-2000; 2000GB-0008049.
 XX
 PR 02-OCT-2000; 2000US-237159P.
 XX
 PA (ANTI-) ANTISOMA RES LTD.
 XX
 PI Young RJ;
 XX
 DR WPI: 2001-662969/76.
 XX
 PT Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity -
 XX
 PS Claim 20; Figure 7; 176pp; English.
 XX
 CC The invention relates to a compound which comprises a target
 CC cell-specific portion, comprising an humanised monoclonal antibody,
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.
 XX
 SQ Sequence 731 AA;

Query Match 93.3%; Score 2348.5; DB 22; Length 731;
 Best Local Similarity 93.0%; Pred. No. 8.8e-133;
 Matches 437; Conservative 20; Mismatches 10; Indels 3; Gaps 1;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPGASVKVSCKASGYFTSTYMWQVVKQAP 60
 DB 1 mgwsciiilflvatatgshsqvqlvqsgaevkpgasvkvsckasgyftsfayviewrvqap 60
 QY 61 GQGLEWNGEIDPSDSTNYNOKFKGKATITVDTSSTAYMELSLRSDEDTAVYYCARNRD 120
 DB 61 gqglewngeidpsdstnyynokfkgkatitvdtststaymelslrsedtdavyyccarsyd 120
 QY 121 YSNWNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 DB 121 ysnwnyfdvwgqglvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvtvs 177
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNFKVDKRVPE 240

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.
 xx Sequence 729 AA;
 SQ

Query Match	93.1%	Score	2343.5	DB	22	Length	729
Best Local Similarity	93.0%	Pred. NO.	1.7e-132				
Matches	436	Conservative	20	Mismatches	10	Indels	3
Gaps							
Qy	1	MGWSCIIILFLVATATGVHSQVOLVQSGAEVKKPGASVKVSKCASGYTTFTSYWQWVKQAP	60				
Db	1	mgwscillflvatatgvhsqvolvqsgaevkpgasvkvcasgyttfsayviewrqap	60				
Qy	61	QGGLWEWGEIDPDSQSYTNYNQFKGKATITVDSTSTAYMELSSLSRSEDATVYYICARNRD	120				
Db	61	qgglewgeidlpdgannsnrynekfgrvtvtdstntaymelslsrseadvyyearysd	120				
Qy	121	YSNNWYFDVWGGGTLTVTYSSASTKGPVSFFPLAPSSKSTSGGTAALGCLVKDYDFPFPVTVS	180				
		:::					
Db	121	fa---wafaywgggtltvtyssastkgsfvflapssktsggtaalgclvdkyfppevtvs	177				
		:::					
Qy	181	WNSGALTSGVHTFPAVLQSSGLYLSLSSVVTVPPSSSLGTQTVICNVNHNKPSNTKYDKRVEP	240				
Db	178	wnsгалtsgvhtfpavlqssglyslssvvtvppssslgtqtvicnvnhkpsntkvdckvpe	237				
Qy	241	KSCDKTHPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPVEKFNW	300				
Db	238	kscdkthtccpcpapelligpsvflfppkpkdtlmisrtpevtcvvdvshedpevkfnw	297				
Qy	301	YVDGVEVHNATKPREQGYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS	360				
Db	298	yvdgvevhnatkpreedynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis	357				
Qy	361	KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGYFSPYDIAVEWESNGQPENNYKTTTPV	420				
Db	358	kakgqprepvytlppsrreeltnqvsltcclvkgyfspydiavewesngqpennyktttpv	417				
Qy	421	LDSDGSFFLYSKLTVDKRWQOGNVFSCSVMEALHNHYTQKSLSLSPG	469				
Db	418	ldsдgsfflyskltdkdrwqognvfscsvmhealhnhytqkslsisq	466				

RESULT	14	
AA	52161	
ID	AA52161	standard; Protein; 739 AA.
XX	AC	
XX	AC	AA52161;
XX	DT	05-FEB-2002 (first entry)
XX	DE	Humanised HMFG-1 heavy chain/DNase I fusion protein 6.
XX	KW	Humanised monoclonal antibody; polymorphic epithelial mucin; PEWL;
KW	KW	cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX	OS	Homo sapiens.
OS	OS	Synthetic.
XX	PN	WO200174905-A1.
XX	PD	11-OCT-2001.
XX	PF	26-MAR-2001; 2001WO-GB01324.
XX	PR	03-APR-2000; 2000GB-0008049.
XX	PR	02-OCT-2000; 2000US-237159P.
XX	PA	(ANTI-) ANTISOMA RES LTD.
XX	XX	

PI	Young RJ;
XX	
XX	WPI; 2001-662969/76.
DR	
XX	
PT	Novel compound used to treat cancer has target cell-specific portion
PT	comprising humanised monoclonal antibody having specificity for
PT	polymorphic epithelial mucin, and cytotoxic portion having
PT	endonucleolytic activity -
XX	
XX	Claim 20; Figure 12; 176pp; English.
PS	
XX	
CC	The invention relates to a compound which comprises a target
CC	cell-specific portion, comprising a humanised monoclonal antibody,
CC	having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC	binding fragment and a cytotoxic portion having endonucleolytic activity,
CC	exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABAA02728. The
CC	compound has cytostatic activity useful for treating cancer and acting as
CC	a potential inducer of apoptosis.
XX	
XX	Sequence 739 AA;
SQ	

Query Match	93.1%	Score 2343.5	DB 22	Length 739
Best Local Similarity	93.0%	Pred. No. 1.8e-132		
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Db 1	mgwsciiilfvatgthsgvqlvgsgaeavkkgpaskvskcasgyftsfayiewvriqap 60			
Qy 61	GGLEWGEIIPDSYNTYNNOKFKGKATITVDITSTSTAYMELSSLRSEDATVAYICARRND 120			
Db 61	gglewgeiipdsynnsnnsnfkrvtrdrtdstntaymelslrsedatvayycarsyd 120			
Qy 121	YSNNWYFDWQGGTLVTYSSASTKGPVSFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180			
Db 121	fa--wfa-ywgggtlvtvssastkgsfvplapskstsggtaalgclvkdypfpvptvs 177			
Qy 181	WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPPSSSLGHTQTVICNVNHNKPSNTKYDKRVEP 240			
Db 178	wnsгалtsgvhtfpavlgssglyslssvvtvpssslgtqtiyicnvnhkpsntkvdkkvep 237			
Qy 241	KSCDKTHCTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNW 300			
Db 238	kscdkthctcpcpapelilggpsvflfppkpkdtlmisartpevtcvvvdvshedpevfnnw 297			
Qy 301	YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360			
Db 298	yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwnlmgkeykckvsnkalpapiektis 357			
Qy 361	KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEESGQPENNYKTTPPV 420			
Db 358	kakgqprepqvtylppsrdeitknqvsitclvkgyfypsdiaveesngqpennkyttppv 417			
Qy 421	LDSDGSFFLYSKLLNVDSRWQGGNWFVSCVMHEALHNHYTQKSLSLSPG 469			
Db 418	ldsdgsfflyskllvdksrwgaqgnwfscsvmhcalhnhytckslslspq 466			

RESULT	15
AA052157	
ID	AA052157 standard; Protein; 730 AA.
XX	
XX	AA052157;
XX	
DT	05-FEB-2002 (first entry)
XX	
DE	Humanised HMFG-1 heavy chain/DNase I fusion protein 2.
XX	
KW	Humanised monoclonal antibody; polymorphic epithelial mucin
KW	cytotoxic; endonuclease; DNase I; human; cytostatic; cancer
XX	
OS	Homo sapiens.

Search completed: August 14, 2002, 15:15:38
Job time: 836 sec

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OS Synthetic.
XX WO200174905-A1.
PN
XX
XX PD 11-OCT-2001.
XX
XX PF 26-MAR-2001; 2001WO-GB01324.
XX
XX PR 03-APR-2000; 2000GB-0008049.
XX
XX PR 02-OCT-2000; 2000US-237159P.
XX
XX PA (ANTI-) ANTISOMA RES LTD.
XX
XX PI Young RJ;
XX
XX DR WPI; 2001-662969/76.
XX
XX PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
XX PS Claim 20; Figure 8; 176pp; English.
XX
XX CC The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX CC binding fragment and a cytotoxic portion having endonucleolytic activity,
XX CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX CC compound has cytostatic activity useful for treating cancer and acting as
XX CC a potential inducer of apoptosis.
XX
XX SQ Sequence 730 AA;

Query Match          92.9%; Score 2337.5; DB 22; Length 730;
Best Local Similarity 92.9%; Pred. No. 4e-132;
Matches 435; Conservative 20; Mismatches 10; Indels 3; Gaps 1;

QY 1 MGWSCILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFSTYMWQWVKQAP 60
DB 1 mgwscilflvatatgvhsqqlvqsgaevkpgasvkvsckasgytfsaywiewvrqap 60

QY 61 GQGLEWMEIDPSDSTNTNNQKFKGATITVDTSTAYMELSSLSRSEDYAVYICARNRD 120
DB 1 gqglewmeidpsdntnnqkfgatitvdtstaymelsslsrsedtavyycarsyd 120

QY 121 YSNWYFDVWGQTLVTVSSASTKGFSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
DB 1 ysnwyfdvwgqtlvtvssastkgsfpvplapsskstsggtaalgclvkdyfpeptvs 177

QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHKPSNTKVKDKRVEP 240
DB 178 wnsгалtsgvhtfpavlsqsglyslssvstvpssslgtqtyicnvnhkpsntkvdkkvep 237

QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEYKFNW 300
DB 238 kscdkthtccpcpapelggpsvflfppkpkdtlmisrtpvctcvvvdvshedpevkfnw 297

QY 301 YVDGVEVHNAKTPREEQVNSRYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
DB 298 yvdgvevhnaktpreeqvnsryrvsvltrlhqdwlngkeykckvsnkalpapiektis 357

QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
DB 358 kagqprepqvylppsrdeitknqvsitclvkgyfypsdiavewesngqpennnykttppv 417

QY 421 LQSDGSFFLYSKLTVDKSRWQQGNFSCSVMHEALHNHYTQKSLSLSP 468
DB 418 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhytqkslsislsp 465
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:05 ; Search time 82.88 Seconds
(without alignments)
138.514 Million cell updates/sec

Title: US-09-499-662-145
Perfect score: 2517
Sequence: 1 MGWSCIILFLVATGTVHVSQ.....MHEALHNYTOKSLSPCK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2232	88.7	476	2	US-08-378-939-10
2	2230	88.6	449	1	US-08-458-516-13
3	2200.5	87.4	467	4	US-09-049-672A-8
4	2198.3	87.3	452	3	US-09-027-449-71
5	2198.5	87.3	452	4	US-09-026-985-71
6	2177	86.5	468	4	US-09-485-737B-67
7	2177	86.5	711	4	US-09-485-737B-90
8	2159.5	85.8	454	2	US-07-934-373C-22
9	2159.5	85.8	454	3	US-08-437-642B-22
10	2159.5	85.8	454	5	PCT-US93-07832-22
11	2146	85.3	472	4	US-08-793-450-8
12	2126	84.5	451	2	US-08-887-352B-14
13	2126	84.5	451	2	US-08-887-352B-16
14	2126	84.5	451	3	US-08-466-151-65
15	2126	84.5	451	4	US-09-109-207C-14
16	2126	84.5	451	4	US-09-109-207C-16
17	2126	84.5	451	4	US-09-296-005-14
18	2126	84.5	451	4	US-09-296-005-16
19	2123	84.3	478	3	US-08-487-550-8
20	2118	84.1	451	2	US-08-887-352B-18
21	2118	84.1	451	4	US-09-109-207C-18
22	2118	84.1	451	4	US-09-282-505-2
23	2118	84.1	451	4	US-09-054-255-2
24	2118	84.1	451	4	US-09-296-005-18
25	2107	83.7	453	3	US-08-466-151-8
26	2107	83.7	453	4	US-08-466-163B-8
27	2105.5	83.7	467	2	US-07-916-098A-45

28 2104.5 83.6 449 4 US-09-679-397-2 Sequence 2, Appli
29 2101.5 83.5 552 5 PCT-US93-07832-23 Sequence 23, Appli
30 2098.5 83.4 469 2 US-07-934-373C-23 Sequence 23, Appli
31 2098.5 83.4 469 3 US-08-437-642B-23 Sequence 23, Appli
32 2096 83.3 451 4 US-09-247-352-3 Sequence 3, Appli
33 2092.5 83.1 459 1 US-08-157-101A-7 Sequence 7, Appli
34 2074.5 82.4 467 1 US-08-704-744-81 Sequence 81, Appli
35 2072.5 82.3 473 4 US-09-049-672A-4 Sequence 4, Appli
36 2062.5 81.9 445 4 US-08-341-560B-17 Sequence 17, Appli
37 2056.5 81.7 446 3 US-08-397-411-7 Sequence 7, Appli
38 2056 81.7 476 3 US-08-487-550-12 Sequence 12, Appli
39 2024 80.4 442 5 PCT-US96-10043-9 Sequence 9, Appli
40 2024 80.4 476 3 US-08-487-550-4 Sequence 4, Appli
41 2012 79.9 442 1 US-08-461-968A-5 Sequence 5, Appli
42 2012 79.9 442 2 US-08-462-571-5 Sequence 5, Appli
43 1997.5 79.4 450 2 US-08-788-800-12 Sequence 12, Appli
44 1988 79.0 442 1 US-08-480-036-2 Sequence 2, Appli
45 1988 79.0 442 1 US-08-461-968A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-378-939-10

Query Match 88.7%; Score 2232; DB 2; Length 476;
Best Local Similarity 88.7%; Pred. No. 5.2e-159;
Matches 422; Conservative 20; Mismatches 28; Indels 6; Gaps 1;
QY 1 MGWSCIILFLVATGTVHVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKAP 60
| | : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : |||

Db 1 MDWTRFLFVAAATGVQSQAEVKKPGSSVTVSCKSGGTFSNVAISWRQAP 60
QY 61 GQLEWMEIDPSDSTNYNOKFKGKATITVDTSTAYMELSSLRSEDFAVYYCARNR- 119
Db 61 GQLEWNGGIPLFGTPTYSQNFQGRVTITADKSTSTAHMELTSLRSEDFAVYYCATDRY 120
QY 120 -----DYSNNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFP 174
Db 121 ROANFRARVGFDPWGQGLTVTVSSASTKGPSVFPLAPSSKTSGGTAALGCLVKDYFP 180
QY 175 EPTVSWNSGALTSVHTTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNTKV 234
Db 181 EPTVSWNSGALTSVHTTPAVLQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSNTKV 240
QY 235 DKRVEPKSCDKTHTCCPAPELLGSPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDP 294
Db 241 DKRVEPKSCDKTHTCCPAPELLGSPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDP 300
QY 295 EVKFNWYDGVGVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAP 354
Db 301 EVKFNWYDGVGVHNAKTPREQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAP 360
QY 355 IEKTIKAKGQPREPOVYITLPPSRREEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNY 414
Db 361 IEKTIKAKGQPREPOVYITLPPSRDELTKNQVSLTCLVKGFPYSDIAVEWESNGQPENNY 420
QY 415 KTTTPVLDSDGSPFLYSLKLTVDKSRQOQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 421 KTTTPVLDSDGSPFLYSLKLTVDKSRQOQGNVFCSCVMHEALHNHYTKLSLSPGK 476

RESULT 2
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-458-516-13
Query Match 88.6%; Score 2230; DB 1; Length 449;
Best Local Similarity 92.9%; Pred. No. 6.8e-159;
Matches 419; Conservative 15; Mismatches 15; Indels 2; Gaps 2;
QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAPGGQLEWMGIDPSDSYTN 79
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Db 119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSVHTFPAVLQ 178
QY 200 SGLYSLSVVTVVPSSSLGTQYICNVNHPKSNTKVDKRVPEKSCDKTHTCCPPAPPELLG 259
Db 179 SGLYSLSVVTVVPSSSLGTQYICNVNHPKSNTKVDKRVPEKSCDKTHTCCPPAPPELLG 238
QY 260 GPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 319
Db 239 GPSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 298
QY 320 NSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVYITLPPSRE 379
Db 299 NSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVYITLPPSRE 358
QY 380 EMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 439
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QY 440 WQGNVFCSCVMHEALHNHYTKLSLSPGK 470
Db 419 WQGNVFCSCVMHEALHNHYTKLSLSPGK 449

RESULT 3
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PP-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGTU11
; CLONE: 2747531
;
US-09-049-672A-8

Query Match      87.4%  Score 2200.5;  DB 4;  Length 467;
Best Local Similarity 89.0%;  Pred. No. 1.1e-156;
Matches 413;  Conservative 20;  Mismatches 28;  Indels 3;  Gaps 1;

Qy  7  ILFLVATATGVHVSQVQLVQSGAEVKKPGASVKASKASYTFTSYMMQWVQKAPQGQGLEW 66
Db  7  ILFLVAAATGTHAQVQLVQSGAEVKKPGASVQVSTGFTLSDLSLVHVVHQAPQGQGLEW 66

Qy  67  MGEIDPSDSYNYNQKFKGKATIIVDSTSTAYMELSLRSEDATVYYCARNRDYSNNWY 126
Db  67  MGGLAPENGEAVYAKQKFLGRITLSEDTSDATYAFMLNNGLSEDSAIYYCARQH---YDFF 123

Qy  127  FDVWGQGLTVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGAL 186
Db  124  FDFWQCGTMVTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGAL 183

Qy  187  TSGVHTFPVAVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNNTKVDKRVKPSCKDKT 246
Db  184  TSGVHTFPVAVLOSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNNTKVDKRVKPSCKDKT 243

Qy  247  HTCPCPAPELGLGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFKNWYVDGVE 306
Db  244  HTCPCPAPELGLGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFKNWYVDGVE 303

Qy  307  VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 366
Db  304  VHNAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 363

Qy  367  REPQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS 426
Db  364  REPQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGS 423

Qy  427  FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db  424  FFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

```
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-027-449-71

Query Match      87.3%  Score 2198.5;  DB 3;  Length 452;
Best Local Similarity 89.8%;  Pred. No. 1.5e-156;
Matches 406;  Conservative 28;  Mismatches 17;  Indels 1;  Gaps 1;

Qy  20  QVQLVQSGAEVKKPGASVKASKASYTFTSYMMQWVQKAPQGQGLEWGEIDPSDSYNY 79
Db  1  EVQLVQSGGLVQPQGLSLRLSCAASGYSFSSHYMHWRQAPGKGLIEWGYIDPSNGETTY 60

Qy  80  NQKFKGKATIIVDSTSTAYMELSLRSEDATVYYCAR- NRDYSNNWYFDVWGQGLTVTV 138
Db  61  NQKFKGRTLTSLRDNSKNTAYLQMNLSRAEDTAVYYCARGDYRYNGDWFVDMGQGLTVTV 120

Qy  139  SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGALTSGVHTTTPAVLQ 198
Db  121  SSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYRPEPTVTSNNSGALTSGVHTTTPAVLQ 180

Qy  199  SSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNNTKVDKRVKPSCKDKTHTCCPCPAPELL 258
Db  181  SSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNNTKVDKRVKPSCKDKTHTCCPCPAPELL 240

Qy  259  GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFKNWYVDGVEVHNNAKTKPREEQ 318
Db  241  GGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFKNWYVDGVEVHNNAKTKPREEQ 300

Qy  319  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db  301  YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 360

Qy  379  EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 438
Db  361  EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS 420

Qy  439  RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db  421  RWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-026-985-71
```

; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-71

Query Match 87.3%; Score 2198.5; DB 4; Length 452;
Best Local Similarity 89.8%; Pred. No. 1.5e-156;
Matches 406; Conservative 28; Mismatches 17; Indels 1; Gaps 1;
QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAPGGLEWMGIDPSDVTNY 79
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSSHYMHWRQAPGKGLWGVYIDPSNGETTY 60
QY 80 NQKFKGKATITVDSTSTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGLTIV 138
Db 61 NQKFKGKATITVDSTSTAYMELSSLRSEDTAVYYCAR-NRDYSNNWYFDVWGQGLTIV 120
QY 139 SSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 121 SSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 180
QY 199 SSGLYSLSSVYVTPSSSLGQTQYICNVNHNKPSNTKVDKRVKPSKCDKTHTCPCPAPELL 258
Db 181 SSGLYSLSSVYVTPSSSLGQTQYICNVNHNKPSNTKVDKRVKPSKCDKTHTCPCPAPELL 240
QY 259 GGPSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPREEQ 318
Db 241 GGPSVFLFPKPKDGLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPREEQ 300
QY 319 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGPREPQVYTLPPSR 378
Db 301 YNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKGPREPQVYTLPPSR 360
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 420
QY 439 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 470

Db 421 RWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 452
RESULT 6
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-09-485-737B-67

Query Match 86.5%; Score 2177; DB 4; Length 468;
Best Local Similarity 88.2%; Pred. No. 6.5e-155;
Matches 410; Conservative 20; Mismatches 31; Indels 4; Gaps 1;

QY 6 IILFLVATATGVHSGVQVLSGAEVKKPGASVKVSCKASGYTFTSYMMQWVKQAPGGLE 65
Db 7 IFSEFLIISASVILSQVQLVQSGSELKPKGASVKISKASGYTFTDYGMNVVKQAPGGGLK 66
QY 66 WMGEIDPSDYSYNNQKFKGKATITVDSTSTAYMELSSLRSEDTAVYYCARNRDYSNNW 125
Db 67 WMGWIINTYTGESTYVDDFKGRFVSLDTSVSAAYLQISLKAEDTATYFCARRGFYA--- 123
QY 126 YEDVWGQGLTIVTSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGA 185
Db 124 -MDYWGQGLTIVTSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVSWNSGA 182
QY 186 LTSGVHTFPAVLQSSGLYSLSSVYVTPSSSLGQTQYICNVNHNKPSNTKVDKRVKPSKCDK 245
Db 183 LTSGVHTFPAVLQSSGLYSLSSVYVTPSSSLGQTQYICNVNHNKPSNTKVDKRVKPSKCDK 242
QY 246 THTCPCPAPELLGGPSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVFNWYVDGV 305
Db 243 THTCPCPAPELLGGPSVFLFPPKPKDGLMISRTPEVTCVVDVSHEDPEVFNWYVDGV 302
QY 306 EVHNATKPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKG 365
Db 303 EVHNATKPREEQNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIETKISKAKG 362
QY 366 PREPQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 425
Db 363 PREPQVYTLPPSREMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 422
QY 426 SFELYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 470
Db 423 SFELYSKLTVDKSRWQOGNVFSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B

Patent No. 6350860
GENERAL INFORMATION:
APPLICANT: Buysse, Marie-Ange
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 711
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match 86.5%; Score 2177; DB 4; Length 711;
Best Local Similarity 88.2%; Pred. No. 1.1e-154;
Matches 410; Conservative 20; Mismatches 31; Indels 4; Gaps 1;

Qy 6 ILFLVATATGVHSQVLVQSGAEVKKPGASVKYCKASGTFSTSYMMQWVKQAPGCGLE 65
Db 7 IFSELLISASVLSQVLVQSGSELKPGASVKISCKASGYTFDDYGNMVKQAPGCGLK 66
Qy 66 WMGEIDPSDSTYNQKFKGKATITVDSTSTAYMELSLRSEDATVYYCARNRDYSNNW 125
Db 67 WMGLINTYTGESTYVDDFKGRFVSLDTSVAAYLIQISLKAEDATYFCARRGFYA --- 123
Qy 126 YFDVMGQGTLYTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 185
Db 124 -MDYWGQGTITVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 182
Qy 186 LTSVGHTEPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKRVKPSCDK 245
Db 183 LTSVGHTEPAVLQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKRVKPSCDK 242
Qy 246 THTCPPCAPPELLGGPSVFLPDKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGV 305
Db 243 THTCPPCAPPELLGGPSVFLPDKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGV 302
Qy 306 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQ 365
Db 303 EVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQ 362
Qy 366 PREPOVYTLPPSREEMTNQVSLCLVKGFPYPSDIAVWESNGQPENNYKTTTPPVLDSDG 425
Db 363 PREPOVYTLPPSREEMTNQVSLCLVKGFPYPSDIAVWESNGQPENNYKTTTPPVLDSDG 422
Qy 426 SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 423 SFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 467

RESULT 8
US-07-934-373C-22
Sequence 22, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-22

Query Match 85.8%; Score 2159.5; DB 2; Length 454;
Best Local Similarity 89.2%; Pred. No. 1.3e-153;
Matches 405; Conservative 18; Mismatches 28; Indels 3; Gaps 1;
Qy 20 QVOLVQSGAEVKKPGASVKYCKASGYTFSTSYMMQWVKQAPGQGLEWMEIDPSDSTYN 79
Db 1 QVOLQSGPELVKPGASVKISCKTSGYTFETYMHWKQSHGKSLWIGGFPNKGSSH 60
Qy 80 NQKFKGKATITVDSTSTAYMELSLRSEDATVYYCARNRDYSNNW ---YFDVMGQGTLY 136
Db 61 NQREMDKATLAVDKSTSTAYMELSLTSEDSGIYYCARNRGLNYGFDVRYFDWVGAGTIV 120
Qy 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 196
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 180
Qy 197 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKRVKPSCDKTHTCPPCAPE 256
Db 181 LQSSGLYSLSSVTVPPSSSLGTQTYICNVNHHKPSNTKVDKRVKPSCDKTHTCPPCAPE 240
Qy 257 LLGGPSVFLPDKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVVEVHNAKTKPRE 316
Db 241 LLGGPSVFLPDKPKDPLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVVEVHNAKTKPRE 300
Qy 317 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREQVYTLPP 376
Db 301 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGPREQVYTLPP 360
Qy 377 SREEMTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTV 436
Db 361 SREEMTKNOVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTV 420
Qy 437 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 421 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 454

Db 61 NQRFMDATLAVDKSTSTAYMELSLTSEDSGIYYCARWGLNYGFOVRYFDMVAGGTV 120
Qy 137 TVSSASTKGPVFFPLAPSSKSTSGTAAALGCLVRDYFPEPVTVSWNSGALTSGVHTFPV 196
Db 121 TVSSASTKGPVFFPLAPSSKSTSGTAAALGCLVRDYFPEPVTVSWNSGALTSGVHTFPV 180
Qy 197 LQSSGLYSLSSVTVVPSSLSGTQYICNVNHPKNTKVDKRVKPCSDKTHCPCPAPE 256
Db 181 LQSSGLYSLSSVTVVPSSLSGTQYICNVNHPKNTKVDKRVKPCSDKTHCPCPAPE 240
Qy 257 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTPRE 316
Db 241 LGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNAKTPRE 300
Qy 317 EYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 376
Db 301 EYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPP 360
Qy 377 SREMTKNOVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVD 436
Db 361 SREMTKNOVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVD 420
Qy 437 KSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 470
Db 421 KSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 454

RESULT 11
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-793-450-8

Query Match 85.3%; Score 2146; DB 4; Length 472;
Best Local Similarity 85.1%; Pred. No. 1.4e-152;
Matches 404; Conservative 26; Mismatches 37; Indels 8; Gaps 3;
Qy 1 MGWSCILFLVATATGTVHSGVQVLOSAGAEVKKPGASVKVSKCKASGYTTSYWMQVWQAP 60
Db 1 MGWSCILFLVATATGTVHSGVQVLOSAGAEVKKPGASVKVSKCKASGYTTSYWMQVWQAP 60
Qy 61 GQGLEWMEIDPSDSTNYNOKFKGKATITVDITSTSTAYMELSSLSRSEDATVYYICARNRD 120
Db 61 GQGLEWMEIDPSDSTNYNOKFKGKATITVDITSTSTAYMELSSLSRSEDATVYYICARPE 119
Qy 121 YSNWN-----YFVWVGQGLTVTVSSASTKGPVFFPLAPSSKSTSGTAAALGCLVRDYFPE 175
Db 120 Y--KWKYHGDFDPWGQGTITTVSSASTKGPVFFPLAPSSKSTSGTAAALGCLVRDYFPE 177
Qy 176 PVTYSWNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSLSGTQYICNVNHPKNTKVD 235
Db 178 PVTYSWNSGALTSGVHTFPVAVLQSSGLYSLSSVTVVPSSLSGTQYICNVNHPKNTKVD 237
Qy 236 KRVEPKSCDKTHCPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPE 295
Db 238 KKAEPKSCDKTQTCTPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPE 297
Qy 296 VKFNWYVDGVEVHNAKTPREEQYNSTYRVYSVLTVTLHODWLNKGEYKCKVSNKALPAPI 355
Db 298 VKFNWYVDGVEVHNAKTPREEQYNSTYRVYSVLTVTLHODWLNKGEYKCKVSNKALPAPI 357
Qy 356 EKTISKAKGQPREPQVYITLPPSREEMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYK 415
Db 358 EKTISKAKGQPREPQVYITLPPSREELTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYK 417
Qy 416 TTPPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 470
Db 418 TTPPVLDSDGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 472
RESULT 12
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 84.5%; Score 2126; DB 3; Length 451;
Best Local Similarity 87.8%; Pred. No. 4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQMWVKQAPGOGLEWMGEIDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNWIRQAPGKLEWVASI-TYDGS 59

QY 79 YNOKFKGKATITVDITSTAYMELSSLRSEDYAVYYCARNRDYSNNYFDVWGQGLTV 138
Db 60 YNPVKGRITISRDSDKNTFYLQMSLRAEDYAVYYCARGSHYFGHWFHFAVWGQGLTV 119

QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179

QY 199 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAP 258
Db 180 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAP 239

QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 318
Db 240 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 299

QY 319 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378
Db 300 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 419

QY 439 RWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451

RESULT 15

US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

;
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
; US-09-109-207C-14

Query Match 84.5%; Score 2126; DB 4; Length 451;
Best Local Similarity 87.8%; Pred. No. 4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQMWVKQAPGOGLEWMGEIDPSDSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAIVSGYSITSGYSWNWIRQAPGKLEWVASI-TYDGS 59

QY 79 YNOKFKGKATITVDITSTAYMELSSLRSEDYAVYYCARNRDYSNNYFDVWGQGLTV 138
Db 60 YNPVKGRITISRDSDKNTFYLQMSLRAEDYAVYYCARGSHYFGHWFHFAVWGQGLTV 119

QY 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179

QY 199 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAP 258
Db 180 SSGLYSLSSVVTVPSSSLGQTQYICNVNHPKSNTKVDKRVKPKSCDKTHTCPCPAP 239

QY 259 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 318
Db 240 GGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 299

QY 319 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 378
Db 300 YNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 359

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 419

QY 439 RWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVFSCSVMEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:06
Job time: 689 sec

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:19:00 ; Search time 108.64 Seconds
(without alignments)
415.703 Million cell updates/sec

Title: US-09-499-662-145
Perfect score: 2517
Sequence: 1 MGWSCIILFLVATGVHSQ.....MHEALHNHYTQKSLSPGK 470
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1758	69.8	330	1	GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2	A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2	A60764	Ig gamma-3 chain C
4	1611.5	64.0	469	2	S37483	Ig gamma-2a chain C
5	1610	64.0	326	1	G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1	G4HU	Ig gamma-4 chain C
7	1547	61.5	474	1	G2MS11	Ig gamma-2b chain C
8	1545	61.4	446	2	S40295	Ig gamma-2a chain C
9	1502.5	59.7	475	2	S01321	Ig gamma-2b chain C
10	1476	58.6	470	2	S22080	Ig heavy chain pre
11	1469	58.4	472	2	S31459	Ig gamma-1 chain -
12	1434	57.0	374	2	S69339	Ig heavy chain v r
13	1428.5	56.8	444	2	PC4436	monoclonal antibod
14	1267	50.3	328	2	I47159	Ig gamma 2a chain
15	1261	50.1	328	2	I47160	Ig gamma 2b chain
16	1253	49.8	255	4	S31866	Ig gamma-1 chain C
17	1245	49.5	234	2	PT0207	Ig gamma chain C r
18	1235	49.1	328	2	I47158	Ig gamma 1 chain c
19	1231.5	48.9	323	1	GHRB	Ig gamma chain C r
20	1231	48.9	328	2	I47161	Ig gamma 3 chain c
21	1210.5	48.1	329	1	G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2	C30554	Ig heavy chain C r
23	1157	46.0	289	1	G3HUW1	Ig gamma-3 heavy c
24	1155	45.9	326	2	FS0017	Ig gamma-1 chain C
25	1150	45.7	329	1	G3MSC	Ig gamma-3 chain C
26	1145	45.5	324	1	G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2	PS0018	Ig gamma-2b chain C
28	1140	45.3	393	1	G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1	G3MSM	Ig gamma-3 chain C

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C:Accession: A93433; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaudo, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the Glm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein NI

igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Comment: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,111/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 69.8%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 4.5e-93;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 200
|||||
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60
QY 201 GLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKTKVDRKVEKLTPLGDTHTCPRCPEPKSC 260
|||||
Db 61 GLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKTKVDRKVEKLTPLGDTHTCPRCPEPKSC 120
QY 261 PSVFLEPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 320
|||||
Db 121 PSVFLEPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYN 180
QY 321 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRREE 380
|||||
Db 181 STYRVSVLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 440
|||||
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRW 300
QY 441 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
|||||
Db 301 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2

A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1639.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 2.8e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 200
|||||
Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLQSS 60
QY 201 GLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKTKVDRKVEKLTPLGDTHTCPRCPEPKSC 238
|||||
Db 61 GLYSLSSVTVPSSSSLGTQTYICNVNHPKSNKTKVDRKVEKLTPLGDTHTCPRCPEPKSC 120
QY 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPKDT 273
|||||
Db 121 DTPPCPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPEPKPKDT 180
QY 274 LMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLH 333
|||||
Db 181 LMSRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVSVLTVLH 240
QY 334 QDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 393
|||||
Db 241 QDWLNKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEMTKNQVSLTCLVK 300
QY 394 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQGNVFSCSYMHE 453
|||||
Db 301 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQGNVFSCSYMHE 360
QY 454 ALHNHYTQKSLSLSPGK 470
|||||
Db 361 ALHNHYTQKSLSLSPGK 377

RESULT 3

A60764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A60764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A60764; MUID:90007613
A:Accession: A60764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 3.7e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

QY 141 ASTKGPSVFLAPSSKSTSGTAAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFLAPCSRSTSGTAAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSVTVVPSLSLGTQYICNVNHPKNTKVKRY----- 238
Db 61 GLYSLSVTVVPSLSLGTQYICNVNHPKNTKVKRY----- 120
QY 239 -----EPKSCDKHTHCPCPAPELGGPSVFLFPKPKDT 273
Db 121 DTPPCPCPEPKSCDTPPCPCPEPKSCDTPPCPCPELGGPSVFLFPKPKDT 180
QY 274 LMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLH 333
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLH 240
QY 334 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRREEMTKNQVSLTCLVK 393
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSRREEMTKNQVSLTCLVK 300
QY 394 GFYPDSIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVWHE 453
Db 301 GFYPDSIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVWHE 360
QY 454 ALHNHYTQKSLSLSPGK 470
Db 361 ALHNRYTQKSLSLSPGK 377

RESULT 4
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 1611.5; DB 2; Length 469;
Best Local Similarity 64.4%; Pred. No. 1.4e-84;
Matches 304; Conservative 60; Mismatches 103; Indels 5; Gaps 4;

QY 1 MGWSCIILFLVATATGVHSQVLVQSGAEVKKPGASVKVSCKASGYFTFTSYMQWQVKAOP 60
Db 1 MGWSWIFLISGTPAGVHCQIQLOQSGPELVKPGASVKISCKASGYFTFTDYIYNVKQKP 60
QY 61 GQGLEWMEIDPDSYNYNOKPKGKATITVDTSSTAYMELSLRSDDTAVYYCARNRD 120
Db 61 GQGLUKWGIWYPSGNTRYENFKGKATLVTDTSSTAYMQLSLTSDDTAVYYFCARAMG 120
QY 121 YNNWYFDVNGQGLTVTVSSASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYFPEPTVTS 180
Db 121 -ATATLLDYGQGTTLTVSSAKTAPSVYPLAPVCGDTTSSVTLGCLVKGYPPEPTLT 179
QY 181 WNSGALTSGVHTFPFPAVLQSSGLYSLSSVTVVTPSSSLGTQTQYICNVNHPKNTKVKRVEP 240

Db 180 WNSGSLSSGVHTFPFPAVLQSD-LYTLSSSVTVTSTWFSQSTICNVNHPASSTKVDKKTIEP 238
QY 241 KSCDKTHTCPP-CPAPELGGPSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298
Db 239 RG-PTIKPCPCPKCPANLLGGPSVFFPPPKIKDVLMLSLSPITCVTVVVDVSEDDPDVQI 297
QY 299 NWYVDGVEVHNNAKTKPREQYNSTYRVVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKT 358
Db 298 SWFVNNVEVHTAQQTQTHREDYNSTLRVVSALPIQHDQMSGKERCKVKVNNKDLPAPIERT 357
QY 359 ISKAKGQPREPOVYITLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTP 418
Db 358 ISKPKGSVRAPQVTVLPPPEEETKKQVTLTCMTVDFPEDIYVEMTWNGTELNKNTE 417
QY 419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFCSVNMEALHNHYTQKSLSLSPGK 470
Db 418 PVLDSDGSFYFYSKLREKKNWERNVSVCSSVWHEGLNHHHTTKSFSTRTPCK 469
RESULT 5
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C;Accession: A93906; A92809; A90752; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain
A;Reference number: A93906; MUID:82197621
A;Accession: A93906
A;Molecule type: DNA
A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A;Reference number: A92809; MUID:81007873
A;Contents: myeloma protein T11
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A;Note: Trp-156 is at or near the complement-binding site
R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of
A;Reference number: A90752; MUID:80001357
A;Contents: myeloma protein Zie
A;Accession: A90752
A;Molecule type: protein
A;Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',1
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Reference number: A93132; MUID:80114419
A;Contents: Zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253; MUID:72033500
A;Contents: annotation; myeloma protein Sa, disulfide bonds
R;Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124

A:Contents: annotation; Sa, disulfide bonds
C:Genetics:

A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83-140-200-246-304/Disulfide bonds: #status experimental
F:102-103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.0%; Score 1610; DB 1; Length 326;

Best Local Similarity 91.8%; Pred. No. 1.1e-84;

Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

QY 141 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 200

Db 1 ASTKGPSVEPLAPCSRSTSESTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 60

QY 201 GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRPKSCDKTHCTCPCPAPPELLGG 260

Db 61 GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRPKSCDKTHCTCPCPAPPELLGG 116

QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Db 117 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176

QY 321 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380

Db 177 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 236

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440

Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 296

QY 441 QQGNFSCSVMEALHNHYTQKSLSLSPGK 470

Db 297 QQGNFSCSVMEALHNHYTQKSLSLSPGK 326

RESULT 6

G4HU

Ig gamma-4 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C:Accession: A90933; A90249; A02150

R:Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A:Reference number: A90933; MUID:83157104

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Note: the sequence was determined from the germline gene

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of the gamma4 chain.

A:Reference number: A90249; MUID:70207560

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30;81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83-141-201-247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;

Best Local Similarity 91.8%; Pred. No. 4.5e-84;

Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 200

Db 1 ASTKGPSVEPLAPCSRSTSESTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQSS 60

QY 201 GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRPKSCDKTHCTCPCPAPPELLGG 260

Db 61 GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRPKSCDKTHCTCPCPAPPELLGG 117

QY 261 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320

Db 118 PSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 177

QY 321 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380

Db 178 STYRVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 237

QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440

Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 297

QY 441 QQGNFSCSVMEALHNHYTQKSLSLSPGK 470

Db 298 QQGNFSCSVMEALHNHYTQKSLSLSPGK 327

RESULT 7

G2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000

C:Accession: S25057; A02157; A26235; A26233; A53598

R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25057

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>

A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827

R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.

Nature 283, 786-789, 1980

A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from

A:Reference number: A02157; MUID:80120716

A:Contents: a allele

A:Accession: A02157

A:Molecule type: DNA

A:Residues: 138-161, 'L', 'I', 'P', '193-474 <YAM>

A:Cross-references: GB:J00461

A:Note: the sequence was determined from the germline gene

R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain
A:Reference number: A26235; MUID:80081501
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <TU1>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain
A:Reference number: A26232; MUID:80081502
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172,'p',174-189,'FP',193-376,'T',378-474 <TU2>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain
A:Reference number: A26233; MUID:82173203
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474 <OLL>
A:Cross-references: GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359
A:Accession: A53598
A>Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Insertions: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:157-222/Domain: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglobulin homology
F:236-257/Region: hinge
F:281-350/Domain: immunoglobulin homology <IM2>
F:387-454/Domain: immunoglobulin homology <IM3>
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220,288-348,394-452/Disulfide bonds: #status predicted
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.58; Score 1547; DB 1; Length 474;
Best Local Similarity 61.28; Pred. No. 6,7e-81;
Matches 292; Conservative 67; Mismatches 108; Indels 10; Gaps 3;

Qy 1 MGWSCIIFLVATATGVSQVQVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVQKAP 60
Db 1 MENSWIFLUSGAGVHSEVQLOQSGPELVNPGASVKMSCKASGYFTITVTHWVKOKP 60

Qy 61 GQLEWMEIDPSYTNYNQKFGKATITVDSTSTAYMELSLRSEDSTAYTCARNRD 120
Db 61 GQGLEWIGYINPNKDGTKFNEKFKGKATLTSDKSNTAYMELSLRSEDSTAYTCARDYD 120

Qy 121 YSNWYFDVWQGGTLVTVSSASTKGPVFLAPLAPSKSTSGGTAALGCLVKDYFPEPTVVS 180
Db 121 YD---WFAYWQGGTLVTVSSAKTTPPSYIPLAPGDDTGGSSVTSGCLVKGYFPESVTVT 177

Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQTYICNVNHPKSTKVDKRVPE 240
Db 178 WNSGSLSSVHTLSQALLQSSGLYTHSSSVTPVSSVTFWTSQVTCVAHPASSTITVDKKLEP 237

Qy 241 KSCDKT-HTCPP-----CPAPELLGGPSVFLPFPKPKDLMISRTPEVTCVVDVSHED 293
Db 238 SGPISTINPCPKCKECHKCAPNLEGGPSVFIFFPNKIDVLMISLTIPKVTCTVVDVSEDD 297

Qy 294 PEVKFNWYDGVVHNAKTPREEQYNSTYRVSVLTVLHQDLNKGKEYKCKVSNKALPA 353

Db 298 PDVQISWFMVNNVEVHTAQTHREDYNTIRVSTPLQHQDMGSGKEFKCKVNNKNDLPS 357
Qy 354 PIEKTISKAKQOPREPQVYITLPPGREEMTKNQVSLTCLVKGFYPSDIAVEWESNGSPENN 413
Db 358 PIERTISKIKGLVRAQVYIILPPAEQLSRKDVSLTCLVGFNPGDISVEWTSNGTTEEN 417
Qy 414 YKTPPVLDSGSPFLYSKLVDSKRWQOQGNVFCSSVMHEALHNYHTOKSLSPGK 470
Db 418 YKDTAPVLDSGSPFIYSKLNKTKSWBKTSFSCNVRHEGLKNYLYKTKTISRSPGK 474

RESULT 8
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:237/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.48; Score 1545; DB 2; Length 446;
Best Local Similarity 64.48; Pred. No. 8.1e-81;
Matches 291; Conservative 59; Mismatches 94; Indels 8; Gaps 4;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVQKAPQGLEWMEIDPSDSYNY 79
Db 1 QIQLQSGPELVNPGASVKISCKASGYFTDYIHWVKQRPGEGLWIGWYIPGSGNTKY 60

Qy 80 NQKFKGATITVDSTSTAYMELSLRSEDSTAYTCARNRDYNNWYFDVWQGGTLVTVS 139
Db 61 NEKFKGATITVDSTSTAYMELSLRSEDSTAYTCARNGKFA----MDYWGQGTSTVVS 116

Qy 140 SASTKGPSVFLPAPSKSTSGGTAALGCLVKDYFPEPTVTVSNWNGALTSGVHTFPAVLQ 199
Db 117 SAKTTPSVYPLAPVCGDGTGSSVTGLCLVKGYPEPTVLTWNWNGSLSSGVTFTFAVLQ 176

Qy 200 SGLYSLSVTVTPSSSLGTQTYICNVNHPKSTKVDKRVPEKSCDKTHTCPP--CPAPEL 257
Db 177 D-LYTLSSSVTVSTWPSQSITCNVAHPASSTIKVKKIEPRG-PTIKPCPKCKAPNKL 234

Qy 258 LGGPSVFLPFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNWYVDGYEVNNAKTPREE 317
Db 235 LGGPSVFLPFPKPKIDVLMISLSPWTCVVDVSEDDPDVQISWFMVNNVEVHTAQTHRE 294

Qy 318 QYNSTYRVSVLTVLHQDLNKGKEYKCKVSNKALPAPIETKISKAKGQRPQVTVLPSP 377
Db 295 DYNSTLRVVSALPQHQDMGSGKEFKCKVNNKDLPAIERTISKPKGSVRAPQVTVLPSP 354

Qy 378 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQENNYKTPPVLDSGDSFFLYSKLTVDK 437

A:Accession: S31459

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-472 <PAT>

A:Cross-references: EMBL:X69797

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 58.4%; Score 1469; DB 2; Length 472;
Best Local Similarity 59.6%; Pred. No. 1.8e-76;
Matches 289; Conservative 66; Mismatches 114; Indels 12; Gaps 6;

Qy 3 WSCIILFLVATATGVHSGVQLVQSGAEVKKPKASVKYKSCASGYTF--TSYMWQVKKQAPGQ 62

Db 3 WT--LLFVLSAPRGVLSQVRLQESGPSLATLQLTSLVTCTISGFSLNNGYGVQWVRQAPGK 60

Qy 63 GLEWMGEIDPSDSTYNQKFKGKATITVDSTSTAYMELSSLRSEDATVYYCARNRDS 122

Db 61 ALEWLG--SGYDEIDYNPVLKSLRSLTKDTSKQVSLTLSTVTTEDTAVYYCAR--VDYD 118

Qy 123 NNWYF----DWGOGTLVTVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPV 177

Db 119 SSHAFAYASYDFWGPGLDISVLSASTTPPKVPIPTSCGGDTSSSIIVTIGCLVSSYMPPEV 178

Qy 178 TVNSGALTSGVHTFFAVLQSSGLYSLSSVYVTPSSSLGTQTYICNVNHRKPSNTKVDKR 237

Db 179 TVTWSGALTSGVHTFFAILQSSGLYSLSSVYVTPASTSGAQTFCNVAHPASSTKVDKR 238

Qy 238 VEPKSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 297

Db 239 VEPGCPDPCKHC--RCPPPELPGPSVFLFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQ 297

Qy 298 FNIWYVDGVEVHNAKTPREQYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPTEK 357

Db 298 FSWFVDNVEVHTATKPREQFNSTFRVVSALPIQHQDWTGCKEKFCKVHNEALPAPLVR 357

Qy 358 TISKAGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVWESNGQP--ENNYK 415

Db 358 TISRTKGAREPQVVLAPPQEEELSKSTLSVTCLVTGYPDYIAVWQKNGQPESEDKYG 417

Qy 416 TTPPVLSDSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTKQSLSPGK 470

Db 418 TTTSLQDAGSYFLYSLRVDKNSWQEGDTYACVVMHEALHNHYTKQSLSPGK 472

RESULT 12

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Coqne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687

A:Accession: S69339

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

R:Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140, 'C', 142-374 <KH2>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match

Best Local Similarity 57.0%; Score 1434; DB 2; Length 374;

Matches 282; Conservative 27; Mismatches 58; Indels 102; Gaps 4;

Qy 5 CIIILFLVATATGVHSGVQLVQSGAEVKKPKASVKYKSCASGYTF--TSYMWQVKKQAPGQ 62

Db 5 CSTLLLTIPSWLSQITLKRESGPTLVKPTQTTLTCTFSGLSKSGVGVGWIRQPPGQ 64

Qy 63 GLEWMGEIDPSDSTYNQKFKGKATITVDSTSTAYMELSSLRSEDATVYYCARN--RDY 121

Db 65 ALEWLALIFWDD--KRYSPSLRTRLTITKDTSKNOVLTMTNVDPADTATYYCGYVGEY 123

Qy 122 SNWYFDVWVGOGTLVTVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSW 181

Db 124 GQGYRFHSGOGTLTVSS----- 142

Qy 182 NSGALTSGVHTFFAVLQSSGLYSLSSVYVTPSSSLGTQTYICNVNHRKPSNTKVDKRVPK 241

Db 143 -----BPK 145

Qy 242 SCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNY 301

Db 146 SCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNY 205

Qy 302 VDGVEVHNAKTPREQYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIETISK 361

Db 206 VDGVEVHNAKTPREQYNSTYRVVSVLTVLHODWLNKGEYCKVSNKALPAPIETISK 265

Qy 362 AKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVWESNGOPENNYKTPPV 421

Db 266 AKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVWESNGOPENNYKTPPV 325

Qy 422 DSDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTKQSLSPGK 470

Db 376 DSDGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTKQSLSPGK 374

RESULT 13

PC4436

monoclonal antibody 13-1 heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C:Accession: PC4436

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp

A:Reference number: JC5810; MUID:98063277

A:Accession: PC4436

A:Molecule type: protein

A:Residues: 1-444 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMM>

F:22/Disulfide bonds: interchain (to 98) #status predicted

F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match

Best Local Similarity 56.8%; Score 1428.5; DB 2; Length 444;

Matches 265; Conservative 79; Mismatches 94; Indels 19; Gaps 8;

Qy 20 QVQLVQSGAEVKKPKASVKYKSCASGYTF--TSYMWQVKKQAPGQLEWGEID--PSDSY-T 77

Db 1 EVQXVETGGGLVRCNSLKLSCLTSGFTFSNRYHMLRQPPGKRLEWIAVITVKSNDYGA 60

Qy 78 NYNQKFKGKATITVDSTSTAYMELSSLRSEDATVYYCARNRDSNNYF--DWGQGTGL 135

Db 61 KYAESVGRGRTISRDDSSKSSVYLQMNRLREEDTATYYCCR-----TPWYVAMDCWQGTGS 115

Qy 136 VTVSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 195

Db 116 VIVSSAKTTPPSVPLAPGSAATNSWYTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPA 175

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:14 ; Search time 53.64 Seconds
(without alignments)
339.265 Million cell updates/sec

Title: US-09-499-662-145

Perfect score: 2517

Sequence: 1 MGWSCIIILFLVATAGVHSQ.....MHEALHNHYTQKSLSPQK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	1758	69.8	330	1	GCL_HUMAN
2	1610	64.0	326	1	GCL_HUMAN
3	1599.5	63.5	327	1	GCL_HUMAN
4	1231.5	48.9	323	1	GC_RABIT
5	1210.5	48.1	329	1	GC2_CAVPO
6	1162	46.2	290	1	GCL_HUMAN
7	1155	45.9	326	1	GCL_RAT
8	1150	45.7	329	1	GCL_MOUSE
9	1145	45.5	324	1	GCL_MOUSE
10	1144.5	45.5	333	1	GCB_RAT
11	1140	45.3	393	1	GCL_MOUSE
12	1139	45.3	398	1	GC3M_MOUSE
13	1129	44.9	330	1	GCAA_MOUSE
14	1127.5	44.8	329	1	GCC_RAT
15	1126.5	44.8	335	1	GCAE_MOUSE
16	1124	44.7	399	1	GCAE_MOUSE
17	1115	44.3	322	1	GCA_RAT
18	1085	43.1	336	1	GCB_MOUSE
19	1080	42.9	405	1	GCB_MOUSE
20	560.5	22.3	139	1	HV07_MOUSE
21	526	20.9	117	1	HV06_MOUSE
22	522.5	20.8	137	1	HV11_MOUSE
23	522	20.7	138	1	HV48_MOUSE
24	514	20.4	117	1	HV05_MOUSE
25	508	20.2	140	1	HV02_MOUSE
26	502	19.9	117	1	HV09_MOUSE
27	489	19.4	117	1	HV04_MOUSE
28	486.5	19.3	429	1	EPC_RAT
29	486	19.3	117	1	HV49_MOUSE
30	486	19.3	428	1	EPC_HUMAN
31	481	19.1	136	1	HV15_MOUSE
32	480	19.1	117	1	HV10_MOUSE
33	477	19.0	117	1	HV10_MOUSE

34	471	18.7	421	1	EPC_MOUSE
35	466	18.5	117	1	HV1B_HUMAN
36	458	18.2	117	1	HV12_MOUSE
37	457	18.2	117	1	HV13_MOUSE
38	452.5	18.0	120	1	HV50_MOUSE
39	449	17.8	120	1	HV03_MOUSE
40	448.5	17.8	147	1	HV1C_HUMAN
41	446.5	17.7	455	1	MUC_MOUSE
42	445	17.7	454	1	MUC_HUMAN
43	439	17.4	121	1	HV01_MOUSE
44	439	17.4	458	1	MUC_RABIT
45	436.5	17.3	476	1	MUC_MOUSE

ALIGNMENTS

RESULT 1

ID	GCL_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID=9606;			
FN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Edlison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
FN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
FN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
FN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
FN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
FN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

RT Intrachain disulfide bonds.";
RN Biochemistry 9:3188-3196(1970).
[7]
RP DISULFIDE BONDS.
RA MEDLINE-77070267; PubMed-1002129;
RX Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
[8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RA MEDLINE-81208100; PubMed-7236608;
RX Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -!- MISCELLANEOUS: NIE HAS THE GLM(17) ALLOTYPIC MARKER, 97-K, & THE
CC GLM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GLM(3)
CC MARKER & THE GLM (NON-1) MARKERS.
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
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CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134

FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT STRAND 238 240
FT HELIX 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 69.8%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 1.3e-113;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGPSVFPPLAPSSKSTGGTAALGLCLVKDYFPPETVTVSNWNGALTSGVHTTPAVLQSS 200
|||||
Db 1 ASTKGPSVFPPLAPSSKSTGGTAALGLCLVKDYFPPETVTVSNWNGALTSGVHTTPAVLQSS 60
|||||
QY 201 GLYSLSVVTVPSSSISLGTOTYICNVNHNKPSNTKVDKRVKPKSCDKHTHTCPCPAPPELLGG 260
|||||
Db 61 GLYSLSVVTVPSSSISLGTOTYICNVNHNKPSNTKVDKRVKPKSCDKHTHTCPCPAPPELLGG 120
|||||
QY 261 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREEQYN 320
|||||
Db 121 PSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGVHNAKTKPREEQYN 180
|||||
QY 321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 380
|||||
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240
|||||
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLTKLVDSRW 440
|||||
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFELYSLTKLVDSRW 300
|||||
QY 441 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
|||||
Db 301 QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 330
|||||

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1] SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RN SEQUENCE OF 88-115 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Mikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RN SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RC TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RN SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RN SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=8001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RN SEQUENCE OF 238-375 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RN REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RN SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RN DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RN DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
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CC -----
DR EMBL: J00230; AAB59393.1; -.
DR PIR: A02148; G2HU.
DR HSP; P01857; 1FC1.
DR MIM; 147110; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109 AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64; REMOVED POST-TRANSLATIONALLY (PROBABLE).
S -> A (IN MYELOMA PROTEINS TIL & ZIE).
/FTID=VAR_003889.
C -> S (IN REF. 3).
Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 1.8e-103;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
QY 141 ASTKGSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGSVPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSVVVTPSSSLGTQTYICNVNHPKSNTKVDRKVPKCDKTHTCPPCAPPELLGG 260
Db 61 GLYSLSVVVTPSSSLGTQTYICNVNHPKSNTKVDRKVPKCDKTHTCPPCAPPELLGG 116
QY 261 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 117 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 176
QY 321 STYRVSVLTVLDQWLNGCKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRREE 380
Db 177 STFRVSVLTVVDQWLNGCKEYCKVSNKGLPAPIEKTISKAKGQPREPOVYTLPPSRREE 236
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSGDSFSELYSKLTVDKSRW 440
Db 237 MTRNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPPVLDSGDSFSELYSKLTVDKSRW 296
QY 441 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 470
Db 297 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 326
RESULT 3
ID GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1].
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2].
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSSP; P01842; 7FAB.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IG1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD11EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 9.5e-103;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASKPGSVPLAPSKSTGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
DB 1 ASKPGSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDTHTCPCPAPELLGG 260
DB 61 GLYSLSVTVPPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDTHTCPCPAPELLGG 117
QY 261 PSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
DB 118 PSVFLPPPKDFTLMSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 177
QY 321 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
DB 118 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 380
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DR InterPro: IPR003597; Ig_c1.
DR SMART; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 3540 MW; 69E8AA118D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 1.6e-77;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVEFLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSSGLY 203
DB 4 KAPSVFFLAPCCGTPSTVTLGCLVKGILPEPTVTVNNSGTLTGKVFVPSVQSSGLY 63
QY 204 SLSSVTVTPSSSLGTQYICNVNHNKSPNTKVDKRVKPSCKDTHCTPCPAPELLGGPSV 263
DB 64 SLSSVSVTSSTSS---QPVTGNVAHPATNTKVDKTVAPSTCKSCK---PTCPPPELLGGPSV 116
QY 264 FLPPPKPDILMISRTPEVTCVVDVSHEDPEVKFNVDGVEVHNNAKTKPREQYNSTY 323
DB 117 FIFPPKPKDTLMISRTPEVTCVVDVSDQDPEVQFTWYINNEQVTRTARPLREQQFNSTI 176
QY 324 RVVSVLTVLHDLNGREYKCKVSNKALPAPIETKSKAKGPQEPQVYITLPPSREEMTK 383
DB 177 RVVSTLPTTHDNLGREGKEFKCKVINKALPAPIETKSKAKGPQEPQVYITLPPSREELSS 236
QY 384 NQVSLTCLVKGYFSDIAVEHESNGPENNYKTTTPVLDSDGSPFLSKLVKDRSRWQQG 443
DB 237 RSVSLTCLVINGFYPSDISEVEKNGKAEDNYKTTTPAVLSDGSPFLYLNKLSVPTSEWQRG 296
QY 444 NVFSCSVNHEALHNHYTQKSLSLSPGK 470
DB 297 DVFTCSVNHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
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Db 179 ISKTKGQPREPQVYTLPPSREEMTKNOVSLTCLVKGYPYSDIAVENWSSQPPENNYNTTP 238
QY 419 PVLDSGDSFFLYSKLTKDKRWQOQGNVFCVSMHEALHNHYTKQSLSPGK 470
Db 239 PMLDSGDSFFLYSKLTKDKRWQOQGNVFCVSMHEALHNHYTKQSLSPGK 290

RESULT 7
GC1_RAT
ID GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 2.8e-72;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGLCYKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
Db 1 AETAPSVYPLPALTALKSNMTVLTGCLVKGYPPEPTVTWNSGALTSGVHTFPAVLQ-S 59

QY 201 GLYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSGCDKTHTCPCPAPELLGG 260
Db 60 GLYTLTSSVTPSWPSQVTCNVNHNKPSNTKVDKRVKPSGCDKTHTCPCPAPELLGG 113

QY 261 ---PSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 317
Db 114 SEVSVFIFPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREE 173

QY 318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 377
Db 174 QFNSTFRSVSELPITLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPS 233

QY 378 REEMTKNOVSLTCLVKGYPYSDIAVENWSSQPPENNYNTTPVLDSDGSFFLYSKLTVDK 437
Db 234 KEEMTKNOVSLTCLVKGYPYSDIAVENWSSQPPENNYNTTPVLDSDGSFFLYSKLTVDK 293
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QY 438 SRWQOQGNVFCVSMHEALHNHYTKQSLSPGK 470
Db 294 EKWOQGNFTFCVSLHEGLNHNHTEKSLSPGK 326

RESULT 8
GC3_MOUSE
ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.;
RA Tucker P.W.; Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
CC PIR; B02156; G3MSC.
CC HSSP; P01857; IFC1.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00410; IG_Like; 1.
CC SMART; SM00407; IGcl; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
Best Local Similarity 65.0%; Pred. No. 6.2e-72;
Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

QY 142 STKGPSVFPLAPSSKSTSGGTAALGLCYKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSG 201
Db 1 TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYPPEPTVKWNYGALSSGVRTVSSVLIQ-SG 59

QY 202 LYSLSVVTVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSGCDKTHTCPC--PCPAPELLG 259
Db 60 FYSLSVVTVPSSVTPSWPSQVTCNVNHNKPSNTKVDKRVKPSGCDKTHTCPC--PCPAPELLG 118

QY 260 GPSVFLFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQY 319
Db 119 GPSVFIFFPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTPREEQY 178

QY 320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRE 379
Db 179 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSRE 238
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QY 380 EMTKNQVSLTCLVKGFPSPDIKAVESNGQPNENYKTPPVLDSDGSGFFLYSKLTVDKSR 439
Db 239 GSKKKVSLTCLVTTFEFAISWERNGEQDKNTPTPILSDGDTFYLYSKLTVDKSR 298
QY 440 WQGNVFCSCVMEALHNNHYTKSLSPGK 470
Db 299 WLOGEFTCSVWHEALHNNHYTKSLSPGK 329

RESULT 9
GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma1 chain";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).

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DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; GLMS
DR HSSP; P01842; 7FAB.

DR GlycosuitedB; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_Cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97
FT CH1.
FT DOMAIN 98 110
FT HINGE.
FT DOMAIN 111 217
FT CH2.
FT DOMAIN 218 324
FT CH3.
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 104 104
FT DISULFID 107 107
FT DISULFID 109 109
FT DISULFID 138 198
FT DISULFID 174 174
FT CARBOHYD
FT N-LINKED (GLCNAC. . .).
FT /FTIG-CAR_000055.
FT DISULFID 244 302
FT MOD_RES 324 324
FT REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276
FT N -> D (IN REF. 3).
FT CONFLICT 278 278
FT N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 45.5%; Score 1145; DB 1; Length 324;
Best Local Similarity 62.3%; Pred. No. 1.3e-71;
Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
QY 141 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNGALTSGVHTFPAVLQSS 200
Db 1 AKTTPSVPLAPGSAQAQNSMTLGLCLVKGYFPEPTVWSNGSLSSGSHVHTFPAVLQSD 60
QY 201 GLYSLSVVTVPSSTLGTQYICNVNHNKPSNTKVDKRVKPKCDKTHTCPP--CPAPELL 258
Db 61 -LYTLSSSVTVPSPPRSETVTCNVAHPASSTKVDKKIVPRDGG---CKPCICTVPEV- 114
QY 259 GGPVSFLFPKPKDLMISRTDEVTCVVVDVSHEDPEVFKNVYVDGVVHNNAKTKPREEQ 318
Db 115 --SSVFIFPPKPKDVLITLTPKVTCTVVDVDSKDDPEQVSWFVDDVEVHTAQTQPREQ 172
QY 319 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGPQPVYTLPPSR 378
Db 173 FNSTFRVSELPIMHQDWLNKGEYKCKRVNSAAPPAPIETKISKGRKAPQVYTIPTPK 232
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 438
Db 233 EQMAKDKVSLTCLMTDFFPEDITVEWMQNGQPAENYKNTQPTMNTNGSYFYVSKLVQKS 292
QY 439 RMOQGNVFCSCVMEALHNNHYTKSLSPGK 470
Db 293 NWEAGNTFTCSVLHLEGLHNHTKSLSPGK 324

RESULT 10
GCB_RAT STANDARD; PRT; 333 AA.
ID GCB_RAT
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2b chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;

```

RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_1like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 45.58; Score 1144.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 1.5e-71;
Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;

Oy 141 ASTGSPVPEPLAPSKSGCTAALGCLVDFPEPVTWNSGALTSVHTPEAVLQSS 200
Db 1 AQTAPSYPIAPLAGCGDTTSVTVLGCLVKGYPFVPTVTWNSGALSDVHTPEAVLQ-S 59

Oy 201 GLYLSSVVTVPSSLSGRTQYICNVNHPKSNTKVDKRVKPS-----CDKTHTCPPCPA 254
Db 60 GLYLTSSVT--SSTWPSQTVTCNVAPASSTKVDKVERNGGIGHKCPTCPTCHKCPV 117

Oy 255 PELGGSPVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGEVHNNAKTKP 314
Db 118 PELGGSPVFLFPKPKDILLISQNAKVTCTVVDVSEEPDQVFSWFVNNVEVHTAQTP 177

Oy 315 REEYNTSYRVVSVLTVLHDLQNGKEYCKVSNKALPAPTEKTSKAKGQPREPQVYTL 374
Db 178 REEQNTSYRVVSVLPIQHQDMGSKFCKVNNKALPSPEKTSKPKGLVRKPYQVYM 237

Oy 375 PPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPVLDSDGSFFLYSKLT 434
Db 238 GPPTQLTEQVSLTCLTSGFLPNDIGVEWTNGHIEKNYKNTPEVMDSDGSFFMYSKLN 297

Oy 435 VDKSRWQGNVFSVSMHEALHNHYTKSLSPGK 470
Db 298 VERSRWDSRAPFVCSVHVEGLHNHNVKSIKSRPGK 333

RESULT 11
GCIM_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
```

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RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RL Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=8222190; PubMed=6283537;
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
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DR EMBL; V00793; CAA24172.1; -.
DR EMBL; V00793; CAA24173.1; -.
DR EMBL; V00793; CAA24174.1; -.
DR PIR; P02159; GLMSM.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT DISULFID 244 302
FT TRANSMEM 340 357 POTENTIAL.
FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;
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Query Match 45.3%; Score 1140; DB 1; Length 393;
Best Local Similarity 62.2%; Pred. No. 3.7e-71;
Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;


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RX MEDLINE=81223894; PubMed=6787604;
RA Ollo R., Aulfray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; G2NSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;

Query Match 44.9%; Score 1129; DB 1; Length 330;
Best Local Similarity 63.9%; Pred. No. 1.7e-70;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

QY 141 ASTKGPSVFFPLAPSSKSTSGGTAALGLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
DB 1 AKTTAPSVYPLPACVGTGTSSTVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQSD 60

QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDTHTCPP--CPAPELL 258
DB 61 -LXTLSSSVTVTSSTWPSQSTITCNVAHPASSSTKVDDKIEPRG-PTIKPCPPCKCPAPNLL 118

QY 259 GGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 318
DB 119 GGPSVFIPFPRKIDVLMISLPIVTCVVVDVSDPDQVQISWFENNVYEVHTAQTTHRED 178

QY 319 YNSTYRVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
DB 179 YNSTLRVVSALPQHQDWMGSEKFEKCKVNNKDLPAPIERTISKPKGSVRAPQVYTLPPPE 238
```

```
QY 379 EEMTKNOVSLTCLVKGYFPPSPDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 438
DB 239 EEMTKQVTLTCLVKGYFPPSPDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS 298
QY 439 RWQOGNVFSCSVMEALHNVHTOKSLSLSPCK 470
DB 299 NWVERNSYSCSVVHEGLHNHTTKTSFRTPK 330

RESULT 14
GCC_RAT ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
DR EMBL; X07189; CAA30169.1; -.
DR PIR; S00847; S00847.
DR HSSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 1 97 CHI.
FT DISULFID 98 113 HINGE.
FT DISULFID 114 222 CH2.
FT DISULFID 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 2.1e-70;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

QY 141 ASTKGPSVFFPLAPSSKSTSGGTAALGLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
DB 1 AKTTAPSVYPLPACVGTGTSSTVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPAVLQ-S 59

QY 201 GLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPSCKDTHTCPP--CPAPEL 257
DB 60 GLYTLSSSVTVTPSSSTWSSQVTCTVAHPATKSNLIKRIEPR---RPKRPPTDICSDDN 116
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```
QY 258 LGSPSVFLEPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 LGRPSVFIFFPKPKDILMITLPKVTVVVDVSEEDPDQFSFVDNVRVFTTAQTPHEE 176
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 QYNSTVRVSVLTVLHQDWLNKKEYCKYKSNKALPAPIEKTISKAKGQPREPOVYTPPPS 377
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 QLNGTRVSVTLHIQHDWMSGKEFKCKVKNKDLPSPIEKTISKPRGARTQQVYIIPP 236
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 REEMTKNOVSLACLKVGFPYSDIAVWESNGQPENNYKTTPVLDSDGSFELYSLKLTVDK 437
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 RQMSKNKVSVCMTVTFYPASISVWERNGELEQDKNTLPVLDSDGSFELYSLKLSVD 296
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 DSWMRGDIPTCSVWHEALHNHHTQKLSRSPGK 339
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE P01864;
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
  IgG2a and IgG2b alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
  chain Fc regions of Ig1a and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC !- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
  FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IGCL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
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Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 2.6e-70;

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Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2:
QY 141 ASTKGPSVFLEPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 200
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AKTAPSVTLPVPCGGTIGSSVTIGCLVKGIFFPEPTVTLWNSGSLSSGVHTEFALLQ-S 59
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 201 GLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVKDKRVEPK-----SCDKHTCPCPPCA 254
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GLYTLLSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPIITQNCPPHQRVPVPCAA 119
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PELLGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP 314
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PLLGGPSVFIFFPKIKDVLMSLSPMVTCVVVDVSEDDPDVQISWFWNVNVEVHTAQTT 179
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 315 REEQYNSTVRVSVLTVLHQDWLNKKEYCKYKSNKALPAPIEKTISKAKGQPREPOVYTL 374
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTLRVVSALPIQHDWMSGKEFKCKYKNRRLPSPIEKTISKPRGVPYRAPQVYVL 239
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 PPSREEMTKNOVSLACLKVGFPYSDIAVWESNGQPENNYKTTPVLDSDGSFELYSLKLT 434
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PPPAEEMTKKEFSLTCMITGFLPAETAVDWTSGNRTEQNYKNTATVLDSDGSYFMYSKLR 299
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 VDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 VOKSTWERSLFCACSVVHEVLHNHLLTTTKTSRSLGK 335
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: August 14, 2002, 15:23:15
Job time: 688 sec
```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:16 ; Search time 187.61 Seconds
(without alignments)
433.386 Million cell updates/sec

Title: US-09-499-662-145
Perfect score: 2517
Sequence: 1 MGWSCIIILFLVATATGVHSQ.....MHEALHNYTKSLSPCK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvrius.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1637.5	65.1	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1626.5	64.6	463	11 Q99LC4	Q99lc4 mus musculus
3	1586.5	63.0	473	11 Q99L25	Q99l25 mus musculus
4	1564	62.1	468	11 Q99L31	Q99l31 mus musculus
5	1435.5	57.0	437	11 Q99IA4	Q99ia4 mus musculus
6	1422.5	56.5	473	11 Q91Z05	Q91z05 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96PQ8	Q96pq8 homo sapien
9	984	39.1	278	11 Q92L1K1	Q92lk1 mus musculus
10	929.5	36.9	614	4 Q96GAG	Q96gag homo sapien
11	888.5	35.3	481	11 Q91WT3	Q91wt3 mus musculus
12	857	34.0	500	4 Q9BRV0	Q9brv0 homo sapien
13	834.5	33.2	481	11 Q91WT1	Q91wt1 mus musculus
14	818	32.5	488	11 Q91WR1	Q91wr1 mus musculus
15	814.5	32.4	597	4 Q96BB9	Q96bb9 homo sapien
16	806	32.0	496	4 Q96DK0	Q96dk0 homo sapien

17	764.5	30.4	597	4 Q9BU10	Q9bu10 homo sapien
18	760.5	30.2	597	4 Q9BQ88	Q9bqb8 homo sapien
19	758	30.1	484	11 Q99LA6	Q99la6 mus musculus
20	754.5	30.0	618	4 Q96AA6	Q96aa6 homo sapien
21	736	29.2	494	4 Q96K68	Q96k68 homo sapien
22	731	29.0	613	4 Q96EY0	Q96ey0 homo sapien
23	726.5	28.9	487	11 Q99KA4	Q99ka4 mus musculus
24	720.5	28.6	479	11 Q91WP5	Q91wp5 mus musculus
25	702	27.9	486	11 Q91Z07	Q91z07 mus musculus
26	691.5	27.5	480	11 Q91XE1	Q91xe1 mus musculus
27	658	26.1	482	11 Q91X92	Q91x92 mus musculus
28	654	26.0	479	11 Q99M22	Q99m22 mus musculus
29	643	25.5	496	4 Q96KX8	Q96kx8 homo sapien
30	603	24.0	426	11 Q9DCD9	Q9dcd9 mus musculus
31	582.5	23.1	416	4 Q9NPP6	Q9np66 homo sapien
32	540.5	21.5	143	11 Q91V67	Q91v67 mus musculus
33	528.5	21.0	143	11 Q92AP9	Q92ap9 mus musculus
34	524	20.8	150	4 Q9Y298	Q9y298 homo sapien
35	515	20.3	142	11 Q92AQ2	Q92aq2 mus musculus
36	511.5	20.3	145	11 Q92AR3	Q92ar3 mus musculus
37	507	20.1	157	4 Q95978	Q95978 homo sapien
38	496.5	19.7	143	11 Q92AQ5	Q92aq5 mus musculus
39	495.5	19.7	159	4 Q96Q50	Q96qs0 homo sapien
40	495	19.7	146	11 Q92AR8	Q92ar8 mus musculus
41	494	19.6	144	11 Q92AP5	Q92ap5 mus musculus
42	493.5	19.6	145	11 Q92AQ7	Q92aq7 mus musculus
43	489.5	19.4	145	11 Q92AR4	Q92ar4 mus musculus
44	487.5	19.4	143	11 Q92AQ0	Q92aq0 mus musculus
45	487	19.3	140	11 Q92AP8	Q92ap8 mus musculus

ALIGNMENTS

RESULT	1
Q9D8L4	
ID	Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC	Q9D8L4; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	1810060009RIK PROTEIN.
GN	IGH-1 OR 1810060009RIK.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX	MEDLINE=21085660; PubMed=11217851;
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamane I.,
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA	Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA	Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RT	Hayashizaki Y.;
RT	"Functional annotation of a full-length mouse cDNA collection.";
PL	Nature 409:685-690(2001).
DR	EMBL; AK007918; BAB25349.1; -.
DR	HSSP; P01842; 7FAB.


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DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.0%; Score 1586.5; DB 11; Length 473;
Best Local Similarity 63.4%; Pred. No. 3,7e-125;
Matches 301; Conservative 61; Mismatches 106; Indels 7; Gaps 5;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPKASVKVSKASGYFTTSMWQWVKAP 60
DB 1 MENSWVFLFSLVTTGVHSGVQLVQSGAEVKKPKASVKVSKASGYFTTTHHWVKQP 60
QY 61 GQLEWNGEIDPSDYNYNOKFKGKATITVDTSTSTAYMELSLRSEDATVYYCARNRD 120
DB 61 EQGLEWIGWIDPEDEGTYAPKFDKATITADTSSNTAYLQLSLTSEDATLIYCARNLL 120
QY 121 --YNN--WYFDVWGQGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPV 177
DB 61 EQGLEWIGYIYPRDGTSTKYNKPKGKATLTADKSSSTAYMQLSLTSEDSAVCFCSRGS 120
QY 121 --YNN--WYFDVWGQGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPV 177
DB 121 IYGYGLYIFDYWGQGLTITVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPV 180
QY 178 TVNSGALTSGLVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKR 237
DB 181 TLTWNSGSLSSGVHTFPAVLQSD--LYTLSSSVTVTSSTWPSQSTTCNVNHPASSTKVDKK 239
QY 238 VEPKCDKTHTCPP--CPAPELGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPE 295
DB 240 IEPRG-PTIKPCPCPCAPNLLGGPSVFIPPKIKDVLMSLSPMVTCTVVVDVSEDDPD 298
QY 296 VKFWYVDGVEVHNNAKTPREEQVNSTYRVVSVLTVLHODMLNGEKYCKVSNKALPAPI 355
DB 299 VQISWFVNNVEVLTAQTHREDYNSTLRVVSALPIQHODMWSGKEFKCKVNNKALPAPI 358
QY 356 EKTISKAKGQPREQVTLTPPSREEMTKNQVSLTCLVKGYEPSDIAVEWESNGOPENNYK 415
DB 359 ERTISKPKGSVRAPQVVLPPPEEMTKKQVTLTCMTVDFMPEDIIYVETWNGKTELNYK 418
QY 416 TTPVLDSDGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALNHYTKQSLSLSPGK 470
DB 419 NTEPVLDSDGSFYFMYSLRVEKKNNVERNSVSCSVVHGLNHHHTTKFSRTPGK 473

RESULT 4
Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Iq.
DR InterPro; IPR003597; Iq-cl.
DR InterPro; IPR003600; Iq-like.
DR InterPro; IPR003606; Iq_MHC.
DR InterPro; IPR003606; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 4.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
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```
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;

Query Match 62.1%; Score 1564; DB 11; Length 468;
Best Local Similarity 63.1%; Pred. No. 2.8e-123;
Matches 298; Conservative 60; Mismatches 108; Indels 6; Gaps 4;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPKASVKVSKASGYFTTSMWQWVKAP 60
DB 1 MENSWVFLFSLVTTGVHSGVQLVQSGAEVKKPKASVKVSKASGYFTTTHHWVKQP 60
QY 61 GQLEWNGEIDPSDYNYNOKFKGKATITVDTSTSTAYMELSLRSEDATVYYCARNRD 120
DB 61 EQGLEWIGWIDPEDEGTYAPKFDKATITADTSSNTAYLQLSLTSEDATLIYCARNLL 120
QY 121 YNNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTVS 180
DB 121 YGG--YVDYWGQGLTITVSSAKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLT 178
QY 181 WNSGALTSGLVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVP 240
DB 179 WNSGSLSSGVHTFPAVLQSD--LYTLSSSVTVTSSTWPSQSTTCNVNHPASSTKVDKKIEP 237
QY 241 KSCDKTHTCPP--CPAPELGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 298
DB 238 RG-PTIKPCPCPCAPNLLGGPSVFIPPKIKDVLMSLSPMVTCTVVVDVSEDDPDVQI 296
QY 299 NWYVDGVEVHNNAKTPREEQVNSTYRVVSVLTVLHODMLNGEKYCKVSNKALPAPIERT 358
DB 297 SWFVNNVEVLTAQTHREDYNSTLRVVSALPIQHODMWSGKEFKCKVNNKALPAPIERT 356
QY 359 ISKAKGQPREQVTLTPPSREEMTKNQVSLTCLVKGYEPSDIAVEWESNGOPENNYKTP 418
DB 357 ISKPKGSVRAPQVVLPPPEEMTKKQVTLTCMTVDFMPEDIIYVETWNGKTELNYKNT 416
QY 419 PVLDSDGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALNHYTKQSLSLSPGK 470
DB 417 PVLDSDGSFYFMYSLRVEKKNNVERNSVSCSVVHGLNHHHTTKFSRTPGK 468

RESULT 5
Q99L44 ID Q99L44 PRELIMINARY; PRT; 437 AA.
AC Q99L44
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003600; Iq-like.
DR InterPro; IPR003606; Iq_MHC.
DR InterPro; IPR003596; Iq_v.
DR Pfam; PF00047; Iq; 4.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR NON_TER 1
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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QY 375 PPSREEMTKNOVSLTCLVKGYFSPSDIAVEWESNGQP--ENNYKTTTPVLDSDGSGFFLYSK 432
Db 240 APHPDELKSKSVSTCLVKDFYFPEIINWQSGNGQPELETXYSTQAQDSGSGFFLYSK 299
QY 433 LTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 300 LSVDRNRWQGGTTTCGVMHEALHNHYTKQVSKNPGK 337

RESULT 8
Q96PQ8 ID Q96PQ8 PRELIMINARY; PRT; 701 AA.
AC Q96PQ8: 2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL: AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.9%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 3.5e-97;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 239 EPKSCDTHCTCPCPAPBELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
Db 470 EPKSCDTHCTCPCPAPBELGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 529
QY 299 NWYVDGVEVHNNAKTPREEQVNSYRVSVLTVLHQDLNGKEYCKVKSNKALPAIEKT 358
Db 530 NWYVDGVEVHNNAKTPREEQVNSYRVSVLTVLHQDLNGKEYCKVKSNKALPAIEKT 589
QY 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTP 418
Db 590 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTP 649
QY 419 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 650 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 701

RESULT 9
Q921K1 ID Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1: 2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC012207; AAH12207.1; -.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 39.1%; Score 984; DB 11; Length 278;
Best Local Similarity 67.1%; Pred. No. 8.8e-75;
Matches 186; Conservative 33; Mismatches 50; Indels 8; Gaps 3;
QY 1 MGWSCIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVKQAP 60
Db 1 MGWSCIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVKQAP 60
QY 61 GQGLEWMEIDPDSYTNYNOKFKGKATITVDSTSTAYMELSSLRSSEDTAYVYCARNRD 120
Db 61 GQGLEWMEIDPDSYTNYNOKFKGKATITVDSTSTAYMELSSLRSSEDTAYVYCARNRD 120
QY 121 YSNWYFDVWQGTTLTVSSASTKGPSPVPLAPLAPSKSTSGTAAAGCLVKDYFPEPPTVS 180
Db 121 Y-DVYFDVWQGTTLTVSSASTKGPSPVPLAPLAPSKSTSGTAAAGCLVKDYFPEPPTVS 179
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHRPSTNPKVDKRYEP 240
Db 180 WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQYICNVNHRPSTNPKVDKRYEP 238
QY 241 K-----SCDKTHCTCPCPAPPELLGGPSVFLFPPKPK 271
Db 239 RVPITQNPCLPKCEPCCAAPDLLGGPSVFIFPPPSR 275

RESULT 10
Q96GA6 ID Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6: 2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 36.9%; Score 929.5; DB 4; Length 614;
Best Local Similarity 36.7%; Pred. No. 1.1e-69;
Matches 212; Conservative 84; Mismatches 166; Indels 115; Gaps 17;
QY 1 MGWSCIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVKQAP 60
Db 1 MDWTWRIILFLVAANTDAYSQMQLVQSGAEVKKPGASVKVSCKASGYTFTSYLHWVRQAP 60
QY 61 GQGLEWMEIDPDSYTNYNOKFKGKATITVDSTSTAYMELSSLRSSEDTAYVYCARNRD 120
Db 61 GQALEWMEITPFGNGNTNYAQKFDQRYTITRDRSMNTAYMELSSLRSSEDTAYVYCARG-- 118
QY 121 YSNW--YFDVWQGTTLTVSSASTKGPSPVPLAPLAPSKSTSG-GTAAAGCLVKDYFPEPVP 177
Db 119 YSSWDDAFDIWGGTWTWVSSGSASAPTLFPLVSCENSPSDTSSVAVGCLAQFLPDSI 178
QY 178 TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL--GTQTY-ICNVNHRPSTN 231
Db 179 TFSWKYKNNSDISSTRGFPVLR-GGKYAATSQVLLPSSKDVWQGTDEHVCKVQHPGNK 237
QY 232 -----TKVDKRYEPKS-----CDKTHCTP----- 250
Db 238 EKNVPLPVIAELPKKVSFVFPDRGFGNPRKSKLICQATGFSRQIQVSWLREGQVGS 297
QY 251 -----PCPAPELLGGPS----- 262
Db 298 GVTTDQVOAEAKESGPTTYKVTSTLTIKESDWLSQSMTFCRVDHRGLTFOQNASSMCMCPVD 357

Qy	263	-----VLFPPKPKFLMISRPETVCVVVDVSHEDPEKFNWYDGVGVHNAKTKPRE	316
Db	358	QDTAIRFAIPPS--FASIFLTKTSLTCLVTLDTLTYD--SVTISWTRQNGEAVKTHTNISE	415
Qy	317	EQYNSTRVYVSVLTVLHODWLNKEYKCKYSNKALPAIEKTIISKAKQP--REPQVYITLP	375
Db	416	SHPNATTSVAGEASICEDDDNGSERFTCTVTHDLSPLKQTISSRKGVALHRDPDYLLP	475
Qy	376	PSREMT--KNOVSLTCLVLKGFYPSDIAVESNGQP--ENNYKTTTPPVLDD--SDGSFFLY	430
Db	476	PARQLMLRNSAITCLVTGFSADVFVQMQRQGLPSPEKIVYTSAPMPEQAPGRIFAH	535
Qy	431	SKLTVDKSRWQQGVNFSCSYMHALNNHYTKQSLSLS	467
Db	536	SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS	572
RESULT	11		
ID	Q91WT3	PRELIMINARY; PRT; 481 AA.	
AC	Q91WT3		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	HYPOTHETICAL 52.0 KDA PROTEIN.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=COLON;		
RA	Strausberg R.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC013488; AAH13488.1; -		
KW	Hypothetical protein.		
SQ	SEQUENCE 481 AA; 52022 MW; 4EEB5C253038B718 CRC64;		

Query Match	35.3%	Score	888.5	DB	11	Length	481
Best Local Similarity	42.7%	Pred.	No. 2.le-66				
Matches	206	Conservative	73	Mismatches	172	Indels	31
Gaps	16						
QY	1	MGWSCIIILFVATATGVHSHQVQLVQSGAEVKKPGASVKSCAKSGYTTSYMMQWVKQAP	60				
Db	1						
QY	1	MRWSCIIILFVATATGVNSVQLQPGAEIVRPGASVKLSCKTSGYTFDTRMMNWVKQRP	60				
Db	1						
QY	61	GGQLEWMGEIDPDSYTNYNQKFKGATITVDTSTSTAYMELSSLSRSEDTRVYYTCARNRD	120				
Db	61						
QY	61	GGQLEWGAIDPDSYTSYNQKFKG-TTLTVDTSSSAYMLLSLTSEDSAVFYFCARGPR	119				
Db	61						
QY	121	YSNNWYFDVWCGTILTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLVKQYFPE-PVTV	179				
Db	121						
QY	120	DSSGY---WQGGTTLTVSSSPAREPTIYPLT-PPQALSDPVIIGLHIHDFPSGTMMNV	175				
Db	120						
QY	180	SWNSGALTSGYHTFPAPVLQSSGLYSLSSVATVPSSSLGT-QTYICNVNHHKPSNTKVKRRV	238				
Db	176						
QY	239	EPKSCDKTHICPPAPAEELGPGSVFVLPFPKPKDTLMISRTPEVTCVVDVSHEDPE-VK	297				
Db	235						
QY	298	FNWYVDGVGEVHNATKPREEQYNT---YRVVSVLTVLHQDLNGKEYKCKVSKNSKALPAP	354				
Db	288	FTW-----EPSTGDAVQKKAQVNSCGCYSVSSVLPQCAERMSNGSPKCVITHPESDT-	341				
QY	355	IEKTIISKAKGPPEQYVTLPPSREMTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ---P	410				
Db	342	LTGTIAKVTYVNTFPVQVHLLPPPSSEALNELSVLTLCLVRAFNPEKVLVRLWLGNEELSP	401				
QY	411	ENNTKTPPVLDSDG---SFFLYSKLTVDKSRWQOQNVFSCSMHEALHNHYTKQSLSLSP	468				

```
Db    402 ESYLVFPEKPGEGATYLTVSLRVSAEINWKGQDYSCMWGHEALPMNFOTKTIDRLS 461  
      | :   |   |   |   |   |   |   |   |   |   |   |   |   |   |  
Oy    469 GK 470  
      ||  
Db    462 GK 463  
  
RESULT 12  
Q9BRV0  
ID Q9BRV0 PRELIMINARY; PRT; 500 AA.  
AC Q9BRV0;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 54.2 KDA PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PROSTATE;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC005951; AAH05951.1; -  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig_cl.  
DR InterPro; IPR003600; Ig_like.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig_4.  
DR SMART; SM00409; IG; 4.  
DR SMART; SM00407; IGc1; 2.  
DR SMART; SM00406; IGv; 1.  
DR SMART; SM00410; IG_like; 1.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 500 AA; 5A154 MW; 0A9BF43F2A3CC6D9 CRC64;
```

Query Match	34.08;	Score	857;	DB	4;	Length	500;
Best Local Similarity	40.9%;	Pred.	No.	9,9e-64;			
Matches	205;	Conservative	69;	Mismatches	177;	Indels	50;
Gaps	18;						

Qy	1	MGWSCIIILFVATATGVHSSOVOLVQSGAEVKKPGASVKVSKCASGYTPTSYVMOWVKQAP	60
Db	1	MDWTWSILFLVAATGAQSQVHLVQSGAEVMPGASVRVSKTSGYAPHYTSIIIVRQAP	60
Qy	61	GGQLEWMEIDPDSYTYNKNOKFGKATITVDTSTAYMELSLRSDTAVYYCARNR-	119
Db	61	GGQLEWGMWISPSDNTRFKKFGQGVTLTDTSTSTVYMELSLRSDTAVYYCARRYC	120
Qy	120	DYS---NNWYF--DVGQGLTVTVSSASTKGPVFPLAPSSKSTSGGTALGCLVKDYF	173
Db	121	SYSCQNDYIIYYMDVWGKGTIVTVSSASPTSPKVFSLGCS-QTPDGNVVIACLVGGFF	179
Qy	174	P-EPVTVSWNSGALTSGVHTTTPAVLQSSG-LYSLSSVVTVPSSS-LGTQTICVNNHKPS	230
Db	180	POEPLSVTWSESGGVYARNPPSQDASGDLYTTSSQLTLPATOCLAGKSVTCHKVY-T	238
Qy	231	NTKYDKRVEPKSCDKTHTCCPAPPELLGGPSVFLFPPKPK-----DTLM	275
Db	239	NPSQDVT-----PCVPVPTPTTSPST-PPTPSPSCCHPRLSLRPAEDLL	285
Qy	276	ISRTPEVTGVVDYSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVYSLVTLVHOD	335
Db	286	LGSEANLTCTLTGL-RDASGVYFTWTVSSGK--SAVQGPDRDLCCGYSSVSVLSGCAEP	342
Qy	336	WLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYTLPPSRREMTKNQ-VSUTCLVKG	394
Db	343	WNHGKTFCTAAYPEKSTPLTATLSKS-GNTRFREVHLLPPPSBELALNELVTLTCLARG	401

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:38 ; Search time 230.21 Seconds
(without alignments)
226.770 Million cell updates/sec

Title: US-09-499-662-147

Perfect score: 2517

Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALHNHYTKSLSLSPCK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_032802.*

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3:	/SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA1982.DAT.*
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22:	/SIDSL/gcgdata/hold-geneseq/geneq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2517	100.0	470	21	AAW90935 Humanised anti-Fas
2	2514	99.9	470	21	AAW90933 Humanised anti-Fas
3	2512	99.8	470	21	AAW90934 Humanised anti-Fas
4	2511	99.8	470	19	AAW83037 Anti-Fas humanised
5	2511	99.8	470	21	AAW84779 Humanised anti-Fas
6	2511	99.8	470	21	AAW90929 Humanised HFE7A de
7	2498	99.2	470	19	AAW83036 Anti-Fas humanised
8	2498	99.2	470	21	AAW84776 Humanised anti-Fas
9	2498	99.2	470	21	AAW90926 Humanised HFE7A de
10	2498	99.2	470	21	AAW90936 Humanised HFE7A de
11	2349.5	93.3	731	22	AAW52156 Humanised HMFG-1 h

12	2349.5	93.3	741	22	AAW52159	Humanised HMFG-1 h
13	2344.5	93.1	729	22	AAW52158	Humanised HMFG-1 h
14	2344.5	93.1	739	22	AAW52161	Humanised HMFG-1 h
15	2338.5	92.9	730	22	AAW52157	Humanised HMFG-1 h
16	2338.5	92.9	740	22	AAW52160	Humanised HMFG-1 h
17	2307	91.7	652	19	AAW48650	Heavy chain of hMA
18	2293.5	91.1	465	22	AAW72228	Humanised 323/A3 (
19	2288.5	90.9	464	22	AAW72232	Humanised 323/A3 (
20	2284	90.7	470	21	AAW80826	A dimeric anti-CD2
21	2283	90.7	466	22	AAW03755	Chimeric 2403 IgG
22	2258	89.7	476	20	AAW88464	Monoclonal antibod
23	2254.5	89.6	481	13	AAW24442	Sequence of antibo
24	2251	89.4	472	20	AAW50166	Human reshaped F19
25	2235	88.8	449	14	AAW43339	Completely humanis
26	2235	88.8	449	14	AAW49816	Amino acid sequenc
27	2233	88.7	476	14	AAW31023	Antibody D heavy c
28	2236.5	88.5	583	22	AAW83156	Ganglioside GM2 an
29	2205.5	87.6	467	22	AAW36210	Human immune syste
30	2203.5	87.5	452	20	AAW29458	Recombinant immuno
31	2203.5	87.5	452	21	AAW30322	Humanised anti-IL-
32	2203.5	87.5	452	21	AAW77766	Humanised anti-IL-
33	2203	87.2	452	19	AAW50157	Chimeric mouse/hum
34	2194.5	87.2	452	19	AAW69316	Anti-IL-8 humanise
35	2191.5	87.1	473	22	AAW64475	Human type antihum
36	2190	87.0	592	22	AAW83858	Amino acid sequenc
37	2189	87.0	474	22	AAW14177	Human novel protei
38	2188.5	86.9	473	22	AAW64471	Human type antihum
39	2187	86.9	595	20	AAW86003	Anti-5T4 single ch
40	2184.5	86.8	475	22	AAW63640	Amino acid sequenc
41	2183.5	86.8	473	22	AAW64459	Human type antihum
42	2176.5	86.5	473	22	AAW64473	Human type antihum
43	2174	86.4	468	20	AAW85689	D9D10 heavy chain
44	2174	86.4	711	20	AAW85692	MoTABII fusion pro
45	2165	86.0	470	13	AAW22757	Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1

AAW90935

ID AAW90935 standard; Protein; 470 AA.

AC AAW90935;

XX DT 08-AUG-2000 (first entry)

XX DE Humanised anti-Fas designed heavy chain Heu 3 protein.

XX KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

XX OS Synthetic.

XX PN EP990663-A2.

XX PD 05-APR-2000.

XX PF 29-SEP-1999; 99EP-0307711.

XX PR 30-SEP-1998; 98JP-0276881.

XX PR 30-SEP-1998; 98JP-0276882.

XX PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 DR N-PSDB; AAA11646.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 PS Claim 2; Page 180-182; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC anti-rheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis, myasthenia gravis, viral
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 3
 CC which is described in the method of the invention.
 XX
 SQ Sequence 470 AA;
 Query Match 100.0%; Score 2517; DB 21; Length 470;
 Best Local Similarity 100.0%; Pred. No. 1.7e-144;
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWSCIILFLVATATGHSQVQLVSGDVRKPKGASVKSCASGTFTSYMQWVRQAP 60
 DB 1 mgwscililflvatatgvsqglvsgdaevkpgasvkscasgytftsyvmqvrqap 60
 QY 61 GQGLEWMMGEIDPSDYNTNQRKFKATLTVDTSSTAYMELSSLRSEDTAVYYCARNRD 120
 DB 61 gggglewmeidpsdyntnyqkfkakatltdtststaymelsslrse dtavyyca rdn 120
 QY 121 YSNNNYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB 121 ysnnyf dwgggtltv tvssastkpsvfplapsskstsggtaalgclvkdyfpeptvys 180
 QY 181 WNSGALTSCVHTFPVAVLQSGGLYSLSSVTVVPSSSLGQTQYTCNVNHPKNTKDKRVEP 240
 DB 181 wnsгалтсгvhtfpavlvqsgglyslssv tvvpssslgtqtqytcnvnhkpsntkdkrv ep 240
 QY 241 KSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
 DB 241 kscdkthtccpcpapellggpsvflfppkpkdtlmisrtpevtcvv dvsh edpevkfnw 300
 QY 301 YVDGVEVHNNAKTPREQYNSTYRVVSVLTVLUQDLNKGKEYCKVSKNKPAPIEKTIIS 360
 DB 301 yvdgvevhnaktpreqynstyrvvsvltvluqdlngkeyckvskvsnkalp iektis 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYGPPSDIAVEWESNGQPENNYKTTTPV 420
 DB 361 kakgqprepqv ytlppsreemtknqvsltclvkgyppspdia vewesngqpenn ykttppv 420

Db 361 kakgqprepqv ytlppsreemtknqvsltclvkgyppspdia vewesngqpenn ykttppv 420
 QY 421 LDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALNHHYTKQKLSLSLSPGK 470
 DB 421 ldsdgsfflyskltvdksrwqgnvfscsvmh ealnhhytqkslsispgk 470
 RESULT 2
 AAW90933
 ID AAW90933 standard; Protein; 470 AA.
 XX
 AC AAW90933;
 XX
 DT 08-AUG-2000 (first entry)
 DE Humanised anti-Fas designed heavy chain Heu 1 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX
 DR WPI: 2000-258930/23.
 DR N-PSDB; AAA11644.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 PS Claim 2; Page 169-170; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively

CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.9%; Score 2514; DB 21; Length 470;
Best Local Similarity 99.8%; Pred. No. 2.6e-144; Indels 0; Gaps 0;
Matches 468; Conservative 1; Mismatches 0;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYWMQVRRQAP 60
DB 1 mgwscililflvatatgshsqvqlvqsgaeavkpkgsasvkvsckasgytftsywmqvrrqap 60
QY 61 GQGLEWMEIDPDSYNTYNNQKFGKATLTVDSTSTAYMELSLRSEDVAVYCARNRD 120
DB 61 gqglewmgeidpsdysntynqkfgkatltvdststaymelsslrseavvyccarnrd 120
QY 121 YSNWYFDWVGQGLTVTVSSASTKGPSVEPLAPSKSTSGCTAALGCLVKDYFPEPTVTS 180
DB 121 ysnwyfdwvggglvtvssastkgpsvfplapsksts gctaalgcivkdyfpeptvts 180
QY 181 WNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRVPE 240
DB 181 wnsгалtsvhtfpavlsqssglyslssvtpssslgtqtyicnvnhkpsntkvdkrvpe 240
QY 241 KSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVGVVDSHEDPEVKFNW 300
DB 241 kscdkthtcpcpapelggpsvflfppkpkdtlmisrtpevtcvvvdsghedpevkfnw 300
QY 301 YVDGVEVHNATKPREQYNSTYRVSVLTVLHODWLNKGEYCKVSNKALPAPTEKTS 360
DB 301 yvdgvevhnatkpreeqynstyrsvsvltvlhqdwlngkeyckvsnkalpapektis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEFESNQGNPNVKTTPPV 420
DB 361 kaksqprepqvtytlppsreemtknqvsltcivkgfypsdiavefvesngqpnnykttppv 420
QY 421 LDSGSEFLYSLKLVKDSRWQGNVFCVSNMHEALHNHYTKSLSPGK 470
DB 421 ldsdgsfplysklvkdsrwqgnvfscvsnmhealhnhytkslspgk 470

RESULT 3

AAW90934 standard; Protein: 470 AA.

AC AAW90934;

DT 08-AUG-2000 (first entry)

DE Humanised anti-Fas designed heavy chain Heu 2 protein.

XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
XX anti-allergic; human; anti-arthritis; antitumor; immunomodulatory; cardiac;
XX dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
XX nephrotropic; anti-infectivity; neuroprotective; antiarteriosclerotic;
XX hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
XX Hashimoto disease; rheumatoid arthritis; graft versus host disease;
XX Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
XX Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
XX multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
XX insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
OS Synthetic.
XX EP990663-A2.

XX 05-APR-2000.
XX 29-SEP-1999; 99EP-0307711.
XX 30-SEP-1998; 98JP-0276881.
XX 30-SEP-1998; 98JP-0276882.
XX (SANY) SANKYO CO LTD.
XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
XX WPI: 2000-259930/23.
XX N-PSDB; AAA11645.

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems

XX Claim 2 ; Page 174-176; 263pp; English.

XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
CC antiartherosclerotic, cardiatic and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody heavy chain construct designated Heu 2
CC which is described in the method of the invention.

XX SQ Sequence 470 AA;

Query Match 99.8%; Score 2512; DB 21; Length 470;
Best Local Similarity 99.6%; Pred. No. 3.5e-144;
Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGHSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYWMQVRRQAP 60
DB 1 mgwscililflvatatgshsqvqlvqsgaeavkpkgsasvkvsckasgytftsywmqvrrqap 60
QY 61 GQGLEWMEIDPDSYNTYNNQKFGKATLTVDSTSTAYMELSLRSEDVAVYCARNRD 120
DB 61 gqglewmgeidpsdysntynqkfgkatltvdststaymelsslrseavvyccarnrd 120
QY 121 YSNWYFDWVGQGLTVTVSSASTKGPSVEPLAPSKSTSGCTAALGCLVKDYFPEPTVTS 180
DB 121 ysnwyfdwvggglvtvssastkgpsvfplapsksts gctaalgcivkdyfpeptvts 180
QY 181 WNSGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRVPE 240
DB 181 wnsгалtsvhtfpavlsqssglyslssvtpssslgtqtyicnvnhkpsntkvdkrvpe 240
QY 241 KSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTVGVVDSHEDPEVKFNW 300

Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqkslspsgk 470

RESULT 5

AA14779

AA14779 standard; Protein; 470 AA.

XX

AC AA14779;

XX

DT 24-NOV-2000 (first entry)

XX

DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.

XX

KW Anti-Fas antibody; monoclonal antibody HFE7A; PERM-BP-5828;

KW murine; humanised antibody; complementarity determining region; CDR;

KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;

KW autoimmune disease; allergy; atopy; arteriosclerosis; myocardiitis;

KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;

KW hepatitis; AIDS; graft rejection; heavy chain.

XX

OS Chimeric - Mus musculus.

OS Chimeric - Homo sapiens.

XX

PN JP2000169393-A.

XX

PD 20-JUN-2000.

XX

PF 30-SEP-1999; 99JP-0278301.

XX

PR 30-SEP-1998; 98JP-0276883.

XX

FA (SANY) SANKYO CO LTD.

XX

DR WPI; 2000-485645/43.

DR N-PSDB; AAA72184.

XX

PT Preventive or treating agent for the diseases caused by an abnormality

PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains

PT anti-Fas antibody -

XX

PS Claim 21; Page 108-109; 139pp; Japanese.

XX

CC The invention relates to compositions for the prevention or treatment

CC or diseases caused by an abnormality in the Fas/Fas ligand system

CC containing an anti-Fas antibody as the active component. The anti-Fas

CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,

CC or a humanised version of HFE7A containing identical CDRs

CC (complementarity determining regions) to antibody HFE7A. Via its

CC interaction with Fas, the antibody of the invention acts as a modulator

CC of apoptosis. The compositions of the invention may therefore be used in

CC the treatment or prevention of conditions such as autoimmune diseases,

CC allergy, atopy, arteriosclerosis, myocardiitis, cardiomyopathy,

CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS

CC and organ graft rejection. Sequences AA14775-14776 and AA14779

CC represent the heavy chains (or fragments thereof) of various humanised

CC HFE7A-derived anti-Fas antibodies.

XX

SQ Sequence 470 AA;

Query Match 99.88; Score 2511; DB 21; Length 470;

Best Local Similarity 99.68; Pred. No. 4e-144;

Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGWSCIIILFVATATGVHSQVQLVQSGAEVKKPGASVKVCKASGYTFTSYMMQVROAP 60

Db 1 mgwscilflvatatgvhsqvlvqsgaevkpgasvkscasgytftsywmgvqkqap 60

Qy 61 GQGLEWMEIDPSDYTNYNQKFKGKATLTVDSTSTAYMELSSLRSDTAVYVCARRRD 120

Db 61 ggglewmeidpsdytnynqkfgkatltvdststaymelslrsdtaavyccarrnd 120

Qy 121 YSNWYFDVWCGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180

Db 121 ysnwfyfdwgegtlvtvssastkgsvfplapsskstsggtaalgclvkdyfpepvtvs 180

Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVKDKRVEP 240

Db 181 wnsгалтsgvhtfpavlgssglyslssvvtvpssslgtqtyicnvnhkpsntkvdkrvep 240

Qy 241 KSCDTHTCPCPAPPELLGGPSVFLFPPPKPDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300

Db 241 kscdthtcpcpapellggpsvflfppkpktlmlsrtpetvctcvvdvshedpevkfnw 300

Qy 301 YVDGVEVNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360

Db 301 yvdgvevnnaktkpreedynstyrvsvlvtlhdwlngkeyckvsnkalpapietktis 360

Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNGOPENNYKTTTPV 420

Db 361 kagqprepytlppstreemtknqvslclvkgfypsdiavewesngopennykttppv 420

Qy 421 LDSGGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNYHTQKSLSLSPGK 470

Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqkslspsgk 470

RESULT 6

AAW90929

ID AAW90929 standard; Protein; 470 AA.

XX

AC AAW90929;

XX

DT 08-AUG-2000 (first entry)

XX

DE Humanised HFE7A designed heavy chain protein #2.

XX

KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;

KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;

KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;

KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;

KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;

KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;

KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;

KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;

KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;

KW insulin dependent diabetes mellitus; arteriosclerosis; myocardiitis;

KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

OS Synthetic.

XX

PN EP990663-A2.

XX

PD 05-APR-2000.

XX

PF 29-SEP-1999; 99EP-0307711.

XX

PR 30-SEP-1998; 98JP-0276881.

PR 30-SEP-1998; 98JP-0276882.

XX

PA (SANY) SANKYO CO LTD.

XX

PI Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;

XX

DR WPI; 2000-258930/23.

DR N-PSDB; AAA11622.

XX

PT New humanized anti-Fas antibody, useful for treating or preventing e.g.

PT inflammatory or autoimmune disease, induces apoptosis selectively in

PT cells with abnormal Fas-Fas ligand systems -

XX

PS Example reference 22; Page 150-152; 263pp; English.

XX

CC This invention describes a novel humanized anti-Fas antibody-like

CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas

CC ligand system, by binding to Fas on the cell surface, and prevents

CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, anti-diabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antifertility, neuroprotective,
 CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) Induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (II) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocardiitis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (A, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention.

XX SQ Sequence 470 AA;

Query Match 99.8%; Score 2511; DB 21; Length 470;
 Best Local Similarity 99.6%; Pred. No. 4e-144;
 Matches 468; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKYSCKASGVTFTSYMMQWVROAP 60
 Db 1 mgwscilflvatatgvhsqqlvqsgaevkpgasvksckasgytftsymbwqvkqap 60

QY 61 GQGLEWNGEIDPSDSTYNNKPKFATLVDTSTAYMELSSLSRSEDFAVYYCARNRD 120
 Db 61 gqglewngelidpsdsytnynqkfkgtatlvdtststaymelsslsrsedtavyyccarnrd 120

QY 121 YSNWYFDVWGQGLTVTVSSASPKGSVPFLAPSSKSTSGGTAALGCLYKDYFPEPVTVS 180
 Db 121 ysnwyfdvwgqgltlvtvssastkgsvpflapsskstsggtaalgclvdyfpepvtvs 180

QY 181 WNSGALTSGVHTPPAVLQSGGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVPE 240
 Db 181 wnsгалtsgvhtppavlqsgglyslssvstvpssslgtqtyicnvnhnkpntkvdkrvpe 240

QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNW 300
 Db 241 kscdkhtccpcpapelggpsvflfppkpkdtlmisrtpetvctcvvdvshedpevkfnw 300

QY 301 YVDGVEVHNAKTKPREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
 Db 301 yvdgvevhnaktkpreeqvnstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 360

QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTPPV 420
 Db 361 kkgqprepqvylppsreemtknqvslclvkgyfypsdiavewesngoppennyktppv 420

QY 421 LQSDGFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
 Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhytqkslsispkg 470

RESULT 7

AAW83036 standard; Protein: 470 AA.

XX AC AAW83036;

XX DT 15-MAR-1999 (first entry)

DE Anti-Fas humanised antibody HFE7A heavy chain.
 XX HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocardiitis; cardiomyopathy; AIDS;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Reptide 1..19 /label= Sig_peptide
 FT Protein 20..470 /label= Mat_protein
 FT Region 20..140 /label= Variable
 FT Region 141..464 /label= Constant
 FT Region 50..54 /label= CDR_H1
 FT /note= "Claim 9"
 FT Region 69..84 /label= CDR_H2
 FT /note= "Claim 9"
 FT Region 118..129 /label= CDR_H3
 FT /note= "Claim 9"
 XX AU9859701-A.
 XX 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 XX 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 XX (SANY) SANKYO CO LTD.
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 DR WPI: 1998-543440/47.
 DR N-PSDB; AAV70079.
 XX New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocardiitis, hepatitis and AIDS
 XX Claim 22; Page 212-213; 292pp; English.
 XX This is the amino acid sequence of the VD type humanised heavy
 CC chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
 CC pGHS7A62 SANK 73397 harbors plasmid pGHS7A62 carrying a fusion
 CC fragment of the humanised VD type HFE7A heavy chain and DNA
 CC encoding human IgG1 constant region (see AAV70079), and is deposited
 CC as FERM BP-6074 (claimed). The invention provides methods for
 CC producing humanised antibodies by culturing host cells. Humanised
 CC versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
 CC of inducing apoptosis in abnormal cells expressing Fas, and of
 CC inhibiting Fas-induced apoptosis in normal cells. The humanised
 CC antibodies are used to evaluate, in animal models, treatments of
 CC diseases that involve Fas/Fas ligand interactions, and also to

CC treat such diseases, including autoimmune disease (e.g. systemic
CC lupus erythematosus, Hashimoto's disease, graft versus host disease,
CC Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
CC Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
CC autoimmune haemolytic anaemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, and
CC insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
CC myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
CC anaemia, hepatitis, AIDS and transplant rejection (all claimed).
XX
SQ Sequence 470 AA;

Query Match 99.2%; Score 2498; DB 19; Length 470;
Best Local Similarity 99.1%; Pred. No. 2.5e-143;
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVRQAP 60
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkpgasvkvsckasgyftsyymmqqvkgap 60
QY 61 GQGLEWNGEIDPDSYNTYNNOKFKGKATLTVDSTSTAYMELSLRSEDYAVYICARNRD 120
Db 61 gqglewngeidpsdysntynngkfkgkatltvdststaymelslrse dtavyyicarnrd 120
QY 121 YSNWNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVTS 180
Db 121 ysnwnwyfdv wqgl tvvssastkgpsvfplapssktsstgtaalgclvkd yfpeptvts 180
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
Db 181 wnsгалтsgvhtfpav lqssglys lssv tvtpssslgtqt yicnvnhkpsntkvdkrv ep 240
QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNW 300
Db 241 kscdkhtccp capellggpsvflfppkpkdtlmisrtpevtcvvyv dshedpevkfnw 300
QY 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHDWLNKGKEYCKVSNKALPAPIETKIS 360
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhdwlngkeyckvsnkalpapietkis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 361 kagqprepqv ytlppsreemtknqvsl tclvkgyf psdiave wesngqpennyktttppv 420
QY 421 LDSGSPFLYSLKLTVDKSRWQOGNWFSCSVNHEALHNYHTOKSLSPGK 470
Db 421 ldsdgsf flyskltvdksrwqognw fscsvnmheal hnyhtoksls pgk 470

RESULT 8
AAB14776
ID AAB14776 standard; Protein: 470 AA.
XX
AC AAB14776;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.

XX 30-SEP-1999; 99JP-0278301.
XX
XX 30-SEP-1998; 98JP-0276883.
PR
PA (SANY) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
DR N-PSDB; AAA72159.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
XX Claim 21; Page 95-96; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment
CC or diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;

Query Match 99.2%; Score 2498; DB 21; Length 470;
Best Local Similarity 99.1%; Pred. No. 2.5e-143;
Matches 466; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWVRQAP 60
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkpgasvkvsckasgyftsyymmqqvkgap 60
QY 61 GQGLEWNGEIDPDSYNTYNNOKFKGKATLTVDSTSTAYMELSLRSEDYAVYICARNRD 120
Db 61 gqglewngeidpsdysntynngkfkgkatltvdststaymelslrse dtavyyicarnrd 120
QY 121 YSNWNWYFDVWGQGLTVTVSSASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPTVTS 180
Db 121 ysnwnwyfdv wqgl tvvssastkgpsvfplapssktsstgtaalgclvkd yfpeptvts 180
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEP 240
Db 181 wnsгалтsgvhtfpav lqssglys lssv tvtpssslgtqt yicnvnhkpsntkvdkrv ep 240
QY 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNW 300
Db 241 kscdkhtccp capellggpsvflfppkpkdtlmisrtpevtcvvyv dshedpevkfnw 300
QY 301 YVDGVEVHNAKTKPREQYNSTYRVVSVLTVLHDWLNKGKEYCKVSNKALPAPIETKIS 360
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhdwlngkeyckvsnkalpapietkis 360
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 361 kagqprepqv ytlppsreemtknqvsl tclvkgyf psdiave wesngqpennyktttppv 420
QY 421 LDSGSPFLYSLKLTVDKSRWQOGNWFSCSVNHEALHNYHTOKSLSPGK 470
Db 421 ldsdgsf flyskltvdksrwqognw fscsvnmheal hnyhtoksls pgk 470

RESULT 9
AAW90926

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
PI WPI: 2000-258930/23.
DR N-PSDB; AAA11655.
XX
XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
PT inflammatory or autoimmune disease, induces apoptosis selectively in
PT cells with abnormal Fas-Fas ligand systems
XX
XX Claim 2: Page 188-189; 263pp; English.
XX
XX This invention describes a novel humanized anti-Fas antibody-like
CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
CC ligand system, by binding to Fas on the cell surface, and prevents
CC apoptosis in cells with a normal system, by inhibiting binding between
CC Fas and its ligand. The products of the invention have anti-inflammatory,
CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
CC immunomodulatory, dermatological, immunosuppressive, thrombolytic,
CC antirheumatic, nephrotropic, antifertility, neuroprotective,
CC antiarteriosclerotic, cardiac and hepatotropic activity. (I) induce
CC apoptosis by binding to cell surface Fas or inhibit it by competitive
CC inhibition of ligand binding. (I) are used to treat and/or prevent
CC diseases associated with the Fas/Fas ligand system, especially systemic
CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
CC versus host disease, Sjogren's syndrome, pernicious or hypoplastic
CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
CC inhibit apoptosis in normal cells but selectively induce it in abnormal
CC cells. They bind to both human and murine Fas, so can be evaluated in
CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
CC the native ligand, do not induce liver disease, and have reduced risk of
CC inducing a human anti-murine antibody response. This sequence represents
CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
CC which is described in the method of the invention.
XX
XX Sequence 470 AA:

Query Match 99.2%; Score 2498; DB 21; Length 470;
Best Local Similarity 98.9%; Pred. No. 2.5e-143;
Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWSCIIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 mgwscililflvatatgvsqvlqsgaevkpgasvkvsckasgytftsymbwvrrqap 60
Qy 61 GQGLEWMGEIDPDSYNTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYICARNRD 120
Db 61 gggglewmgeidpsdyntynqkfkgrvtrtdtsstaymelslrsedtavycarnrd 120
Qy 121 YSNWNYFDVWGQGLIVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 ysnwnyfdwdegltvtvssastkgpsvfplapssksts ggtaalgclvkdypfpvptvs 180
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240
Db 181 wnsгалtsгvhtfpavlgssglyslssvttvtpssslgqtqyicnvnhkpsntkvdkrvpe 240
Qy 241 KSCDKHTCCPPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkhtccppapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 300
Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVKSNKALPAPIETIS 360
Db 301 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvksnkalpapietis 360
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
Db 361 kakgqprepqvtytlppsreemtknqvsltclvkgfypsdiavewesngqpennkttppv 420

Db 361 kakgqprepqvtytlppsreemtknqvsltclvkgfypsdiavewesngqpennkttppv 420
Qy 421 LDSGGSFFLYSKLTVDKSRWQGNVFCVSVMHEALHNHYTQKSLSLSPK 470
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhcalhnhytqkslslspsgk 470
RESULT 11
AAM52156
ID AAM52156 standard; Protein; 731 AA.
XX
XX AAM52156;
AC
XX
XX 05-FEB-2002 (first entry)
DT
XX
XX Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
DE
XX
XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
XX Homo sapiens.
OS
XX
XX Synthetic.
OS
XX
XX WO200174905-A1.
PN
XX
XX 11-OCT-2001.
PD
XX
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX
XX 03-APR-2000; 2000GB-0008049.
XX
XX 02-OCT-2000; 2000US-237159P.
PR
XX
XX (ANTI-) ANTISOMA RES LTD.
XX
XX Young RJ;
PI
XX
XX WPI: 2001-662969/76.
DR
XX
XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity
XX
XX
XX Claim 20; Figure 7; 176pp; English.
PS
XX
XX The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
XX
XX Sequence 731 AA;

Query Match 93.3%; Score 2349.5; DB 22; Length 731;
Best Local Similarity 93.2%; Pred. No. 3.8e-134;
Matches 438; Conservative 19; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MGWSCIIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 mgwscililflvatatgvsqvlqsgaevkpgasvkvsckasgytftsymbwvrrqap 60
Qy 61 GQGLEWMGEIDPDSYNTYNNQKFKGKATLTVDTSSTAYMELSSLRSEDVAVYICARNRD 120
Db 61 gggglewmgeidpsdyntynqkfkgrvtrtdtsstaymelslrsedtavycarsyd 120
Qy 121 YSNWNYFDVWGQGLIVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 ysnwnyfdwdegltvtvssastkgpsvfplapssksts ggtaalgclvkdypfpvptvs 177
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGQTQYICNVNHHKPSNTKVDKRVPE 240
Db 181 wnsгалtsгvhtfpavlgssglyslssvttvtpssslgqtqyicnvnhkpsntkvdkrvpe 240

|||||
Db 178 wnsгалtsghvfapvlgssylslsvvtpssslgtqtyicnvnhkpsntckvdkkvep 237
QY 241 KSCDKTHTCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300
Db 238 kscdkhtcpcpcapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREOYNSTYRVVSVLTVTLHODWLNKGKCKVSNKALPAPIETKTS 360
Db 298 yvdgvevhnaktkpreeqnystyrvvsvltvlnhqdwlngkeyckvsnkalpapietkts 357
QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 358 kagqgpreqvvtlppsrdeitcknqvsitclvkgfypsdiavewesngqpennnykttppv 417
QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 418 ldsdgsfflyskltvdksrwggnvfscsvmhealhnhytqkslsispkg 467

RESULT 12
AAM52159
ID AAM52159 standard; Protein; 741 AA.
AC AAM52159;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 4.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity -
XX
PS Claim 20; Figure 10; 176pp; English.
XX
CC The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
XX
SQ Sequence 741 AA;

Query Match 93.3%; Score 2349.5; DB 22; Length 741;
Best Local Similarity 93.2%; Pred. No. 3.8e-134;
Matches 438; Conservative 19; Mismatches 10; Indels 3; Gaps 1;

QY 1 MGWSCIILFLVATGVHSQVLQVSGAERKPKGSKVSKASGYTFTSYWQWVRQAP 60
Db 1 mgwscililflvatgvhsqvlvsgaerkkpgskvskasgytftsaywiewrqp 60
QY 61 GCGLEMMGEIDPSDSTYNNYKFKGKATLVDTSTSTAYMELSSLSRSEDTAVYYCARNRD 120
Db 61 gkglewvgeilpgsnnsrynekfgrvtvtrdtstntaymelsslrsestavyycarsyd 120
QY 121 YSNWYFVWVGOGTLTVYSSASTKGPSVPLAPSSKSTSGGTAALGCLVLDYFEPVTVS 180
Db 121 fa---wfywgggtltvtssastkgpsvplapsskstsggtaalgclvdyfepvttvs 177
QY 181 WNSGALTSGVHTFPVAVLQSSGLYSLSVVTVPSSSSLGTQTYICNVNHKPSNTKVKDRVEP 240
Db 178 wnsгалtsghvfapvlgssylslsvvtpssslgtqtyicnvnhkpsntckvdkkvep 237
QY 241 KSCDKTHTCPCPCAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300
Db 238 kscdkhtcpcpcapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297
QY 301 YVDGVEVHNAKTPREOYNSTYRVVSVLTVTLHODWLNKGKCKVSNKALPAPIETKTS 360
Db 298 yvdgvevhnaktkpreeqnystyrvvsvltvlnhqdwlngkeyckvsnkalpapietkts 357
QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 358 kagqgpreqvvtlppsrdeitcknqvsitclvkgfypsdiavewesngqpennnykttppv 417
QY 421 LDSGSEFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 418 ldsdgsfflyskltvdksrwggnvfscsvmhealhnhytqkslsispkg 467

RESULT 13
AAM52158
ID AAM52158 standard; Protein; 729 AA.
XX
AC AAM52158;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 3.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX
OS Homo sapiens.
OS Synthetic.
PN WO200174905-A1.
XX
PD 11-OCT-2001.
XX
PF 26-MAR-2001; 2001WO-GB01324.
XX
PR 03-APR-2000; 2000GB-0008049.
PR 02-OCT-2000; 2000US-237159P.
XX
PA (ANTI-) ANTISOMA RES LTD.
XX
PI Young RJ;
XX
DR WPI; 2001-662969/76.
XX
PT Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity -
XX
PS Claim 20; Figure 9; 176pp; English.
XX
CC The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis.
XX
SQ Sequence 741 AA;

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 729 AA;

Query Match 93.1%; Score 2344.5; DB 22; Length 729;
Best Local Similarity 93.2%; Pred. No. 7.5e-134;
Matches 437; Conservative 19; Mismatches 10; Indels 3; Gaps 1;
Qy 1 MGWSCIIILFVATATGVSQVQLVQSGAEVKKPGASVKASKASYTFTSTWQWVRQAP 60
Db 1 mgwsciiilfvatatgvsqvlvqsgaevkpgasvkaskasytftsaywiewvrdqap 60
Qy 61 GQLEWMEIDPDSYTYNOKFKGKATLTVDTSSTAYMELSSLRSEDATVYYCARNRD 120
Db 61 gglewmeidpdsytynokfkgkatltvdtsstaymelslsrseadtavyycarsyd 120
Qy 121 YSNWNYFDWQGGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvts 177
Qy 181 WNSGALTSGVITFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRV 240
Db 178 wnsгалтsgvitfpavlgssglyslsvtvtpssslgtqtyicnvnhkpsntkvdkkv 237
Qy 241 KSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 238 kscdkthcpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297
Qy 301 YVDGVEVHNATKPREOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 360
Db 298 yvdgevhnatkpreedynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420
Db 358 kakgqprepqvytlppsrdeltknqslclvkgfypsdiavewesngqpennykttppv 417
Qy 421 LDSGSPFLYSLKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPG 469
Db 418 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispg 466

RESULT 14
AAM52161
ID AAM52161 standard; Protein; 739 AA.
XX

AC AAM52161;

XX 05-FEB-2002 (first entry)

XX Humanised HMEG-1 heavy chain/DNase I fusion protein 6.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX

OS Homo sapiens.

OS Synthetic.

XX WO200174905-A1.

XX 11-OCT-2001.

XX 26-MAR-2001; 2001WO-GB01324.

XX 03-APR-2000; 2000GB-0008049.

XX 02-OCT-2000; 2000US-237159P.

XX (ANTI-) ANTISOMA RES LTD.

XX

PI Young RJ;

XX WPI; 2001-662969/76.

XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX

PS Claim 20; Figure 12; 176pp; English.

XX The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX

SQ Sequence 739 AA;

Query Match 93.1%; Score 2344.5; DB 22; Length 739;
Best Local Similarity 93.2%; Pred. No. 7.6e-134;
Matches 437; Conservative 19; Mismatches 10; Indels 3; Gaps 1;

Qy 1 MGWSCIIILFVATATGVSQVQLVQSGAEVKKPGASVKASKASYTFTSTWQWVRQAP 60

Db 1 mgwsciiilfvatatgvsqvlvqsgaevkpgasvkaskasytftsaywiewvrdqap 60

Qy 61 GQLEWMEIDPDSYTYNOKFKGKATLTVDTSSTAYMELSSLRSEDATVYYCARNRD 120

Db 61 gglewmeidpdsytynokfkgkatltvdtsstaymelslsrseadtavyycarsyd 120

Qy 121 YSNWNYFDWQGGTLVTYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180

Db 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepvts 177

Qy 181 WNSGALTSGVITFPAVLQSSGLYSLSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKRV 240

Db 178 wnsгалтsgvitfpavlgssglyslsvtvtpssslgtqtyicnvnhkpsntkvdkkv 237

Qy 241 KSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300

Db 238 kscdkthcpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297

Qy 301 YVDGVEVHNATKPREOYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI 360

Db 298 yvdgevhnatkpreedynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357

Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 420

Db 358 kakgqprepqvytlppsrdeltknqslclvkgfypsdiavewesngqpennykttppv 417

Qy 421 LDSGSPFLYSLKLTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPG 469

Db 418 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispg 466

RESULT 15

AAM52157

ID AAM52157 standard; Protein; 730 AA.

XX AAM52157;

XX 05-FEB-2002 (first entry)

XX Humanised HMEG-1 heavy chain/DNase I fusion protein 2.

XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
XX

OS Homo sapiens.

Search completed: August 14, 2002, 15:15:40
Job time: 838 sec

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OS Synthetic.
XX WO200174905-A1.
XX PD 11-OCT-2001.
XX PF 26-MAR-2001; 2001WO-GB01324.
XX PR 03-APR-2000; 2000GB-0008049.
XX PR 02-OCT-2000; 2000US-237159P.
XX PA (ANTI-) ANTISOMA RES LTD.
XX PI Young RJ;
XX WPI; 2001-662969/76.
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity
XX Claim 20; Figure 8; 176pp; English.
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX compound has cytostatic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX Sequence 730 AA;
SQ
Query Match 92.9%; Score 2338.5; DB 22; Length 730;
Best Local Similarity 93.2%; Pred. No. 1.7e-133;
Matches 436; Conservative 19; Mismatches 10; Indels 3; Gaps 1;
QY 1 MGWSCIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVCKRSGYFTSYWMQWVRQAP 60
DB 1 mgwscililflvatatgvhsqqlvqsgaevkpgasvkvsckasgytfsaywiewvraqp 60
QY 61 GQGLEWMGEIDSDSTNYNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYICARNRD 120
DB 61 gkglewvgeilpgsnnsrynekfgrvtvtrdtstntaymelsslrse dtavvycarsyd 120
QY 121 YSNWYFDYVGQTLVTSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 121 fa---wfywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdyfpeptvts 177
QY 181 WNSGALTSVHTFPFPAVLQSGLYSLSSVTVSPSSSLGTQYICNVNHRKPSNTKVKDKRVEP 240
DB 178 wnsгалtsvghtfpavqlqsglyslssvstvpssslgtqtyicnvnhkpsntkvdkkvep 237
QY 241 KSCDKTHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300
DB 238 kscdkthtccpcpapellggpsvflfppkpkdtlmsrtpevtcvvvdvshedpevkfnw 297
QY 301 YVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
DB 298 yvdgvevhnaktkreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 357
QY 361 KAKGPQEPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPV 420
DB 358 kagqppepqvyltppsrdeltknqvsitclvkgyfypsdiavewesngqpennnykttppv 417
QY 421 LQSDGSFFLYSKLTVDKSRWQQGNVFCSMVHEALHNHYTQKSLSLSP 468
DB 418 ldsdgsfflyskltvdksrwqggnvfscsmvhealhnhytqkslsislsp 465
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:17:06 ; Search time 82.88 Seconds
(without alignments)
138.514 Million cell updates/sec

Title: US-09-499-662-147
Perfect score: 2517
Sequence: 1 MGWSCIILFLVATATGVHSQ.....MHEALHNYTKSLSPCK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2235	88.8	449	1	US-08-458-516-13
2	2233	88.7	476	2	US-08-378-939-10
3	2205.5	87.6	467	4	US-09-049-672A-8
4	2203.5	87.5	452	3	US-09-027-449-71
5	2203.5	87.5	452	4	US-09-026-985-71
6	2174	86.4	468	4	US-09-485-737B-67
7	2174	86.4	711	4	US-09-485-737B-90
8	2158.5	85.8	454	2	US-07-934-373C-22
9	2158.5	85.8	454	3	US-08-437-642B-22
10	2158.5	85.8	454	5	PCT-US93-07832-22
11	2147	85.3	472	4	US-08-793-450-8
12	2127	84.5	451	2	US-08-887-352B-14
13	2127	84.5	451	2	US-08-887-352B-16
14	2127	84.5	451	3	US-08-466-151-65
15	2127	84.5	451	4	US-09-109-207C-14
16	2127	84.5	451	4	US-09-109-207C-16
17	2127	84.5	451	4	US-09-296-005-14
18	2127	84.5	451	4	US-09-296-005-16
19	2124	84.4	478	3	US-08-487-550-8
20	2119	84.2	451	2	US-08-887-352B-18
21	2119	84.2	451	4	US-09-109-207C-18
22	2119	84.2	451	4	US-09-282-505-2
23	2119	84.2	451	4	US-09-054-255-2
24	2119	84.2	451	4	US-09-296-005-18
25	2108	83.8	453	3	US-08-466-151-8
26	2108	83.8	453	4	US-08-466-163B-8
27	2106.5	83.7	467	2	US-07-916-098A-45

28	2105.5	83.7	449	4	US-09-679-397-2	Sequence 2, Appl
29	2102.5	83.5	552	5	PCT-US93-07832-23	Sequence 23, Appl
30	2099.5	83.4	469	2	US-07-934-373C-23	Sequence 23, Appl
31	2099.5	83.4	469	3	US-08-437-642B-23	Sequence 23, Appl
32	2096	83.3	451	4	US-03-247-352-3	Sequence 3, Appl
33	2093.5	83.2	459	1	US-08-157-101A-7	Sequence 7, Appl
34	2073.5	82.5	467	1	US-08-704-744-81	Sequence 81, Appl
35	2073.5	82.4	473	4	US-09-049-672A-4	Sequence 4, Appl
36	2063.5	82.0	445	4	US-08-341-560B-17	Sequence 17, Appl
37	2057.5	81.7	446	3	US-08-397-411-7	Sequence 7, Appl
38	2057	81.7	476	3	US-08-487-550-12	Sequence 12, Appl
39	2025	80.5	442	5	PCT-US96-10043-9	Sequence 9, Appl
40	2025	80.5	476	3	US-08-487-550-4	Sequence 4, Appl
41	2013	80.0	442	1	US-08-461-968A-5	Sequence 5, Appl
42	2013	80.0	442	2	US-08-462-571-5	Sequence 5, Appl
43	1998.5	79.4	450	2	US-08-788-800-12	Sequence 12, Appl
44	1989	79.0	442	1	US-08-480-036-2	Sequence 2, Appl
45	1989	79.0	442	1	US-08-461-968A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: TSO, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-13

Query Match 88.8%; Score 2235; DB 1; Length 449;
Best Local Similarity 93.3%; Pred. No. 6,6e-159;
Matches 421; Conservative 13; Mismatches 15; Indels 2; Gaps 2;

QY 20 QVOLVSGAEVKKPGASVKKVSKASGYTFTSYWMQVROAPGQGLEWMGIDPSDSTYNY 79
Db 1 QVOLVSGAEVKKPGASVKKVSKASGYTFTSYWMQVROAPGQGLEWMGIDPSDSTYNY 60
QY 80 NQKFKGKATLTDSTSTAYMELSLRSEDATAYYCARNRDYNNHYFDVWGQGTILTVTS 139
Db 61 NQKFKGKATLTDSTSTAYMELSLRSEDATAYYCARNRDYNNHYFDVWGQGTILTVTS 118
QY 140 SASTKGPSVFLPAPSSKSTSGGTAALGCLVGVKDYFPPVTVSNWNGALTSQVHFFPAVLQS 199
Db 119 SASTKGPSVFLPAPSSKSTSGGTAALGCLVGVKDYFPPVTVSNWNGALTSQVHFFPAVLQS 178
QY 200 SGLYSLSSVTVVSSSLGQTQYICNVNHNKPSNTKVDKRVKPSKCDKTHTCPPCAPPELLG 259
Db 179 SGLYSLSSVTVVSSSLGQTQYICNVNHNKPSNTKVDKRVKPSKCDKTHTCPPCAPPELLG 238
QY 260 GPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVNNAKTKPREQY 319
Db 239 GPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVNNAKTKPREQY 298
QY 320 NSTYRVVSVLTVLHQDWLNGKEYCKVKVSNKALPAPTEKTIKAKGQPREPOVYTLPPSRE 379
Db 299 NSTYRVVSVLTVLHQDWLNGKEYCKVKVSNKALPAPTEKTIKAKGQPREPOVYTLPPSRE 358
QY 380 EMTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 439
Db 359 EMTKNQVSLTCLVKGPYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 418
QY 440 WQGNVFCFSVHVALHNNHYTKSLSLSPGK 470
Db 419 WQGNVFCFSVHVALHNNHYTKSLSLSPGK 449

RESULT 2

US-08-378-939-10
; Sequence 10, Application US/08378939
; Patent No. 587961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT
; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-378-939-10

Query Match 88.7%; Score 2233; DB 2; Length 476;
Best Local Similarity 88.7%; Pred. No. 1e-150;
Matches 422; Conservative 20; Mismatches 28; Indels 6; Gaps 1;

QY 1 MGWSCILFLVLTATATGSHQVQLVQSGAEVKKPGASVKKVSKASGYTFTSYWMQVROAP 60
Db 1 MDWTWRFELFVAAATGVQSQMQLVQSGAEVKKPGASVKKVSKASGYTFTSYWMQVROAP 60
QY 61 GQGLEWMGIDPSDSTYNYNQKFKGKATLTDSTSTAYMELSLRSEDATAYYCARNR- 119
Db 61 GQGLEWMGIIPLFGTPTYSQNFQGRVTTADKSTSTAHMELTSLRSEDATAYYCATDRY 120
QY 120 ----DYSNNWTFDVMWGQGTILTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVXDYFP 174
Db 121 RQANFDRARVGVFDPWVGQGTILTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVXDYFP 180
QY 175 EPTVTVSNWNGALTSQVHFFPAVLQSSGLYSLSVTVVTPSSSLGQTQYICNVNHNKPSNTKV 234
Db 181 EPTVTVSNWNGALTSQVHFFPAVLQSSGLYSLSVTVVTPSSSLGQTQYICNVNHNKPSNTKV 240
QY 235 DKRVKPSKCDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDP 294
Db 241 DKRVKPSKCDKTHTCPPCAPPELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDP 300
QY 295 EVKFNWYDGVGVNNAKTKPREQYNSYRVVSVLTVLHQDWLNGKEYCKVKVSNKALPAP 334
Db 301 EVKFNWYDGVGVNNAKTKPREQYNSYRVVSVLTVLHQDWLNGKEYCKVKVSNKALPAP 360
QY 355 IEKTSKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 414
Db 361 IEKTSKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 420
QY 415 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVHVALHNNHYTKSLSLSPGK 470
Db 421 KTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCFSVHVALHNNHYTKSLSLSPGK 476

RESULT 3

US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ceirone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LUNGUT11
; CLONE: 2747531
; US-09-049-672A-8

Query Match      87.6%; Score 2205.5; DB 4; Length 467;
Best Local Similarity 89.4%; Pred. No. 1.1e-156;
Matches 415; Conservative 18; Mismatches 28; Indels 3; Gaps 1;

Qy 7 ILFLVATATGVHVSQVLQVSGAEYKKGASVYKSCASGYTFTSYMMQWVRQAPGQGLEW 66
Db 7 ILFLVAAATGTHAQVLQVSGAEYKKGASVYKSCASGYTFTSYMMQWVRQAPGQGLEW 66
Qy 67 MGEIDPSDSYNYKQKFKGKATLVDTSTAYMELSLRSEDYAVYCARNRDYSNNY 126
Db 67 MGLAPENGEAYAKFLGRLTSEDTSADTAYMFLNNGSDESAIYYCARQH---YDFF 123
Qy 127 FDVWGQGLTVTVSSASVYKGPVFLAPSSKSTSGTAAALGCLVKDYRPPVTVSNWNGAL 186
Db 124 FDFWGQGTMTVTVSSASVYKGPVFLAPSSKSTSGTAAALGCLVKDYRPPVTVSNWNGAL 183
Qy 187 TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKSCDKT 246
Db 184 TSGVHTFPVAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKSCDKT 243
Qy 247 HTCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 306
Db 244 HTCPCPAPELLGGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVE 303
Qy 307 VHNARTKPREQYNTYRVVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAKGP 366
Db 304 VHNARTKPREQYNTYRVVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAKGP 363
Qy 367 REPOVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPVLDSDGS 426
Db 364 REPOVYTLPPSREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTTTPVLDSDGS 423
Qy 427 FFLYSLKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 424 FFLYSLKLTVDKSRQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 4
US-09-027-449-71
; Sequence 71, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way

```

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: PI085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-71

Query Match      87.5%; Score 2203.5; DB 3; Length 452;
Best Local Similarity 90.3%; Pred. No. 1.5e-156;
Matches 408; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

Qy 20 QVLQVSGAEYKKGASVYKSCASGYTFTSYMMQWVRQAPGQGLEWGEIDPSDSYNY 79
Db 1 EVQLVQSGGLVQPGSLRLSCAASGYSFSSHYMHWRQAPGKGLWVGYYIDPSNGEITY 60
Qy 80 NQKFKGKATLVLDVDTSTAYMELSLRSEDYAVYCAR-NRDYSNNWYFDVWGQGLTVTV 138
Db 61 NQKFKGRTLSRDNSKNTAYLQMNSLRAEDTAVYVCARGDYRYNGDFWDFVWGQGLTVTV 120
Qy 139 SSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYRPPVTVSNWNGALTSGVHTFPVAVLQ 198
Db 121 SSASTKGPSVFLAPSSKSTSGTAAALGCLVKDYRPPVTVSNWNGALTSGVHTFPVAVLQ 180
Qy 199 SSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKSCDKTHTCCPCPAPELL 258
Db 181 SSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKSCDKTHTCCPCPAPELL 240
Qy 259 GGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREQ 318
Db 241 GGPSVFLFPPPKDRLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREQ 300
Qy 319 YNSTYRVVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAGQPREPOVYTLPPSR 378
Db 301 YNSTYRVVSVLVTLVHODWLNKGYCKVSNKALPAPIETKISKAGQPREPOVYTLPPSR 360
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 438
Db 361 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 420
Qy 439 RWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 RWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 452

RESULT 5
US-09-026-985-71

```

; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-71

Query Match 87.5%; Score 2203.5; DB 4; Length 452;
Best Local Similarity 90.3%; Pred. No. 1.5e-156;
Matches 408; Conservative 26; Mismatches 17; Indels 1; Gaps 1;
QY 20 QYLVQSGAEVKKPGASVKSVCASGYTFSTYMMQVWVROAPGQGLWMEIDPDSYTNV 79
DB 1 EYLVQSGGGLVQPGSLRLSCAASGYSFSSHYMHVWVROAPGKLEWGYIDPSNGETTY 60
QY 80 NQKFKGKATLVDTSTSTAYMELSLRSEDATVYICAR-NRDYSNNWYEDVWGQGTLVTV 138
DB 61 NQKFKGRFTLSRDNSKNTAYLQMNLSRAEDATVYICARGDYRNGDWFFDVWGQGTLVTV 120
QY 139 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSYGHTTFAVLQ 198
DB 121 SSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSYGHTTFAVLQ 180
QY 199 SSGLYSLSSVWTVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDKTKTCPCPAPELL 258
DB 181 SSGLYSLSSVWTVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDKTKTCPCPAPELL 240
QY 259 GGPSVFLFPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYDGVVEVHNKTKPREQ 318
DB 241 GGPSVFLFPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYDGVVEVHNKTKPREQ 300
QY 319 YNSTRVVSVLVTHODWLNKGKCKVSNKALPAIEKTIKAKGCPREPQVYTLPPSR 378
DB 301 YNSTRVVSVLVTHODWLNKGKCKVSNKALPAIEKTIKAKGCPREPQVYTLPPSR 360
QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 438
DB 361 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKS 420
QY 439 RMOQGNVFCSCVMHEALHNHYTKLSLSPGK 470

DB 421 RMOQGNVFCSCVMHEALHNHYTKLSLSPGK 452
RESULT 6
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-67

Query Match 86.4%; Score 2174; DB 4; Length 468;
Best Local Similarity 88.0%; Pred. No. 2.5e-154;
Matches 409; Conservative 21; Mismatches 31; Indels 4; Gaps 1;
QY 6 IILFLVATATGTVHSGVQLVQSGAEVKKPGASVKSVCASGYTFSTYMMQVWVROAPGQGLE 65
DB 7 IFSELLISASVILSQVLQSGSELKKPGASVKSVCASGYTFDYGMNVKQAPQGGLK 66
QY 66 WGEIDPDSYTNVYKQFKGKATLVDTSTSTAYMELSLRSEDATVYICARNRDIYNNW 125
DB 67 WMGWINTYTGESTYVDDFGRFVFLSDTSVSAAYLQISLKAEDTATYFCARRGFYA--- 123
QY 126 YEDVWGQGTLVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 185
DB 124 -MDYWGQGTLVTVSSASTKGPSVFFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 182
QY 186 LTSGVHTTFAVLQSSGLYSLSSVWTVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDK 245
DB 183 LTSGVHTTFAVLQSSGLYSLSSVWTVPSSSLGTQYICNVNHPKSNKTKVDRKVEPKSCDK 242
QY 246 THTCPPCPAPELLGGPSVFLFPPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYDGV 305
DB 243 THTCPPCPAPELLGGPSVFLFPPKPKDLMISRTPVTCVVDVSHEDPEVKFNWYDGV 302
QY 306 EYHNKTKPREQYNSTYRVVSVLVTHODWLNKGKCKVSNKALPAIEKTIKAKGQ 365
DB 303 EYHNKTKPREQYNSTYRVVSVLVTHODWLNKGKCKVSNKALPAIEKTIKAKGQ 362
QY 366 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 425
DB 363 PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDG 422
QY 426 SFELYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 470
DB 423 SFELYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSPGK 467

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B

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; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

```

```

Query Match      86.4%; Score 2174; DB 4; Length 711;
Best Local Similarity 88.0%; Pred. No. 4.3e-154;
Matches 409; Conservative 21; Mismatches 31; Indels 4; Gaps 1;

```

```

QY 6 IILFLVATGVSQVQVQSGAEVKKPGASVKASKASYGTTSTYMWQVVRQAPQGLE 65
DB 7 IFGLISASVILQVQVQSGSELKPGASVKISKASYGTTFTDGMNWKQAPQGLK 66
QY 66 WMGEIDPSDYTNKQFKATLTVDSTSTAYMELSLRSEDYVYICARNRDYNNW 125
DB 67 WMGWINTYGESYVDDFKGRFVSLDTSVAAYLQISSLKAEATATYFCARRGFYA 123
QY 126 YFDVWQOGLTVYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGA 185
DB 124 -MDYWGQGTFTVYSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGA 182
QY 186 LTSVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKRVEPKSCDK 245
DB 183 LTSVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKRVEPKSCDK 242
QY 246 THTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV 305
DB 243 THTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGV 302
QY 306 EVHNAKTKPREQYNSTIRYVSVLTCLVHQLDNLNGKEYCKVSNKALPAPAEKTIKRAKGQ 365
DB 303 EVHNAKTKPREQYNSTIRYVSVLTCLVHQLDNLNGKEYCKVSNKALPAPAEKTIKRAKGQ 362
QY 366 PREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDG 425
DB 363 PREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDG 422
QY 426 SFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
DB 423 SFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 467

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RESULT      8
US-07-934-373C-22
; Sequence 22, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:

```

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; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA: 07/715272
; APPLICATION NUMBER:
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-22

```

```

Query Match      85.8%; Score 2159.5; DB 2; Length 454;
Best Local Similarity 89.2%; Pred. No. 3.4e-153;
Matches 405; Conservative 18; Mismatches 28; Indels 3; Gaps 1;
QY 20 QVOLVQSGAEVKKPGASVKASKASYGTTSTYMWQVVRQAPQGLEWMEITDPSDSTNY 79
DB 1 QVOLQSGPELVKPGASVKISKCTGYTFTYTHHMKQSHGKSLWIGFNPKNKGGSSH 60
QY 80 NQKFKGKATLTVDSTSTAYMELSLRSEDYVYICARNRDYNNW---YFDVWQOGLTV 136
DB 61 NQRFMDKATLAVDKSTSTAYMELSLRSEDYVYICARNRDYNNWYFDVWQOGLTV 120
QY 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 196
DB 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 180
QY 197 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKRVEPKSCDKTKTCPCPAPE 256
DB 181 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKYDKRVEPKSCDKTKTCPCPAPE 240
QY 257 LLGSPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPRE 316
DB 241 LLGSPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPRE 300
QY 317 EYQNSTYRVVSVLTCLVHQLDNLNGKEYCKVSNKALPAPAEKTIKRAKGQPREPOVYTLPP 376
DB 301 EYQNSTYRVVSVLTCLVHQLDNLNGKEYCKVSNKALPAPAEKTIKRAKGQPREPOVYTLPP 360
QY 377 SREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYSKLTV 436
DB 361 SREEMTKNQVSLTCLVKGYFSPDIAVEWESNGOPENNYKTTTPVLDSDGSEFFLYSKLTV 420
QY 437 KSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
DB 421 KSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 454

```

RESULT 9
 US-08-437-642B-22
 ; Sequence 22, Application US/08437642B
 ; Patent No. 6054297
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul J. Carter
 ; APPLICANT: Leonard G. Presta
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/437,642B
 ; FILING DATE: 09-May-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/934373
 ; FILING DATE: 21-AUG-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/146206
 ; FILING DATE: 17-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/05126
 ; FILING DATE: 15-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/715272
 ; FILING DATE: 14-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0709P2C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 454 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; IS-08-437-642B-22

Query Match	85.8%;	Score	2158.5;	DB	3;	Length	454;
Best Local Similarity	89.2%;	Pred.	No. 3.4e-153;				
Matches	405;	Conservative	18;	Mismatches	28;	Indels	3;
Gaps							
QY	20	QVQLVQSGAEVKKPGASVKSCASGYYFTSYVMQWVRQAPGQGLEWNGEIDPDSDSYTNY	79				
DB	1	QVQLQSGPELVKPGASVKISCKTSGYFTETYMHWKQSHGKSLIEWIGGNPKNGGSSH	60				
QY	80	NQKFKGKATLVDTSTSTAYMELSLRSEDATVAYVCARNRDYSNNW---	136				
DB	61	NOREFMDKATLAVDKSTSTAYMELRLSITSDSGIYYCAWRGRLNYGDFRYDFVMGAGTIV	120				
QY	137	TVSSASTKGPSVFPEPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWSGALTSGVHTFPFV	196				
DB	121	TVSSASTKGPSVFPEPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWSGALTSGVHTFPFV	180				
QY	197	LOSSGLYLSLSSVTVVPSSLSGTQTYICNVNHNKPSNTKVDKRVKPSCKDKTTCPCCPAPE	256				
DB	181	LOSSGLYLSLSSVTVVPSSLSGTQTYICNVNHNKPSNTKVDKRVKPSCKDKTTCPCCPAPE	240				
QY	257	LAGGGSVFLFPEPKPKDITLMISRTPEVTCVVDVDSHEDPEVKFNWTVDGVGVHNAKTKPRE	316				

```

Query Match      85.8%; Score 2150.5; DB 5; Length 454;
Best Local Similarity 89.2%; Pred. No. 3.4e-153;
Matches 405; Conservative 18; Mismatches 28; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKSCASGYFTFTSYNMQWVRQAPGQGLEWMGIEDPDSYINY 79
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLVQSGPELVKPGASVKISCTSTGYTFEYTHMHWKQSHGKSLGIGGPNPNKGGSSH 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QV 80 NQKFKGKATLVDTSTSTAYMELSSLSRSEDATVYICARNRDYSNNW---YFDVWGQGFLV 136

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Db 61 NQFMDKATLAVDKSTSTAYMELSLTSEDSGIIYICARWGLNGYFVRYFDVWGAGTV 120
Qy 137 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFFPEPVTVSNWSGALTSGVHTFPAP 196
Db 121 TVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFFPEPVTVSNWSGALTSGVHTFPAP 180
Qy 197 LQSGLYSLSSVTVVPSSSLGTQYIYICNVNHPKSNKVDKRVKPKSCDKTHTCPCPAP 256
Db 181 LQSGLYSLSSVTVVPSSSLGTQYIYICNVNHPKSNKVDKRVKPKSCDKTHTCPCPAP 240
Qy 257 LLGGSVFLFPKPKDTHMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKTRPE 316
Db 241 LLGGSVFLFPKPKDTHMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNKTRPE 300
Qy 317 EQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPP 376
Db 301 EQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPIEKTSKAKGQPREPQVYTLPP 360
Qy 377 SREEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 436
Db 361 SREEMTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVD 420
Qy 437 KSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 470
Db 421 KSRWQGNVFCSCVMHEALHNNHYTKLSLSPGK 454

RESULT 11
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABAHLI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-793-450-8

Query Match 85.3%; Score 2147; DB 4; Length 472;
Best Local Similarity 85.18; Pred. No. 2.6e-152;
Matches 404; Conservative 26; Mismatches 37; Indels 8; Gaps 3;
Qy 1 MGWSCIIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSKKASGYTFTSYMMQWRQAP 60
Db 1 MGWSCIIILFLVATATGVHSGAELVQSGAEVKKPGASVKVSKKASGYTFTSYMMQWRQAP 60
Qy 61 GGLGEMGEIDPSDSTYNNQKFKGKATLTVDSTSTAYMELSSRSDTAVIYICARNRD 120
Db 61 GGLGEMGEIDPSDSTYNNQKFKGKATLTVDSTSTAYMELSSRSDTAVIYICARNRD 119
Qy 121 YSNWN-----YFDVMGQGLTVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPE 175
Db 120 Y--FKYHGDWFDWQGGTTTVTVSSASTKGPVFPPLAPSSKSTSGGTAALGCLVKDYFPE 177
Qy 176 PVTYSNWSGALTSGVHTFPAPVLSQSGLYSLSSVTVVPSSSLGTQYIYICNVNHPKSNKVD 235
Db 178 PVTYSNWSGALTSGVHTFPAPVLSQSGLYSLSSVTVVPSSSLGTQYIYICNVNHPKSNKVD 237
Qy 236 KRVEPKSCDKTHTCPCPAPPELLGQPSVFLPPPKDKDTLMISRTPEVTCVVVDVSHEDPE 295
Db 238 KKAEPKSCDKTQTCPCPAPPELLGQPSVFLPPPKDKDTLMISRTPEVTCVVVDVSHEDPE 297
Qy 296 VKFNWYVDGVEVHNKTRPEEYQNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPI 355
Db 298 VKFNWYVDGVEVHNKTRPEEYQNSTYRVSVLTVLHODWLNKREYKCKVSNKALPAPI 357
Qy 356 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 415
Db 358 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 417
Qy 416 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSPGK 470
Db 418 TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKLSLSPGK 472
RESULT 12
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-14

Query Match 84.5%; Score 2127; DB 2; Length 451;
Best Local Similarity 87.8%; Pred. No. 7.4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVSGAEVKKPGASVKVSCKASGTYTTS-YWMQWVROAPQGGLWGEIDPDSYIN 78
Db 1 EVLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIROAPGKGLWVASI-TYDGSIN 59
QY 79 YNOKFKGKATLVTDSTAYMELSLRSEDATVYYCARNRDYSNNYFDVWGQGLTVTV 138
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTV 119
QY 139 SSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQ 179
QY 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPNTKVDKRVKPKSCDKTHTCPPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPNTKVDKRVKPKSCDKTHTCPPCPAPELL 239
QY 259 GGPVFLFPFKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPVFLFPFKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299
QY 319 YNSTYRWVSVLVTHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRWVSVLVTHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
QY 379 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 419
QY 439 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 470
Db 420 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 451

RESULT 13
US-08-887-352B-16
; Sequence 16, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-887-352B-16

Query Match 84.5%; Score 2127; DB 2; Length 451;
Best Local Similarity 87.8%; Pred. No. 7.4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

QY 20 QVQLVSGAEVKKPGASVKVSCKASGTYTTS-YWMQWVROAPQGGLWGEIDPDSYIN 78
Db 1 EVLVESGGGLVQPGGSLRLSCAVSYISITSGYSWNIROAPGKGLWVASI-TYDGSIN 59
QY 79 YNOKFKGKATLVTDSTAYMELSLRSEDATVYYCARNRDYSNNYFDVWGQGLTVTV 138
Db 60 YNPVSKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHHFAVWGQGLTVTV 119
QY 139 SSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPVFPPLAPSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLQ 179
QY 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPNTKVDKRVKPKSCDKTHTCPPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNKPNTKVDKRVKPKSCDKTHTCPPCPAPELL 239
QY 259 GGPVFLFPFKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPVFLFPFKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299
QY 319 YNSTYRWVSVLVTHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
Db 300 YNSTYRWVSVLVTHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 359
QY 379 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 438
Db 360 EEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSLKLTVDKS 419
QY 439 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 470
Db 420 RMQOGNVFSCVSMHEALHNNHYTKLSLSPGK 451

RESULT 14
US-08-466-151-65
; Sequence 65, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/466163
;; FILING DATE: 06-Jun-1995
;; APPLICATION NUMBER: 08/405617
;; FILING DATE: 15-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/185899
;; FILING DATE: 26-JAN-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/879495
;; FILING DATE: 07-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/744768
;; FILING DATE: 14-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Svoboda, Craig G.
;; REGISTRATION NUMBER: 39, 044
;; REFERENCE/DOCKET NUMBER: P0718P2C1D1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1489
;; TELEFAX: 650/952-9881
;; INFORMATION FOR SEQ ID NO: 65:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 451 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-08-466-151-65

Query Match 84.5%; Score 2127; DB 3; Length 451;
Best Local Similarity 87.8%; Pred. No. 7.4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVOLVQSGAEVKKPGASVKVSCKASGYFTFS-YMQWVRQAPGQGLEWMGEIDPSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSCYSNNWIRQAPGKGLEWVASI-TYDGSN 59
Qy 79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGLTVTV 138
Db 60 YNPVKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTV 119
Qy 139 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 198
Db 120 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPPAPELL 239
Qy 259 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHODWLNKGEYKCKYSNKKALPAPIEKTISKAKGQPREPOVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKYSNKKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 419
Qy 439 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-109-207C-14
; Sequence 14, Application us/09109207C
; Patent No. 617213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

;; FILE REFERENCE: P1123R1
;; CURRENT APPLICATION NUMBER: US/09/109,207C
;; CURRENT FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/051,554
;; PRIOR FILING DATE: 1997-07-03
;; NUMBER OF SEQ ID NOS: 44
;; SEQ ID NO 14
;; LENGTH: 451
;; TYPE: PRT
;; ORGANISM: Artificial
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-451
;; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-109-207C-14

Query Match 84.5%; Score 2127; DB 4; Length 451;
Best Local Similarity 87.8%; Pred. No. 7.4e-151;
Matches 397; Conservative 23; Mismatches 30; Indels 2; Gaps 2;

Qy 20 QVOLVQSGAEVKKPGASVKVSCKASGYFTFS-YMQWVRQAPGQGLEWMGEIDPSDSYTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSCYSNNWIRQAPGKGLEWVASI-TYDGSN 59
Qy 79 YNQKFKGKATLTVDSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGQGLTVTV 138
Db 60 YNPVKGRITISRDSDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQGLTVTV 119
Qy 139 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 198
Db 120 SSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKRVKPKSCDKHTHTCCPPAPELL 239
Qy 259 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHODWLNKGEYKCKYSNKKALPAPIEKTISKAKGQPREPOVYTLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNKGEYKCKYSNKKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKS 419
Qy 439 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 470
Db 420 RWOQGNVFSCSYMHHEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:08
Job time: 691 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:19:01 ; Search time 108.64 Seconds
(without alignments)
415.703 Million cell updates/sec

Title: US-09-499-662-147
Perfect score: 2517
Sequence: 1 MWSCIIILFLVATATGVHSQ.....MHEALHHYTKSLSPCK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.1	377	2 A60764	Ig gamma-3 chain C
4	1610.5	64.0	469	2 S37483	Ig gamma-2a chain
5	1610	64.0	326	1 G2HU	Ig gamma-2 chain C
6	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
7	1546	61.4	474	1 G2MS11	Ig gamma-2b chain
8	1544	61.3	446	2 S40295	Ig gamma-2a chain
9	1501.5	59.7	475	2 S01321	Ig gamma-2b chain
10	1477	58.7	470	2 S22080	Ig heavy chain pre
11	1470	58.4	472	2 S31459	Ig gamma-1 chain -
12	1435	57.0	374	2 S69339	Ig heavy chain v r
13	1429.5	56.8	444	2 PC4436	monoclonal antibod
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.5	234	2 PT0207	Ig gamma chain C r
18	1235	49.1	328	2 I47158	Ig gamma 1 chain C
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain C
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	46.0	289	1 G3H0W1	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G1MSC	Ig gamma-3 chain C
26	1145	45.5	324	1 G1MS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain
28	1140	45.3	393	1 G1MSM	Ig gamma-1 chain C
29	1139	45.3	398	1 G3MSM	Ig gamma-3 chain C

RESULT 1
GHU

Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence-revision 18-Aug-1982 #text-change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berison, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: Implications for evolution of

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

* C; keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin homology <IMM>

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Query Match          65.1%; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 2.8e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

Qy 141 ASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ASTKGPSVFPLAPCSRSTSGTGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

Qy 201 GLYSLSVVTVTPSSSLGTQYICNVNHPKSTKVDKRV----- 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GLYSLSVVTVTPSSSLGTQYICNVNHPKSTKVDKRVKLTPLGLDTHTCPRCPPEPKSC 120

Qy 239 -----EPKSDKTHTCPCPAPELLGGPSVFLFPPPKPDT 273
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 DTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPPKPDT 180

Qy 274 LMISRTPEVTCVVVDVSHEDPEVKFNQYVDSGEVFNHNAKTTPREQYNSTYRVVSVLTVLH 333
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKVYVDGEVFNHNAKTTPREQYNSTYRVVSVLTVLH 240

Qy 334 ODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRREEMTKNQVSLTCLVK 393
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ODWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRREEMTKNQVSLTCLVK 300

Qy 394 GFYPDSIAVEVESGQPNENYKTPPPVLDSDGSFFLYSLKLTVDKSRWQOGNPFVSCSVNHE 453
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GFYPDSIAVEVESGQPNENYKTPPPVLDSDGSFFLYSLKLTVDKSRWQOGNPFVSCSVNHE 360

Qy 454 ALHNHYTQKSLSLSPGK 470
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 ALHNRYTQKSLSLSPGK 377

RESULT 4
S37483
Ig gamma-2a chain - mouse
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Accession: S37483
R; Duncanson, F.F.D.
submitted to the EMBL Data Library, February 1993
A; Reference number: S37483
A; Accession: S37483
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-469 <DUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: immunoglobulin
F; 276-345/Domain: immunoglobulin homology <IMM>

Query Match          64.0%; Score 1610.5; DB 2; Length 469;
Best Local Similarity 64.4%; Pred. No. 1.2e-84;
Matches 304; Conservative 60; Mismatches 103; Indels 5; Gaps 4;

Qy 1 MGWSCIILFLVATYATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYFTFTSWMMQWRQAP 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MGWSIIFLLSAGTAGVHCQIQQLQSGPELVKPGASVKISCKASGYFTFTDYIYNWVKQP 60

Qy 61 GQGLEWMEIDPSDSTYNQKFKATLTVDSTSTAYMELSLRSEDTPAVYICARNRD 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GQGLKRWGIYPASGNTKYINENFGKATLTVDSTSTAYMQLSSLTSEDTPAVYFCARAMG 120

Qy 121 YNNWYIFDVMWGQTLTVTSSASTKGPSVFPLAPSSKTSSTGTAALGCLVKDYFPEPVTVS 180
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| :
Db 121 -ATATLLDYGQGTLLTVSSAKTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLT 179

Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTQYICNVNHPKSTKVDKRVPE 240
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Db 180 WNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSTICNVNHPASSTKVDKKTIEP 238
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 KSCDKTHTCTPP-CPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 298
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 RG-FTIRPCPCPKCPAPNLLGGPSVFPPPKIKDVLMLSLSPFITCVVVDVSEDDPDVQI 297
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 299 NWYVDGVEVHNNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 358
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 298 SWFNNVEVHTAQQTQTHREDYNSTLRVVSALPQIQHQMWSGKEFKCKVNNKDLPAPIERT 357
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 359 ISKAKGQPREPQVYITLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEVWESNGQPENNYKTP 418
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 ISKPKGSVRAPQVYITLPPPEEEMTKKQVTLCTMTDFPEDIYVEWTWNGKTELKYNKTE 417
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 419 PVLDSGDSFFLYSLKLTVDKSRWQOGNPFVSCSVNHEALHNHYTQKSLSLSPGK 470
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 PVLDSGDSFYFYSKLRYEKKNNVERNYSVCSVVHGLEHNNHHTKTSFSRTPGK 469
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
G2HU
Ig gamma-2 chain C region - human
C; Species: Homo sapiens (man)
C; Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C; Accession: A93906; A92809; A93132; A02148
R; Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A; Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain.
A; Reference number: A93906; MUID:82197621
A; Accession: A93906
A; Molecule type: DNA
A; Residues: 1-326 <ELL>
A; Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A; Note: Lys-326 is probably removed posttranslationally
R; Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A; Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, a
A; Reference number: A92809; MUID:81007873
A; Contents: myeloma protein T11
A; Accession: A92809
A; Molecule type: protein
A; Residues: 1-19, Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A; Note: Trp-156 is at or near the complement-binding site
R; Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A; Title: The amino acid sequences of the three heavy chain constant region domains of
A; Reference number: A90752; MUID:80001357
A; Contents: myeloma protein Zie
A; Accession: A90752
A; Molecule type: protein
A; Residues: 1-24, 'E', 26-57, 'EV', 60-85; 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 'L',
A; Note: this sequence has since been revised
R; Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A; Reference number: A93132; MUID:80114419
A; Contents: Zie
A; Accession: A93132
A; Molecule type: protein
A; Residues: 238-275 <HOF>
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A; Reference number: A94591
A; Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A; Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R; Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A; Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A; Reference number: A90253; MUID:72033500
A; Contents: annotation; myeloma protein Sa, disulfide bonds
R; Frangione, B.; Milstein, C.; Pink, J.R.L.
```


A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain
A:Reference number: A26235; MUID:80081501
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>
A:Note: Lys-474 is probably removed posttranslationally
R:Rucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain
A:Reference number: A26232; MUID:80081502
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain genes
A:Reference number: A26233; MUID:82173203
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
A:Cross-references: GB:000461
R:Kim, H.; Yamauchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359
A:Accession: A53598
A>Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
C:Genetics:
A:Introns: 138/1; 236/1; 258/1; 368/1
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:157-222/Domain: immunoglobulin C region; immunoglobulin homology
F:157-222/Domain: immunoglobulin C region; immunoglobulin homology
F:157-222/Domain: immunoglobulin C region; immunoglobulin homology
F:281-350/Domain: immunoglobulin C region; immunoglobulin homology
F:387-454/Domain: immunoglobulin C region; immunoglobulin homology
F:152/Disulfide bonds: interchain (to light chain) #status predicted
F:164-220,288-348,394-452/Disulfide bonds: #status predicted
F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.48; Score 1546; DB 1; Length 474;
Best Local Similarity 61.29; Pred. No. 5.8e-81;
Matches 292; Conservative 67; Mismatches 108; Indels 10; Gaps 3;

Qy 1 MGWSCIILFLVATATGTHSVQVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAP 60
Db 1 MENSWIFLLSCTAGVHSEVQLQSGPELVNPGASVKMSCKASGYTFTSYMMHWKQKP 60

Qy 61 QGGLWMEIDPSYTNYNOKFGKATLTVDSTSTAYMELSLRSDDTAIVYICARNRD 120
Db 61 QGGLWIGIYNPNKDGTKFNEKFKGKATLTSDKSNTAYMELSLTSDDSAIVYICARDYD 120

Qy 121 YSNWYFDVWQGLTLVTVSSASTKGPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
Db 121 YD---WFAYWQGLTLVTVSSAATTPPSYIPLAPCGDFTGSSVTSGCLVKGYFPESVFT 177

Qy 181 WNSGALTSVHTFAVLSGLSYSLSSVTVPSSSLTGTQYICNNHNPSTKVDKRVPE 240
Db 178 WNSGSLSSVHTLSQLQSLGSLYSSVTVPSSTWPSQVTCSVAHPASSTVTDKKLEP 237

Qy 241 KSCDKT-HTCPP-----CPAPELLGSPSVFLFPKPKDRLMISRTPEVTCTVVDVSHED 293
Db 238 SGPISTINPCPKCKECPAPNLEGGSPSVFLFPKPKDRLMISRTPEVTCTVVDVSHED 297

Qy 294 PEVFNWTVDGVVHNAKTPREQYNSTYKRVSVLTVLHODWLNKGYCKKVSNAKALPA 353

Db 298 PDVQISWFNVEVHTAQOTHRDYNSTIRVVSFLPIQHDQMSGKFKCVNKKDLPS 357
Qy 354 PIEKTISKAGOPREPQVYITLPPSREEMTKNOVSLTCLVGFYPSDIAVWESNGOPENN 413
Db 358 PIERTISKIKGLVRAPQVYITLPPPAEQLSRKDVSLTCLVGFNPGDISVETWTSNGTEEN 417
Qy 414 YKTPPVLDSDGSPFLYSKLTVDKSRWQGVNFGVSCVMHEALHNHYTKSLSPGK 470
Db 418 YKDTAPVLDSDGSPFIYSKLNKTKWETDSEFSCNVRHEGLKNYLLAKTKTSRSPGK 474

RESULT 8
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Kiebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 agl.in
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglyutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMH>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.38; Score 1544; DB 2; Length 446;
Best Local Similarity 64.4%; Pred. No. 7e-81;
Matches 291; Conservative 59; Mismatches 94; Indels 8; Gaps 4;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGQGLEWMGEIDPSDSTYNY 79
Db 1 QIQLQQSGPELVNPGASVKISCKASGYTFTDYIHWVKQRPGEGLWIGIYVPSGNTKY 60

Qy 80 NOKFKGKATLTVDSTSTAYMELSLRSDDTAIVYICARNRDYNNWYFDVWQGLTVTS 139
Db 61 NEKTAGKATLTVDSTSTAYMELSLRSDDTAIVYICARNRDYNNWYFDVWQGLTVTS 116

Qy 140 SASTKGPSVFLPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSVHTFAVLQS 199
Db 117 SAKTAPSVYIPLAPCGDFTGSSVTGLCLVKGYFPEPTVLTWNSGSLSSGVHTFAVLQS 176

Qy 200 SGLYSLSVTVTPSSSLGTQYICNNHNPSTKVDKRVKPEKCDKTTCTPP--CPAPEL 257
Db 177 D-LYTLSSSVTVTSSTWPSQSTICNVAPASSTKVDKKIEPRG-PTIKCPCKCPAPNL 234

Qy 258 LGGPSVFLFPKPKDRLMISRTPEVTCTVVDVSHEDPEVFNWTVDGVVHNAKTKPRE 317
Db 235 LGGPSVFLFPKPKDRLMISRTPEVTCTVVDVSHEDPEVFNWTVDGVVHNAKTKPRE 294

Qy 318 QYNSTIRVSVLTVLHODWLNKGYCKKVSNAKALPAIEKTSKAKGPRPQVITLPPS 377
Db 295 DYNSTIRVSVLTVLHODWLNKGYCKKVSNAKALPAIEKTSKAKGPRPQVITLPPS 354

Qy 378 REEMTKNOVSLTCLVGFYPSDIAVWESNGOPENNKTTPVLDSDGSPFLYSKLTVDK 437


```

RESULT 12
S69339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
R:Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, C', 142-374 <KH2>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

```

[illegible]

QY	196	VLOSSGLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVKDKRVEPKSCDKTHTCPD	---CP	253
DB	176	VLQSD-LYTLSSSVTVPSSTWSPSTVTCNVAHPASSTKVDKIKVPRDGC	---CKP	230
QY	254	APELLGGPSVFLFPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK	313	
DB	231	VPEV---SSVFIPPPAPKDVLTITLPKVTCTVVVDISKDDPEVQFSWFVDVEVHTAQTQ	287	
QY	314	PREEQNSTYRVVSVLTVLHQDLWGANGKEYCKCKVSNKALPAPIETKISKAKQPREPQVYT	373	
DB	288	PREEQNSTFRSVSELPIMHQDLWGANGKEPKCRVNSAAFPAPIETKISKTKGRKPAQVYT	347	
QY	374	LPPSREMTKNQVSLTCLVKYGYPSPDIAVEWESNQCPENNYKTPPVLDSDGSFSLYSLK	433	
DB	348	IPPKPEOMAKDKVSLTCTMTIDFFEDITVEWQMNGQPAENYKNTQPTIMDTGSGFYVSKL	407	
QY	434	TVDKSRWQOQNVFSCSVMEALHNHYTKSLSLSPCK	470	
DB	408	NVQKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPCK	444	
RESULT 14				
I47159				
Ig gamma 2a chain constant region - pig (fragment)				
C:Species: Sus scrofa domestica (domestic pig)				
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000				
C:Accession: I47159				
R:Kacskovics, I.; Sun, J.; Butler, J.E.				
J. Immunol. 153, 3565-3573, 1994				
A:Title: Five putative subclasses of swine IgG identified from the cDNA seq				
A:Reference number: I47158; MUID:95015845				
A:Accession: I47159				
A>Status: preliminary; translated from GB/EMBL/DBJ				
A:Molecule type: mRNA				
A:Residues: 1-328 <KAC>				
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124				
C:Genetics:				
A:Gene: IgG2a				
C:Superfamily: immunoglobulin C region; immunoglobulin homology				
F;133-202/Domain: immunoglobulin homology <IMM>				
Query Match 50.3%; Score 1267; DB 2; Length 328;				
Best Local Similarity 69.9%; Pred. No. 2.9e-65;				
Matches 232; Conservative 42; Mismatches 52; Indels 6; Gaps				
QY	141	ASTKGSVPPLAPSKSTSGGTAAAGCLVXQYFPPEVTVSNWNGALTSYGVHTFPAVLQSS	200	
DB	1	APKTAPSVYPLAPCSRDTSGPNVALGCLASSYFPPEVTVTVNSGALSSGVHTFSPVLQPS	60	
QY	201	GLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPELGG	260	
DB	61	GLYSLSVTVTPASSLSKSYTCNVNHNATTTKVDKRVGTRTKPKPCIPACESP----	116	
QY	261	PSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	320	
DB	117	PSVFIPPPAPKDTLMISRTPQVTCVVVDVSDQENPEVQFSWYVDGVEVHTAQTREKEQFN	176	
QY	321	SYRVVSVLTVLHQDLWGANGKEYCKCKVSNKALPAPIETKISKAKQPREPQVYTLPSPREE	380	
DB	177	SYRVVSVLPIHQDLWGANGKEPKCRVNNKNDLPAPITRIISKAKQGTREPQVYTLPHPAAE	236	
QY	381	MTKNQVSLTCLVKYGYPSPDIAVEWESNQ--PENNYKTPPVLDSDGSFSLYSLTKVDKS	438	
DB	237	LSRSKSVITCLVIGYPPDIDVEWQMNGQPEPEGNYRTTPQQVDVGTGYFLYSKFSVDKA	296	
QY	439	RWQOQNVFSCSVMEALHNHYTKSLSLSPCK	470	
DB	297	SNWGGIFQCAVMEALHNHYTKSGISPTGK	328	

RESULT	15
I47160	

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:15 ; Search time 53.64 Seconds
(without alignments)
339.265 Million cell updates/sec

Title: US-09-499-662-147

Perfect score: 2517

Sequence: 1 MGWSCIILFVATATGVHSQ.....MHEALHHYTKSLSLSPGK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1758	69.8	330	1 GC1_HUMAN	P01857 homo sapien
2	1610	64.0	326	1 GC2_HUMAN	P01859 homo sapien
3	1599.5	63.5	327	1 GC4_HUMAN	P01861 homo sapien
4	1231.5	48.9	323	1 GC_RABIT	P01870 oryctolagus
5	1210.5	48.1	329	1 GC2_CAVPO	P01862 cavia porce
6	1162	46.2	290	1 GC3_HUMAN	P01860 homo sapien
7	1155	45.9	326	1 GC1_RAT	P20759 rattus norv
8	1150	45.7	329	1 GC2_MOUSE	P22436 mus musculu
9	1145	45.5	324	1 GC1_MOUSE	P01868 mus musculu
10	1144.5	45.5	333	1 GCB_RAT	P20761 rattus norv
11	1140	45.3	393	1 GC1M_MOUSE	P01869 mus musculu
12	1139	45.3	398	1 GC3M_MOUSE	P03987 mus musculu
13	1129	44.9	330	1 GCAA_MOUSE	P01863 mus musculu
14	1127.5	44.8	329	1 GCC_RAT	P20762 rattus norv
15	1126.5	44.8	335	1 GCAB_MOUSE	P01864 mus musculu
16	1124	44.7	399	1 GCAM_MOUSE	P01865 mus musculu
17	1115	44.3	322	1 GCA_RAT	P20760 rattus norv
18	1085	43.1	336	1 GCB_MOUSE	P01866 mus musculu
19	1080	42.9	405	1 GCBM_MOUSE	P01867 mus musculu
20	559.5	22.2	139	1 HV07_MOUSE	P01751 mus musculu
21	525	20.9	117	1 HV06_MOUSE	P01750 mus musculu
22	524.5	20.8	137	1 HV11_MOUSE	P01755 mus musculu
23	521	20.7	138	1 HV48_MOUSE	P03980 mus musculu
24	513	20.4	117	1 HV05_MOUSE	P01749 mus musculu
25	507	20.1	140	1 HV02_MOUSE	P01746 mus musculu
26	501	19.9	117	1 HV09_MOUSE	P01753 mus musculu
27	488	19.4	117	1 HV04_MOUSE	P01748 mus musculu
28	486.5	19.3	429	1 EPC_RAT	P01855 rattus norv
29	486	19.3	428	1 EPC_HUMAN	P01854 homo sapien
30	485	19.3	117	1 HV49_MOUSE	P06328 mus sapien
31	480	19.1	117	1 HV1G_HUMAN	P23083 homo sapien
32	479	19.0	117	1 HV10_MOUSE	P01754 mus musculu
33	479	19.0	136	1 HV15_MOUSE	P01759 mus musculu

RESULT 1

ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

34	471	18.7	421	1	EPC_MOUSE	P06336 mus musculu
35	470	18.7	117	1	HV1B_HUMAN	P01743 homo sapien
36	457.5	18.2	120	1	HV50_MOUSE	P06329 mus musculu
37	457	18.2	117	1	HV12_MOUSE	P01756 mus musculu
38	456	18.1	117	1	HV13_MOUSE	P01757 mus musculu
39	452.5	18.0	147	1	HV1C_HUMAN	P01744 homo sapien
40	448	17.8	120	1	HV03_MOUSE	P01747 mus musculu
41	446.5	17.7	455	1	MUC_MOUSE	P01872 mus musculu
42	445	17.7	454	1	MUC_HUMAN	P01871 homo sapien
43	439	17.4	458	1	MUC_RABIT	P03988 oryctolagus
44	438	17.4	121	1	HV01_MOUSE	P01745 mus musculu
45	436.5	17.3	476	1	MUCM_MOUSE	P01873 mus musculu

ALIGNMENTS

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE-77070267; PubMed-1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE-81208100; PubMed-7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC MARKER & THE G1M (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35,116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
CC -----
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CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100;
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134

FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 305 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 69.8%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 6.1e-114;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGSVPFLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 200
DB 1 ASTKGSVPFLAPSSKSTSGGTAALGLVKDYFPEPVTVSWNSGALTSGVHTTFAVLQSS 60
QY 201 GLYSLSVVTVPSSSLSGTQTYICNVNHPKSNKTKVDKRVKPKCDKHTCCPCPAPELLGG 260
DB 61 GLYSLSVVTVPSSSLSGTQTYICNVNHPKSNKTKVDKRVKPKCDKHTCCPCPAPELLGG 120
QY 261 PSVLEFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYDGVGVHNAKTKPREEQYN 320
DB 121 PSVLEFPKPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMYDGVGVHNAKTKPREEQYN 180
QY 321 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSREE 380
DB 181 STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSRDE 240
QY 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 441 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 470
DB 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01559;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RC MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Oeda S., Ohta M., Nikaido T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RC MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
genes.";
RL EMBO J. 1:403-407(1982).
RN [4]
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RL Submitted (MAR-1980) to the PIR data bank.
RN [8]
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=9525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulfide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
RN [11]
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CC EMBL; J00230; AAB59393.1; -.
CC PIR; A02148; G2HU.
CC HSSP; P01857; 1FC1.
CC MIM; 147110; -.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_ci.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00410; IG_like; 1.
CC SMART; SM00407; IGcl; 2.
CC PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109 /FTid=VAR_003889.
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;

Query Match 64.0%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 8.9e-104;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;

Qy 141 ASTKGPSVFPLAPSSKSTSGGTAAIGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Qy 201 GLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKRVKPSCKDTHTCPPCPAPPELLGG 260
Db 61 GLYSLSVVTVPSFSSFGTQTYTCNVDRHPSNTKVDKTVKVERKCCV- --CPPCPAPP-VAG 116
Qy 261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
Db 117 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176
Qy 321 STYRVSVLTVLDHDLNGKEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSREE 380
Db 177 STFRVSVLTIVVHODWLNKEYKCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSREE 236
Qy 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPLDSDGSGSFYSLKLTVDKSRW 440
Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPLDSDGSGSFYSLKLTVDKSRW 296
Qy 441 QQGNVFCFSVMHEALHNHYTOKSLSPGK 470
Db 297 QQGNVFCFSVMHEALHNHYTOKSLSPGK 326

RESULT 3
ID GC4_HUMAN STANDARD; PRY; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RS SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Plunk J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human Immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
CC -----
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSSP; P01842; 7FAB.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT FT DOMAIN 99 110 HINGE.
FT FT DOMAIN 111 220 CH2.
FT FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 4.7e-103;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYPEPVTVSWNSGALTSGVHTFPVLQSS 200
Db | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYPEPVTVSWNSGALTSGVHTFPVLQSS 60

QY 201 GLXLSGVTVTPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHCTCPAPELLGG 260
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
61 GLXLSGVTVTPSSSLGTQTYTCNDVHKPSNTKVDKRVERSK-----VGPPCPSCPAPFLGG 117

QY 261 PSVFLPPPKPDLTMLSRPEVTVCVVVDVSHEDPEVKENWYDGVGVHNAKTKPREEQYN 320
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
118 PSVFLPPPKPDLTMLSRPEVTVCVVVDVSQDEPQEWFNYDGVGVHNAKTKPREEQFN 177

QY 321 STYRVSVTLTVLHQDLNLNGKEYCKYSKNALPAPIEKTIISKAKGPREPQVTVLPSPREE 380
Db | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Dd	178	STYRVSVLTVLHODWLNGKEYCKVKNKGLPSSIEKTISKAKQPREPVQYITLPSPQEE	237
Qy	381	MTKNQVSLTCLVKGFPSDIADAVENSGQPENNKKTPPPVLDSOGSFFLYSKLFTYDKSRW	440
Dd	238	MTKNQVSLTCLVKGFPSDIADAVENSGQPENNKKTPPPVLDSOGSFFLYSRLIVDKSRW	297
Qy	441	QQGVNFSCSYMHEALHNHYTKQSLSLSPGK	470
Dd	298	QEGNVFSCSYMHEALHNHYTKQSLSLILGK	327

RESULT 4

GC-RABBIT ID	GC-RABBIT STANDARD;	PRT;	323 AA.
AC P01870;			
DT 21-JUL-1986 (Rel. 01, Created)			
DT 15-JUL-1986 (Rel. 01, Last sequence update)			
DT 21-JUL-1999 (Rel. 38, Last annotation update)			
DE Ig gamma chain C region.			
OS Oryctolagus cuniculus (Rabbit).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.			
OX NCBI_TaxID=9986;			
[1]			
RN SEQUENCE FROM N.A.			
RP MEDLINE=84030930; PubMed=6313520;			
RX Bernstein K.E., Alexander C.B., Mage R.G.;			
RA "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant			
RT F-1 haplotype." ;			
RL Immunogenetics 18:387-397(1983).			
RN [2]			
RP SEQUENCE OF I-128.			
RX MEDLINE=76135469; PubMed=1243651;			
RA Pratt D.M., Moile L.E.;			
RT "Sequence studies on the constant region of the Fd sections of rabbit			
RL immunoglobulin G of different allotype." ;			
RN Biochem. J. 151:337-349(1975).			
[3]			
RP SEQUENCE OF 88-266 FROM N.A.			
RX MEDLINE=83299917; PubMed=6193512;			
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;			
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma			
RL heavy chain and identification of two genomic C gamma genes." ;			
RN Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).			
[4]			
RP SEQUENCE OF 132-161.			
RX MEDLINE=70110015; PubMed=5461106;			
RA Fruchter R.G., Jackson S.A., Moile L.E., Porter R.R.;			
RT "Sequence studies of the Fd section of the heavy chain of rabbit			
RL immunoglobulin G." ;			
RN Biochem. J. 116:249-259(1970).			
[5]			
RP SEQUENCE OF 129-131 AND 155-322.			
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;			
RL (In) Killander J. (eds.);			
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almquist and Wiksell,			
RL Stockholm (1967).			
-I- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPE MARKER,			
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15			
CC MARKERS AND REF.5 THE E15 MARKER.			

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CC EMBL; M16426; AAA31289.1; --			
DR FIR; A02161; GHRB.			
DR HSSP; P01857; 1FC1.			
DR InterPro: IPR003006; Iq_MHC.			

Query Match	63.5%;	Score 1599.5;	DB 1;	Length 327;
Best Local Similarity	91.8%;	Pred. No. 4.7e-103;		
Matches 303;	Conservative 9;	Mismatches 15;	Indels 3;	Gaps 1;
QY	141	ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYRPEPVTVSWNSGALTSGVHTPEAVLQSS	200	
Db	1	ASTKGPSVFPLAPCSRSTSESTAAGCLVKDYRPEPVTVSWNSGALTSGVHTPEAVLQSS	60	
QY	201	GLYSLGSVTVTPSSSLGTQTYICNVHKKPSNTKVDKRVKPKSCDKTHTCCPCAPPELLGG	260	
Db	61	GLYSLGSVTVTPSSSLGTQTYICNVHKKPSNTKVDKRVKPKSCDKTHTCCPCAPPELLGG	117	
QY	261	PSVFLPPPKPDTLMTSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	320	
Db	118	PSVFLPPPKPDTLMTSRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN	177	
QY	321	STYRVVSVLTVTHQDMLINKKEYCKYKSNKALPAIEKTIISKAKGQREPVVTLTPSREE	380	

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DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 9.1e-78;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVFPLAPSSKSTSGGTAAALGLVDFPEPTVSVNSGALTSGVHTFPAVLQSSGLY 203
DB 4 KAPSVFPLAPCCGTPSTVTLGLVKGYLEPPEPTVTVNSGTLNGLVTFPSVRQSSGLY 63

QY 204 SLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVRPKSCDKTHTCPCPAPPELLGGPSV 263
DB 64 SLSSVTVTPSSS---QPVCNVNHPATNTKVDKTVAPSTCSK----PTCPPPELLGGPSV 116

QY 264 FLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNNAKTKPREQYNSTY 323
DB 117 FIFPKPKDLMISRTPEVTCVVVDVSDQDPEVQFTWYINNEQVTRAPPLREQQFNSTI 176

QY 324 RVSVSLTVLHODWLNKGEYCKVGNKALPAPIETKISKAKGPPEQVYITLPPSREEMTK 383
DB 177 RVSVSLTVLHODWLNKGEYCKVGNKALPAPIETKISKAKGPPEQVYITLPPSREEMTK 383

QY 384 NOVSLTCLVKGFPYSDIAVENESNGQPENNYKTTTPPVVLDSDGSPFLYSLVVDKSRWQQG 443
DB 237 RVSILTCLVKGFPYSDISVENESNGKADNYKTTTPPVVLDSDGSPFLYSLVVDKSRWQQG 443

QY 444 NVFSCSVMEALHNHYTQKSLSLSPGK 470
DB 297 DVFTCSVMHEALHNHYTQKSLSRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;

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RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RT Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RT Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RT Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RT Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RT Biochemistry 10:26-31(1971).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2BP.
DR HSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 48.1%; Score 1210.5; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 2.6e-76;
Matches 233; Conservative 30; Mismatches 62; Indels 9; Gaps 4;

QY 140 SASTKGPSVFPLAPSSKSTSGGTAAALGLVDFPEPTVSVNSGALTSGVHTFPAVLQ 199
DB 1 SARTTAPSVFPLAACVSDTSGSMMTLGCLVKGYPPEPTVTKVNSGALTSGVHTFPAVLQ- 59

QY 200 SGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVRPKSCDKTH--TCPPCPAPEL 257
DB 60 SGLYSLTSMVTPVPSQKAT---CNVAHPASSTKVDKTVETIRTP2BPBCTCPKCPPPEN 115

QY 258 LGGPSVFLFPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNKYVDGVVHNNAKTKPRE 317
DB 116 LGGPSVFLFPKPKDMLISLTPRVTCVVVDVSDQDPEVQFTWYINNEQVTRAPPLREQQ 175

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Db 179 ISKTGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTP 238
 Qy 419 PVLSDSGSFYLYSLKTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
 Db 239 PMLSDSGSFYLYSLKTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 290

RESULT 7
 GC1_RAT
 ID GC1_RAT STANDARD; PRT; 326 AA.
 AC P20759;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-1 chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;
 RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR HSP; PS0017; PS0017.
 DR HSP; P01842; 7FAB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; Igcl; 2.
 DR PROSITE; PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 112 HINGE.
 FT DOMAIN 113 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT CARBOHYD 176 176
 SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;
 Best Local Similarity 63.4%; Pred. No. 1,7e-72;
 Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

Qy 141 ASTKGPSVPEPLAPSSKSTSGGTAALGLVKGDFPEPVTVSNNGALTSGLVHFFAVLQSS 200
 Db 1 AETAPSYIPLAPGALKSNWTLGCLVKGDFPEPVTVTNWNGALSSGVHFFAVLQ-S 59
 Qy 201 GLYLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKRVKPSKCDKTHFCPCPAPPELLGG 260
 Db 60 GLYLTSSVTVFSSVPSQVTCNVNHNKPSNTKVDKRVKPSKCDKTHFCPCPAPPELLGG 113
 Qy 261 ---PSVFLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNHAKTKPREE 317
 Db 114 SEVSSVFIFPKPKDVLITLTLPKVCVVDVSHDEPEVKFNWYVDGVVHNHAKTKPREE 173
 Qy 318 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTSKAKGQPREPQVYTLPPS 377
 Db 174 QFNSTFRSVLPILVHQDWLNGRTFRCKVTSAAPFSPTEKTSKPEGRQTQVPHVVTMSPT 233
 Qy 378 REEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYNTTPVLDSDSGSFYLYSLKTLVDK 437
 Db 234 KEEMTKNOVSLTCLVKGFYPSDIAVEWQMQNQENYKNTPTMTDGSFYLKLVNKK 293

Qy 438 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
 Db 294 EKWQGNVFTCSVLHEGLHNHHTKSLSHSPGK 326

RESULT 8
 GC3_MOUSE
 ID GC3_MOUSE STANDARD; PRT; 329 AA.
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ig gamma-3 chain C region, secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85027161; PubMed=6092053;
 RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner F.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RL EMBO J. 3:2041-2046(1984).
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 CC -----
 CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
 DR PIR; B02156; G3MSC.
 DR HSP; P01857; 1FC1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; Ig_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
 Best Local Similarity 65.0%; Pred. No. 3,7e-72;
 Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

Qy 142 STKGPSVPEPLAPSSKSTSGGTAALGLVKGDFPEPVTVSNNGALTSGLVHFFAVLQSSG 201
 Db 1 TTAPSVIPLVPGCDSTSGSSVTLGCLVKGDFPEPVTVKNWNGALSSGVTVSSVLQ-SG 59
 Qy 202 LYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKRVKPSKCDKTHFCPCPAPPELLGG 259
 Db 60 FYSLSLVTVFSSVPSQVTCNVNHNKPSNTKVDKRVKPSKCDKTHFCPCPAPPELLGG 118
 Qy 260 GPSVFLFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNHAKTKPREEY 319
 Db 119 GPSVFIFFPKPKDMLISRTPEVTCVVDVSHDEPEVKFNWYVDGVVHNHAKTKPREEY 178
 Qy 320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTSKAKGQPREPQVYTLPPSRE 379
 Db 179 NSTFRVVSALPIQHDWNRGKEFKCKVNNKALPAPTEKTSKAKGQPREPQVYTLPPSRE 238

QY 380 EMTKNQVSLCLVKGFPSPDIWESNGQPNKYKTPPVLSDSGSFFLYSLKLTVDKSR 439
 Db 239 QMSKKVSLCLVNTFSEALSWEWNGELEDQYKNTPTILSDGYYFLYSLKLTVDTS 298
 QY 440 QMOGNVFCSCVMEALHNHYTKSLSPGK 470
 Db 299 WLOGEFTCSVMEALHNHYTKSLSPGK 329

RESULT 9
 GCL_MOUSE STANDARD; PRT; 324 AA.
 AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-1 chain C region.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=80202559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
 cloned in a bacterial plasmid";
 RL Gene 9:87-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salser W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
 heavy chain";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242288; PubMed=98524;
 RA Adegugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a
 murine myeloma gammal chain";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein";
 RL Biochem. J. 126:837-850(1972).
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 DR EMBL; V00793; CAA24172.1; -
 DR EMBL; V00793; CAA24173.1; -
 DR EMBL; V00793; CAA24174.1; -
 DR EMBL; V00793; CAA24175.1; -
 DR EMBL; V00795; CAA24176.1; -
 DR PIR; A02159; GIMS.
 DR HSSP; P01842; 7FAB.

DR GlycoSuiteDB: P01868; -
 DR MGI:96446; Igh-4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_CL.
 DR Pfam: PF00047; Ig; 3.
 DR SMART: SM00407; IGc1; 2.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC...).
 FT FTID-CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 276 276 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;
 Query Match 45.5%; Score 1145; DB 1; Length 324;
 Best Local Similarity 62.3%; Pred. No. 8.1e-72;
 Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
 QY 141 ASTKGPSVPLAPSSKSTSGTAALCLVKGFPSPDIWESNGQPNKYKTPPVLSDSGSFFLYSLKLTVDKSR 200
 Db 1 AKTPPSVPLAPGSAQAQNSMVTGLCLVKGFPSPDIWESNGQPNKYKTPPVLSDSGSFFLYSLKLTVDKSR 60
 QY 201 GLYSLSVVTVPSVSSSLGTQYICNVNHNKPSNTKVDKRVKPKCDKTHTCPP--CPAPELL 258
 Db 61 -LYTLSSVTVPSVSSPRPSEITVCNVAHPASTKVDKRVKPKCDKTHTCPP--CPAPELL 114
 QY 259 GGSVFLFPKPKDMLMSRTPEVTCVVDVSHEDPEVKFNWYVDGVEVINATKKPREQ 318
 Db 115 --SSVFIFPPKPKDVLITLTPKVTVCVVDVSHEDPEVKFNWYVDGVEVINATKKPREQ 172
 QY 319 YNSTYRWVSVTLVHODWLNKGVCKVSNKALPAPTEKTIKAKGQPPQVYTLPPSR 378
 Db 173 FNSTFVSSELPIHMQDLNKGKFKVNSAAPAPTEKTIKAKGQPPQVYTLPPSR 232
 QY 379 EEMTKNQVSLCLVKGFPSPDIWESNGQPNKYKTPPVLSDSGSFFLYSLKLTVDKSR 438
 Db 233 EQMAKDKVSLTCMTDFPEDITVWQNGQPAENYKNTQPIINTNGSYFVSKLVNYSK 292
 QY 439 RMOQGNVFCSCVMEALHNHYTKSLSPGK 470
 Db 293 NWEAGNFTCSVLHEGLHNHHTKSLSPGK 324
 RESULT 10
 GCB_RAT STANDARD; PRT; 333 AA.
 AC P20761;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2B chain C region.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89232738; PubMed=3149946;

```
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SQ SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 45.3%; Score 1144.5; DB 1; Length 333;
Best Local Similarity 63.7%; Pred. No. 9e-72;
Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;

QY 141 ASTGSPVEPLAPSSKTSGTALGLVDFPEPTVTVNSGALTSVHTFFAVLOSS 200
Db 1 AQTAPSVYPLAPGCGDTSTVTGLGLVGFPEPTVTVNSGALSSDVHTFFAVLO-S 59
QY 201 GLYSLSSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVRPKS-----CDKTHRCPPCPA 254
Db 60 GLYTLTSSVT--STWPSQVTVCNVHPASTKVDKKVERNGGIGHKCTPCPCCHKCPV 117
QY 255 PELGGPSVFPPPKPKDLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNATKP 314
Db 118 PELGGPSVFPPPKPKDILLISQNAKTCVVDVSEBEPDQVQSFVNNVEVHTAQTP 177
QY 315 REEQNSTYRVVSVLTVHQLWNLGKEYCKVSNKALPAPEIKTSIKRAGQPREQVYTL 374
Db 178 REEQNSTFRVVSALPIQHOHDMGKFKCKVNNKALPSPIEKTISKPKGLVRKPVQVYM 237
QY 375 PPSREEMTKNOVSLTCLVKGFPSPDIAVEWESNGOPENNYKTPPVLDSDGSEFLYSKLT 434
Db 238 GPPEQLTEQVTSITCLTSGFLPNDIGVEWTSNGHIEKNYKNTPEVMDSDGSFFWYSKLN 297
QY 435 VDKSRWQGNVFCSSVMHEALHNHYTKLSLSPEK 470
Db 298 VERSRWDSRAPFCVSVVHEGLNHHVKEKISRPPGK 333

RESULT 11
GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
```

```
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular
domain.";
RT Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]
RP SEQUENCE OF 323-366 FROM N.A.
RX MEDLINE=82115295; PubMed=6799207;
RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
RA Eisenberg D., Wall R.;
RT "Gene segments encoding transmembrane carboxyl termini of
immunoglobulin gamma chains.";
RT Cell 26:19-27(1981).
RN [4]
RP SEQUENCE OF 1-44 FROM N.A.
RX MEDLINE=82222190; PubMed=6283537;
RA Yanawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
immunoglobulin gamma chains.";
RT Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.
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CC EMBL; V00793; CAA24172.1; -
CC EMBL; V00793; CAA24173.1; -
CC EMBL; V00793; CAA24174.1; -
CC PIR; B02159; GIMSM.
CC HSP; P01842; 7FAB.
CC MGD; MGI:96446; Igh-4.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_cl.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; IGcl; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing; Transmembrane.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 N-LINKED (GLCNAC. . .).
FT CARBOHYD 174 174
FT DISULFID 244 302 POTENTIAL.
FT TRANSMEM 340 357 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 358 393
SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 45.3%; Score 1140; DB 1; Length 393;
Best Local Similarity 62.2%; Pred. No. 2.3e-71;
Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
```


RX MEDLINE=81223894; PubMed=6787604;
RA Olio R., Aufray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin:amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges.";
RL Eur. J. Biochem. 30:452-462(1972).
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CC -----
DR EMBL; V00798; CAA24178.1; -;
DR PIR; A02152; G2MSA.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 44.98; Score 1129; DB 1; Length 330;
Best Local Similarity 63.94; Pred. No. 1e-70;
Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;

Qy 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
Db 1 AKTAPSVYPLAPVCGDTGSGSVTLGCLVKGYFPEPTVLTWNSGSLSGVHTFPAVLQSD 60

Qy 201 GLYSLSSVTVPPSSSLGTOTYICNVNHNKPSNTKVDKRVPEKSCDKTHTCPP--CPAPEL 258
Db 61 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKEPRG-PTIKPCPCPKCPAPNLL 118

Qy 259 GGPSVFLPPPKDFTLMSRPEVTCVVDYSHEDPEKFNWYDGVVHNKAKTPREQ 318
Db 119 GGPSVFIEPPKIKDVLMTSLSPITVCVVDVSEDDPQVQISWFVNNVEVHTAQOTHRD 178

Qy 319 YNSTRVVSVLTVLHODNLNCKEYKCKVSNKALPAPIETKISKAKGQPREQVYTLPPSR 378
Db 179 YNSTLRVVSALPIQHDWMSKEFKCKVNNKDLPAPIERTISKPGSVRAPOVYVLPPE 238

Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVWESNGSPENNYKTPPPVLDSDGSFFLYSKLTVDKS 438
Db 239 EEMTKQVTLTCLVMTDFEPDIYVEWTNKGKTELKNTPEVLDSDGSFYFMYSKLRVERK 298
Qy 439 RWQGNVFSQCSVMHEALNHYTKQKSLSPGK 470
Db 299 NWVERNSYSCSVVHGLNHHHTKFSRTPGK 330

RESULT 14
GCC_RAT
ID GCC_RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggemann M., Delmastro-Galfrè P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).
CC -----
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CC -----
DR EMBL; X07189; CAA30169.1; -;
DR PIR; S00847; S00847.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
KW NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 44.8%; Score 1127.5; DB 1; Length 329;
Best Local Similarity 62.8%; Pred. No. 1.3e-70;
Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;

Qy 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 200
Db 1 ARTTAPSVYPLVPGSGTSGSLVTLGCLVKGYFPEPTVTKWNSGALSSGVHTFPAVLQ-S 59

Qy 201 GLYSLSSVTVPPSSSLGTOTYICNVNHNKPSNTKVDKRVPEKSCDKTHTCPP--CPAPEL 257
Db 60 GLYTLSSSVTVPPSSWSQTVCVAHPATKSNLIKRIEPR---RPKPRPPTDICSDDN 116

```
QY 258 LGGPSVFLPPPKDITMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 LGRPSVFIFPPKPKDITMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 176
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 QYNSTRVYVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 QLNSTRVYVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 236
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 REBMTKNVSLTCLVKGFPSPDIJAVWESNGQPNKYKTPPPVLDSDGSFFLYSKLTVDK 437
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 REBMTKNVSLTCLVKGFPSPDIJAVWESNGQPNKYKTPPPVLDSDGSFFLYSKLTVDK 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 438 SRMQQGNVSCSVHHEALHNHYTKQSLSLSPGK 470
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 297 DSMRMGDIIVTCSVVHEALHNHYTKQSLSLSPGK 329
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
  IgG2a and IgG2b alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
  chain Fc regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -!- MISCELLANEOUS; THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
  FROM BALB/C MICE, AT 15% OF THE POSITIONS.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; IFCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS00290; Ig_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
```

Query Match 44.8%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 1.6e-70;

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Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;
QY 141 ASTKGPSVFLPPPKDITMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 200
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 AKTAPSVPLVPVCGGTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGSHVHTFPALLO-S 59
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 201 GLYSLSVVTVSPSSSLGTQTYICNVNHPKSPNTKVDKRVPEK-----SCDKTHTCPPCPA 254
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPIITQNPCTPHQVRVPPCAA 119
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PELLGGPSVFLPPPKDITMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPK 314
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PDLGGPSVFIFPPKPKDITMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPK 179
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 315 REOYNSTRVYVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 374
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTRVYVSVLTVLHODWLNKGYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 239
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 PPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLT 434
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PPAEEMTKKEFSLTCTMITGFLPAETIAVDWTSNGRTEQNKYKNTATVLDSDGSFFLYSKLR 299
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 VDKSRMQQGNVSCSVHHEALHNHYTKQSLSLSPGK 470
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 VDKSRMQQGNVSCSVHHEALHNHYTKQSLSLSPGK 335
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Search completed: August 14, 2002, 15:23:16
Job time: 689 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:18 ; Search time 187.61 Seconds
(without alignments)
433.386 Million cell updates/sec

Title: US-09-499-662-147

Perfect score: 2517

Sequence: 1 MWNSCILFLVATATGVHSQ.....MHEALHNHYTQKSLSPGK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1636.5	65.0	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1625.5	64.6	463	11 Q99LC4	Q99lc4 mus musculus
3	1585.5	63.0	473	11 Q99L25	Q99l25 mus musculus
4	1559	61.9	468	11 Q99L31	Q99l31 mus musculus
5	1436.5	57.1	437	11 Q99L31	Q99l31 mus musculus
6	1423.5	56.6	473	11 Q99L25	Q99l25 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96P08	Q96pq8 homo sapien
9	983	39.1	278	11 Q921K1	Q921k1 mus musculus
10	930.5	37.0	614	4 Q96GA6	Q96ga6 homo sapien
11	887.5	35.3	481	11 Q91WT3	Q91wt3 mus musculus
12	862	34.2	500	4 Q9BRV0	Q9brv0 homo sapien
13	833.5	33.1	481	11 Q91WT1	Q91wt1 mus musculus
14	817	32.5	488	11 Q91WR1	Q91wr1 mus musculus
15	815.5	32.4	597	4 Q96BB9	Q96bb9 homo sapien
16	807	32.1	496	4 Q96DK0	Q96dk0 homo sapien

ALIGNMENTS

RESULT 1

Q9D8L4 ID Q9D8L4 PRELIMINARY; PRT; 473 AA.
AC Q9D8L4;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 181006009RIK PROTEIN.
GN IGH-1 OR 181006009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Okada T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RT Hayashizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.

17 765.5 30.4 597 4 Q9BU10 Q9bu10 homo sapien
18 761.5 30.3 597 4 Q9BQB8 Q9bqb8 homo sapien
19 755.5 30.0 618 4 Q96AA6 Q96aa6 homo sapien
20 755 30.0 484 11 Q99LA6 Q99la6 mus musculus
21 737 29.3 494 4 Q96K68 Q96k68 homo sapien
22 735 29.2 613 4 Q96EY0 Q96ey0 homo sapien
23 727.5 28.9 487 11 Q99RA4 Q99ra4 mus musculus
24 721.5 28.7 479 11 Q91WP5 Q91wp5 mus musculus
25 703 27.9 486 11 Q91Z07 Q91z07 mus musculus
26 692.5 27.5 480 11 Q91XE1 Q91xe1 mus musculus
27 659 26.2 482 11 Q91X92 Q91x92 mus musculus
28 655 26.0 479 11 Q99M22 Q99m22 mus musculus
29 644 25.6 496 4 Q96KX8 Q96kx8 homo sapien
30 605 24.0 426 11 Q9DCD9 Q9dcd9 mus musculus
31 580.5 23.1 416 4 Q9NPP6 Q9npp6 homo sapien
32 539.5 21.4 143 11 Q91V67 Q91v67 mus musculus
33 527.5 21.0 143 11 Q924P9 Q924p9 mus musculus
34 525 20.9 150 4 Q9V298 Q9v298 homo sapien
35 514 20.4 142 11 Q924Q2 Q924q2 mus musculus
36 511 20.3 157 4 Q95978 Q95978 homo sapien
37 510.5 20.3 145 11 Q924R3 Q924r3 mus musculus
38 499.5 19.8 159 4 Q96QSO Q96qso homo sapien
39 495.5 19.7 143 11 Q924Q5 Q924q5 mus musculus
40 494 19.6 146 11 Q924R8 Q924r8 mus musculus
41 493 19.6 144 11 Q924P5 Q924p5 mus musculus
42 492.5 19.6 145 11 Q924Q7 Q924q7 mus musculus
43 488.5 19.4 145 11 Q924R4 Q924r4 mus musculus
44 486.5 19.3 143 11 Q924Q0 Q924q0 mus musculus
45 486 19.3 140 11 Q924P8 Q924p8 mus musculus

DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR SMART; SM00410; IG; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 63.0%; Score 1585.5; DB 11; Length 473;
 Best Local Similarity 63.4%; Pred. No. 1.le-124;
 Matches 301; Conservative 61; Mismatches 106; Indels 7; Gaps 5;

Qy 1 MWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKCKASGYTFTSYWQVVRQAP 60
 Db 1 MWSWVFLFFSVTVGVHSQVQLVQSGDAELVKPGASVKISCKVSGITFTDTHHWKQRP 60

Qy 61 GQLEWMEGIDPSDSTYNVQKFGKATLTVDSTSTAYMELSSRSDEDTAVVYCARNRD 120
 Db 61 EQLEWIGWIDPEGETYAPFQDKATITADTSSNTAYLQLSSLTSEDTAVVYCARNLL 120

Qy 121 --YNN--WYDFWVGQTLTVSSASTKGPSVPLAPSSKTSGGTAALGCLVKDYFPEPV 177
 Db 121 IYGGVLYFYFYGQGTITVSSAKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPV 180

Qy 178 TVSNWGSALTSGVHTFPAVLQSSGLYSLSSVTVVPSVSSISLTQTYICNVNHNKPSNTKDKR 237
 Db 181 TLTNWGSLSGSHVTFPAVLQSD--LYTLSSSVTVTSSTWPSQISITCNVAHPASSTKVDK 239

Qy 238 VEPKSCDTHRCPP--CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPE 295
 Db 240 IEPGR-PTIKPCPPCKCPAPNLGGPSVFIFPKIKDVLMLISLSPMTVCVVVDVSEDDPD 298

Qy 296 VKFNWYDGVVHNNAKTPREQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPI 355
 Db 299 VQISWVFNVEVLTQAOTQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPI 358

Qy 356 EKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYK 415
 Db 359 ERTISKPGSVRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIYVSWTNGKTELNYK 418

Qy 416 TTPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTKSLSLSPGK 470
 Db 419 NTEPVLDSDGSFYFMYSKLVEKKNVVERNSYSCSVVHGLNHHHTKFSRTPGK 473

RESULT 4
 Q99L31
 ID Q99L31 PRELIMINARY; PRT; 468 AA.
 AC Q99L31
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003878; AA03878.1; -.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003600; Ig.like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGv; 1.
 DR SMART; SM00410; IG; 1.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SQ SEQUENCE 468 AA; 51661 MW; 96352328B3332ADB CRC64;

Query Match 61.9%; Score 1559; DB 11; Length 468;
 Best Local Similarity 62.7%; Pred. No. 1.8e-122;
 Matches 296; Conservative 62; Mismatches 108; Indels 6; Gaps 4;

Qy 1 MWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSKCKASGYTFTSYWQVVRQAP 60
 Db 1 MKCSWVIFLMAVVGIVNSEVQLQSGAEVLRPGASVKLSCTASGFNIKDSLMHWKQRP 60

Qy 61 GQLEWMEGIDPSDSTYNVQKFGKATLTVDSTSTAYMELSSRSDEDTAVVYCARNRD 120
 Db 61 EQLEWIGWIDPEGETYAPFQDKATITADTSSNTAYLQLSSLTSEDTAVVYCARNLL 120

Qy 121 YNNWYDFWVGQTLTVSSASTKGPSVPLAPSSKTSGGTAALGCLVKDYFPEPVTVS 180
 Db 121 YGG--YDYWVGQTTITVSSAKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPVTLT 178

Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSVSSISLTQTYICNVNHNKPSNTKDKRVP 240
 Db 179 WNSGSLSGSHVTFPAVLQSD--LYTLSSSVTVTSSTWPSQISITCNVAHPASSTKVDK 237

Qy 241 KSCDTHRCPP--CPAPELLGGPSVFLPPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 298
 Db 238 RG-PTIKPCPPCKCPAPNLGGPSVFIFPKIKDVLMLISLSPMTVCVVVDVSEDDPDVQI 296

Qy 299 NWYDGVVHNNAKTPREQYNSTYRVSVLTVLHODWLNKGYCKVSNKALPAPIKT 358
 Db 297 SHFVFNVEVLTQAOTQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAPIKT 356

Qy 359 ISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYK 418
 Db 357 ISKPGSVRAPQVYVLPPEEEMTKQVTLTCMTDFMPEDIYVSWTNGKTELNYK 416

Qy 419 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTKSLSLSPGK 470
 Db 417 PVLDSDGSFYFMYSKLVEKKNVVERNSYSCSVVHGLNHHHTKFSRTPGK 468

RESULT 5
 Q99L14
 ID Q99L14 PRELIMINARY; PRT; 437 AA.
 AC Q99L14
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.G.; Yu X.; Ekramoddoullah A.K.M.; Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152372; AA040243.1; -.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR003600; Ig_like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 4.
 DR SMART; SM00406; IGv; 1.
 DR SMART; SM00410; IG_like; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 437
 SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EB7D697C CRC64;

Qy	375	PPSREMTKNOVSLTCLVKGYPSDIAVWESNQCP--ENNYKTPPVLDSDGSFFLYSK	432
Db	240	APHDELSKSVSTCLVKDYFPEINEMQSGQPELETYKSTQAQODSDGSFFLYSK	299
Qy	433	LTVDKSRWQOQNVFSCSVMHHEALHNHYTKQSLSLSPGK	470
Db	300	LSVDRNRWQOQTTFCTGVMHHEALHNHYTKQSVKNPGK	337
RESULT	8		
Q96PQ8			
ID	Q96PQ8	PRELIMINARY; PRT; 701 AA.	
AC	Q96PQ8		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RX	SEQUENCE FROM N.A.		
RX	MEDLINE=21477448; PubMed=11593034;		
RA	Hu Z., Garen A.,		
RT	"targeting tissue factor on tumor vascular endothelial cells and tumor		
RT	cells for immunotherapy in mouse models of prostatic cancer.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).		
DR	EMBL; AF272774; AAK58686.1; -.		
SQ	SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;		
Query Match	49.9%;	Score 1257; DB 4; Length 701;	
Best Local Similarity	99.1%;	Pred. No. 6.9e-97;	
Matches	230; Conservative	2; Mismatches 0; Indels 0; Gaps 0;	
Qy	239	EPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVYVSHEDPEVKF	298
Db	470	EPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVYVSHEDPEVKF	529
Qy	299	NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT	358
Db	530	NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT	589
Qy	359	ISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGYFSPYDIAVEWESNGQPENNYKTP	418
Db	590	ISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGYFSPYDIAVEWESNGQPENNYKTP	649
Qy	419	PVLDSGSGFFLYSKLTVDKSRWQOQNVFSCSVMHHEALHNHYTKQSLSLSPGK	470
Db	650	PVLDSGSGFFLYSKLTVDKSRWQOQNVFSCSVMHHEALHNHYTKQSLSLSPGK	701
RESULT	9		
Q921K1			
ID	Q921K1	PRELIMINARY; PRT; 278 AA.	
AC	Q921K1		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	UNKNOWN (PROTEIN FOR MGC:18977).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RX	SEQUENCE FROM N.A.		
RA	Strausberg R.;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC012207; AAK12207.1; -.		
SQ	SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;		

Query Match	39.1%;	Score 983; DB 11; Length 278;	
Best Local Similarity	67.1%;	Pred. No. 1.8e-74;	
Matches	186; Conservative	33; Mismatches 5; Indels 8; Gaps 3;	
Qy	1	MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVRQAP	60
Db	1	MGWNCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMHWVKORR	60
Qy	61	GGLEWMEIDPSDSTYNNQKFKGKATLTVDTSSTAYMELSSLSRSEDATVYYCARNRD	120
Db	61	GGLEWIGNINPNSGCTYNNKFNKATLAVDKSSSTVYMLSSLTSEDSAYYYCTRGVY	120
Qy	121	YSNNWYFDVWGQTLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS	180
Db	121	Y-DDVYFDVWGAGTTVTSSAKTTAPSVPLAPVCGGTTGSSVTLGCLVKGYFPEPTVLT	179
Qy	181	WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKYDKRVEP	240
Db	180	WNSGSLSGVHTFPALLQ-SGLYTLSSSVTVTSNTPSQITFCNVAHFASSTKYDKKIEP	238
Qy	241	K-----SCDKTHCPCPAPPELLGGPSVFLFPPKPK 271	
Db	239	RVPITQNPCLPKCEPCAPDILLGGPSVFIFFPRSR 275	
RESULT	10		
Q96GA6			
ID	Q96GA6	PRELIMINARY; PRT; 614 AA.	
AC	Q96GA6		
DT	01-DEC-2001	(TrEMBLrel. 19, Created)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)	
DT	01-DEC-2001	(TrEMBLrel. 19, Last annotation update)	
DE	UNKNOWN (PROTEIN FOR MGC:15420).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PRIMARY B-CELLS FROM TONSILS;		
RA	Strausberg R.;		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC009851; AAK09851.1; -.		
SQ	SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;		
Query Match	37.0%;	Score 930.5; DB 4; Length 614;	
Best Local Similarity	36.7%;	Pred. No. 1.4e-69;	
Matches	212; Conservative	84; Mismatches 166; Indels 115; Gaps 17;	
Qy	1	MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYWMQVVRQAP	60
Db	1	MDWTWRIILFLVAAATDAYSQMQLVQSGAEVKKPGASVKVSCKASGYTFTYRHLHWVRQAP	60
Qy	61	GGLEWMEIDPSDSTYNNQKFKGKATLTVDTSSTAYMELSSLSRSEDATVYYCARNRD	120
Db	61	GQALEWGWITPFGNTNTYAKQFQDRVTITDRSMTAYMELSSLSRSEDATVYYCARG--	118
Qy	121	YSNNW--YFDVWGQTLTVSSASTKGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPV	177
Db	119	YSSWDDAFDIWQGTQVTVTVSSGASAPTLFPLVSCENSPSDTSSVAVGCLAQDLPDSI	178
Qy	178	TVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSL--GTQTY-ICNVNHRKPSN	231
Db	179	TFSWKYKKNDSISSTRGFPVLR-GGKYAATSOVLLPSKDVQMGQDDEHVCKVQHPGNK	237
Qy	232	-----TKVDRKVEPKS-----CDKTHTCP-----	250
Db	238	EKNVPLPVIAELPPKVSFVFPVRDGFNGPRKSKLICATGFSRQIQVSWLREGKQVGS	297
Qy	251	-----PCPAPELLGGPS-----	262
Db	298	GVTTDQVQAEKESGPTTYTKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQONASSMCPVD	357

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QY 263 -----VFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMVYDGVGEVHNHAKTKPRE 316
|| || : : : : : || : | | | | |
Db 358 QQTAIRFAIPPS-FASIELTKRSTKLTCLVTLDTLTYD-SVTISWTRQNGEAVKTHNISE 415
|| || : : : : : || : | | | | |
QY 317 EOYNSTYRVVSVLTVLHODWLNCKEYKCKVSNKALPAPIEKTIISKAKGQP-REPQVYTL 375
|| || : : : : : || : | | | | |
Db 416 SHPNATFSAVGASICEDDNGSERCTVTHTDPLSPKLTQISRPKGVALHRPDVYLLP 475
|| || : : : : : || : | | | | |
QY 376 PSREEMT-KNOVSLTCLVKGFPYSDIAVEWESNGQP--ENNYKTTTPVLD--SDGSFFLY 430
|| || : : : : : || : | | | | |
Db 476 PAREQLNRESATITCLVTFGSPADVFVQVMQRGQLSPKDYVTSAPMPEPQAPGRYFAH 535
|| || : : : : : || : | | | | |
QY 431 SKLTVDSRWQOQNSVSCVMHEALHNHYTKQSLSL 467
|| || : : : : : || : | | | | |
Db 536 SILTVSEEWNTGETYTCVVAHEALPNRVTERTVDKS 572
|| || : : : : : || : | | | | |

RESULT 11
Q91WT3 PRELIMINARY; PRT; 481 AA.
AC Q91WT3;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 52.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013488; AAH3488.1; -.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52022 MW; 4EB5C253038B718 CRC64;
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Query Match 35.3%; Score 887.5; DB 11; Length 481;
Best Local Similarity 42.7%; Pred. No. 4.1e-66;
Matches 206; Conservative 73; Mismatches 172; Indels 31; Gaps 16;

QY 1 MGWSCILLFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNQWVRQAP 60
|| || : : : : : || : | | | | |
Db 1 MWWSCILLFLVATATGVNSQVQLQPGAEIVRPGASVKLSCKTSGYTFDYHWNVQKRP 60
|| || : : : : : || : | | | | |

QY 61 GOGLEWMEIDPSDSTYNNQKFGKATLTVDTSSTAYMELSSLSRSEDATVYICARNRD 120
|| || : : : : : || : | | | | |
Db 61 GOGLEWIGAIDPDSYTSYNQKFG--TTLTVDTSSTAYMELSSLSRSEDATVYICARNRD 119
|| || : : : : : || : | | | | |

QY 121 YSNMYFDVWGOGTLTVYSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPE-PYTV 179
|| || : : : : : || : | | | | |
Db 120 DSSGYI---WGOGTLTVYSSAPAREPTIYPLT-FPQALSSDPVITGCLIHDFPFGTMNV 175
|| || : : : : : || : | | | | |

QY 180 SNWSGALTSGVITFPAVLQSSGLYSLSSVTVTPSSSLGT-QYICNVNHNKPSNTVDKVR 238
|| || : : : : : || : | | | | |
Db 176 TWGKSGKDTITVTFPALASGGRYTMSSQLTLPAYCEPGESEVSKVQH-DSNPVQELNV 234
|| || : : : : : || : | | | | |

QY 239 EPKSCDKTHTCPCPAPELGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPE-VK 297
|| || : : : : : || : | | | | |
Db 235 NCPGICSPPTTPPPPSQ----PSLSLQRPALD-LLLGSDASITCTLNGL--RDEGAV 287
|| || : : : : : || : | | | | |

QY 298 FNNYVDGVEVHNKTKPREEQYNST--YRVVSVLTVLHODWLNCKEYKCKVSNKALPAP 354
|| || : : : : : || : | | | | |
Db 288 FTW-----EPSTGDAVKQAVQNSCGYSVSVLPFGCAERNWNSGASFKCTVTHPESDT- 341
|| || : : : : : || : | | | | |

QY 355 IEKTIISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVKGYFSPDIAVEWESNGQ---P 410
|| || : : : : : || : | | | | |
Db 342 LTGTIAKVTVNTPPQVHLPPPPSEALNELVSLTCLVRAFNPREVLVRLHGNELSP 401
|| || : : : : : || : | | | | |

QY 411 ENNYKTTTPVLDSDG--SFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTKQSLSLP 468
|| || : : : : : || : | | | | |
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Db 402 ESYLVEPLKEPEGEGATYLVTSVLRVSABIKWQGOYSQVCMVGHEALPMNFTQKTIDRLS 461
|| || : : : : : || : | | | | |
QY 469 GK 470
|| || : : : : : || : | | | | |
Db 462 GK 463
|| || : : : : : || : | | | | |

RESULT 12
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL 54.2 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IG_4.
DR SMART; SM00407; IGcl_2.
DR SMART; SM00406; Igv_1.
DR SMART; SM00410; IG-like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;
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Query Match 34.2%; Score 862; DB 4; Length 500;
Best Local Similarity 41.3%; Pred. No. 6e-64;
Matches 207; Conservative 67; Mismatches 177; Indels 50; Gaps 18;

QY 1 MGWSCILLFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNQWVRQAP 60
|| || : : : : : || : | | | | |
Db 1 MDWTSILFLVAAATGAOSQVHLVQSGAEVMPGASVRSVRSCKTSGYAFHTYSIIWVRQAP 60
|| || : : : : : || : | | | | |

QY 61 GOGLEWMEIDPSDSTYNNQKFGKATLTVDTSSTAYMELSSLSRSEDATVYICARNR- 119
|| || : : : : : || : | | | | |
Db 61 GOGLEWGMHISPDSDNTREFAKFGQGVTLTDTSTSTVYMELESLRSDDTAVYICARRYC 120
|| || : : : : : || : | | | | |

QY 120 DYS---NNMYF---DWGOGTLTVYSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYF 173
|| || : : : : : || : | | | | |
Db 121 SYSSQNDYIIYVMDVWGKGTITVYSSASPTSPKVPPLSLS-TQPDGNVVIACLQVQGF 179
|| || : : : : : || : | | | | |

QY 174 P-EPYTVSNWSGALTSGVITFPAVLQSSG-LYSLSSVTVTPSSS-LGTQYICNVNHNKPS 230
|| || : : : : : || : | | | | |
Db 180 POEPLSVTWSGESQGVTAARNFPFSDQASGDLYTTSQTLTPATQCLAGKSVTCHVKHY-T 238
|| || : : : : : || : | | | | |

QY 231 NTKVDKRVBPKSCDKTHTCPCPAPELGGPSVFLPFPKPK-----DTLM 275
|| || : : : : : || : | | | | |
Db 239 NPSQDVTV-----PCVPSTPTPTSPST-PPTPSPSCCHPRLSLHRALEDLL 285
|| || : : : : : || : | | | | |

QY 276 ISRTPEVTCVVVDVSHEDPEVKFNMVYDGVGEVHNHAKTKPREEQYNSTYRVVSVLTVLHOD 335
|| || : : : : : || : | | | | |
Db 286 LGSEANLFTCTLGL-RDASGVTFWTTPSSGK--SAVGPPDRDLGCGYSVSSVLSGCAEP 342
|| || : : : : : || : | | | | |

QY 336 WLNKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREEMTKNQ-VSLTCLVK 394
|| || : : : : : || : | | | | |
Db 343 WHNGKFTTCTAAYPESKTPTLTATLSKS-GNTPRPEVHLLPPPPSEALNELVTLTCLARG 401
|| || : : : : : || : | | | | |
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Qy 395 FYPSEDIAVENESGQ--PENNYKTTTPPVL-DSDG--SFFLYSKLTVDKSRWQGNVFS 449
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 402 FSPKDLVLRWLGQSQELPREKYLTWASRQEPSQGTTFFAVTSILRYAAEDKKGDTFS 461
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 450 VMHEALHNHYTKQSLSLSPQK 470
      ||||  ||||  |||
Db 462 VGHEALPFTQETIDRLAGK 482
      ||||  ||||  |||

RESULT 13
Q91WT1
ID Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.1 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RC Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC013490; AAH13490.1; -.
SQ Hypothetical protein.
KW SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

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RESULT 14
Q91WRI ID Q91WRI PRELIMINARY; PRT; 488 AA.
AC Q91WRI;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DE HYPOTHETICAL 53.0 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013539; AH13539.1; -
KW Hypothetical protein.
SQ SEQUENCE 488 AA; 52964 MW; F12068460B400B9D CRC64;

Query Match 32.5%; Score 817; DB 11; Length 488;
Best Local Similarity 39.2%; Pred. No. 3.4e-60;
Matches 191; Conservative 85; Mismatches 177; Indels 34; Gaps

Qy 1 MGNSCIILFVATATGVHSQVQLVQSGAEVYKPKGASVYKSCKASGYTFTSYNMOWYRQAP 60
Db 1 MGNNWIFELLSGTAGIYSEVQLQSGPELVKPGASVYKSCKASGYTITDYVYVWVYKQSH 60

Qy 61 GQGLEWGEIDPSDYSYNYNOKFKGATLVTDVSTSTAYMELSSLSRSEDATVAYYCARNRD 120
Db 61 GKSLEWGDINPYNGGTSYNQKFKGATLVTDKSSSIAYMQLNNLTSDDSAVYICARGPV 120

Qy 121 YSNWYF----DWVGQGLTVTVSSASTKGSVFPLAPSSKSGCTAALGCLVKDYFPE 175
Db 121 YYS--YFSYDRGDYWGQGLTVTVSAEPAREPTIYPLT-PPQALLSDPVIIGLIHDYFPS 177

Qy 176 -PVTVSNWNGALTSGVHTFFAVILQSGSLYSLSSVWTVVPSSSLGT-QTYICNVNHHKPSNTK 233
Db 178 GTMNVTWKGSKDITTVNFFPALASGGRYTMSSQLTLPVCEPGESEVKCSVQH-DSNPV 236

Qy 234 VDKRVEPKSDCKHTCCPPAPPELLGGPSVFLPPTPKDTLMTSRPTEVTCVVVDVSHED 293
Db 237 QELNVNCGICSPPTTPPPSPSCQ-----PSLSLQRPALSD-LLLGSDASITCTLNLG--RD 289

Qy 294 PE-VKENVYVDGVEVHNAKTKPREQYNSTP--YRVSVTLTVLHDWLNGKEYCKVSKN 349
Db 290 PEGAVFTW-----EPSTGKDAVKAVQNGCGCYSSVSLPFGCAERNWNGASFCVTTHP 344

Qy 350 ALPAIEKTIKAKGQPREPQVTLPPSRREMTKQ-VSLTCLVKGFIYPSDIAVESNG 408
Db 345 ESDI-LNGTIKTYVNTFPQVHLLPPPSSEALNELVSLTCLVRAFNPKEVLVRLHGN 403

Qy 409 Q---PENNYKTTPLVDSGDG--SEFFLYSKLTVDKSRKQNGQVSCSMHEALHNHTQKS 463
Db 404 EELSPESYLVEPLKEGEGATTYLVTSVLRVSAEIKWQGDQYSCMWGHEALPMNFTQKT 463

Qy 464 LSLSPGK 470
Db 464 IDRLSGK 470

RESULT 15
Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:15:40 ; Search time 230.21 Seconds
(without alignments)
226.770 Million cell updates/sec

Title: US-09-499-662-157
Perfect score: 2518
Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALNHVTKSLSPQK 470

Scoring table:
BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
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19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
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21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2518	100.0	470	21	AAW90936 Humanised HFE7A de
2	2498	99.2	470	19	AAW83037 Anti-Fas humanised
3	2498	99.2	470	21	AAW83037 Humanised anti-Fas
4	2498	99.2	470	21	AAW90929 Humanised HFE7A de
5	2498	99.2	470	21	AAW90935 Humanised anti-Fas
6	2497	99.2	470	21	AAW90934 Humanised anti-Fas
7	2495	99.1	470	21	AAW90933 Humanised anti-Fas
8	2485	98.7	470	19	AAW83036 Anti-Fas humanised
9	2485	98.7	470	21	AAW83036 Humanised anti-Fas
10	2485	98.7	470	21	AAW90926 Humanised HFE7A de
11	2363.5	93.9	731	22	AAW52156 Humanised HMF-1 h

12	2363.5	93.9	741	22	AAW52159 Humanised HMF-1 h
13	2358.5	93.7	729	22	AAW52158 Humanised HMF-1 h
14	2358.5	93.7	739	22	AAW52161 Humanised HMF-1 h
15	2352.5	93.4	730	22	AAW52157 Humanised HMF-1 h
16	2352.5	93.4	740	22	AAW52160 Humanised HMF-1 h
17	2291.5	91.0	465	22	AAW72228 Humanised 323/A3 (
18	2289	90.9	652	19	AAW48650 Heavy chain of hma
19	2286.5	90.8	464	22	AAW72232 Humanised 323/A3 (
20	2274	90.3	470	21	AAW80826 A dimeric anti-CD2
21	2269	90.1	476	20	AAW88464 Monoclonal antibody
22	2264	89.9	466	22	AAW83755 Chimeric 2403 IgG
23	2259.5	89.7	481	13	AAW24442 Sequence of anti-bo
24	2238	88.9	472	20	AAW50166 Human reshaped F19
25	2238	88.9	476	14	AAW31023 Antibody D heavy c
26	2230	88.6	449	14	AAW33339 Completely humanis
27	2230	88.6	449	19	AAW49816 Amino acid sequenc
28	2219.5	88.1	583	22	AAW83156 Ganglioside GM2 an
29	2210.5	87.8	452	20	AAW29458 Recombinant immuno
30	2210.5	87.8	452	21	AAW30322 Humanised anti-IL-
31	2210.5	87.8	452	21	AAW77766 Humanised anti-IL-
32	2207.5	87.7	467	22	AAW36210 Human immune syste
33	2201.5	87.4	452	19	AAW69316 Anti-IL-8 humanise
34	2193	87.1	474	22	AAW14177 Human novel protei
35	2192.5	87.1	473	22	AAW64475 Human type antihum
36	2190	87.0	472	20	AAW50157 Chimeric mouse/hum
37	2189.5	87.0	473	22	AAW64471 Human type antihum
38	2184.5	86.8	473	22	AAW64469 Human type antihum
39	2183.5	86.7	475	22	AAW63640 Amino acid sequenc
40	2177.5	86.5	473	22	AAW64473 Human type antihum
41	2172	86.3	468	20	AAW85689 D9D10 heavy chain
42	2172	86.3	711	20	AAW85692 MoAb1 fusion pro
43	2171	86.2	592	22	AAW83838 Amino acid sequenc
44	2168	86.1	595	20	AAW86003 Anti-5T4 single ch
45	2161	85.8	470	13	AAW22757 Reshaped CAMPATH-1

ALIGNMENTS

RESULT 1
AAW90936
ID AAW90936 standard; Protein; 470 AA.
AC AAW90936;
XX
XX
DT 08-AUG-2000 (first entry)
DE Humanised HFE7A designed heavy chain HHH type protein.
XX
KW Fas; antibody: human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiac;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antifertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Sjogren's disease; rheumatoid arthritis; graft versus host disease;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
XX
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI: 2000-258930/23.
 DR N-PSDB; AAL11655.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Claim 2: Page 188-189; 263pp; English.
 XX
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymomimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A heavy chain construct HHH type
 CC which is described in the method of the invention.
 XX
 XX Sequence 470 AA:

Query Match 100.0%; Score 2518; DB 21; Length 470;
 Best Local Similarity 100.0%; Pred. No. 1.4e-144;
 Matches 470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 mgwscIIILflvatatgvhsqvlqsgaeVkkpgasvkYscKasgytftsyMMqwrqap 60
 QY 61 GQGLEWNGEIDPSDYTNYNQKFKGRVTITRDTSTAYMELSSLRSEDTAVYYCARNRD 120
 DB 61 gqgleWNGeidpsdytnynqkfkgrvtITrdtstAYmELsslrSEdtavYYcarnrd 120
 QY 121 YSNNNYFDVWGGTGLVTWSSASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVVS 180
 DB 121 ysnnnYfdvWggTglvtWssastkGpsvEplapssKstsggTaaLgclvKdyfpeptvs 180
 QY 181 WNSGALTSCVHHFPAVLQSSGLYSLSSVTVPSSSLIGTQTYICNVNHRPSNTKVKRVEP 240
 DB 181 wnsGaltscvHhfpavLqssGLySLssvTVpssSLIGtqTYiCNvNhrpsntKvkRvep 240
 QY 241 KSCDTHTCPPCPAPPELGGPSVEFPKPKDITLMSRTPETCVVDVSHEDPEVKFNW 300
 DB 241 kscdthtcppcpaPElGGpsvEfpkPKdITlmsrtpETcvvDVshEDpeVkfNw 300
 QY 301 YVDGEVHNNAKTPREQNTYRVRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
 DB 301 yvdGEvhnNAktpREqNTyRvrVsvLTvLhqDWlNGKeyCKvsnKAlpAPIeKtIs 360
 QY 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGYGPPVSDIAVEWESNGQPENNYKTPPV 420
 DB 361 kAkGqprePoVytLppSreEMtknQvSLtclvKgyGppvSDiAveWesNgqPeNnykTppv 420

DB 361 kAkGqprePqvYtlppSreemtknqVslTclvKgyfPsdIaveWesngqPenNyktppv 420
 QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKLSLSpgk 470
 DB 421 lQsdgsfflyskltvdKsrwQgnvfCscvMhealhnhytqKlsLsIsPgk 470
 RESULT 2
 AAW83037
 ID AAW83037 standard; Protein; 470 AA.
 XX
 AC AAW83037;
 XX 15-MAR-1999 (first entry)
 DE Anti-Fas humanised antibody HFE7A heavy chain.
 XX
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
 KW apoptosis; HFE7A; autoimmune disease; Hashimoto's disease;
 KW systemic lupus erythematosus; graft versus host disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease;
 KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
 KW rheumatoid arthritis; autoimmune haemolytic anaemia;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease;
 KW thrombopenia purpura; insulin-dependent diabetes; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy.
 XX Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Sig_peptide
 FT Region /label= Mat_protein
 FT Region 20..140
 FT Region /label= Variable
 FT Region 141..464
 FT Region /label= Constant
 FT Region 50..54
 FT Region /label= CDR_H1
 FT Region /note= "claim 9"
 FT Region 69..84
 FT Region /label= CDR_H2
 FT Region /note= "claim 9"
 FT Region 118..129
 FT Region /label= CDR_H3
 FT Region /note= "claim 9"
 XX AU9859701-A.
 PD 08-OCT-1998.
 XX 30-MAR-1998; 98AU-0059701.
 PR 08-OCT-1997; 97JP-0276064.
 PR 01-APR-1997; 97JP-0082953.
 PR 25-JUN-1997; 97JP-0169088.
 PA (SANY) SANKYO CO LTD.
 XX Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
 PI Masahiko O, Nobufusa S, Shin Y, Tohru T;
 XX WPI; 1998-543440/47.
 DR N-PSDB; AAV70080.
 XX
 PT New antibodies and proteins bind conserved epitope of Fas antigen -
 PT used to evaluate drugs in animal models and to treat Fas-associated
 PT diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
 PT myocarditis, hepatitis and AIDS

```
xx Claim 22; Page 225-227; 292pp; English.
xx This is the amino acid sequence of the HV type humanised heavy
cc chain of murine anti-human Fas monoclonal antibody HFE7A. It
cc includes humanising R44G and A76T amino acid substitutions that are
cc are conserved in the human IgG heavy chain. Host Escherichia coli
cc pGHPDHV3 SANK 70298 harbors plasmid pGHPDHV3 carrying a fusion
cc fragment of the humanised HV type HFE7A heavy chain and DNA
cc encoding human IgG1 constant region (see AAV70080), and is deposited
cc as FERM BP-6273 (claimed). The invention provides methods for
cc producing humanised antibodies by culturing host cells. Humanised
cc versions of HFE7A (see AAN83031-37), like native HFE7A, are capable
cc of inducing apoptosis in abnormal cells expressing Fas, and of
cc inhibiting Fas-induced apoptosis in normal cells. The humanised
cc antibodies are used to evaluate, in animal models, treatments of
cc diseases that involve Fas/Fas ligand interactions, and also to
cc treat such diseases, including autoimmune disease (e.g. systemic
cc lupus erythematosus, Hashimoto's disease, graft versus host disease,
cc Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
cc Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
cc autoimmune haemolytic anaemia, sterility, myasthenia gravis,
cc multiple scl rosis, Basedow's disease, thrombopenia purpura and
cc insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
cc myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
cc anaemia, hepatitis, AIDS and transplant rejection (all claimed).
xx
xx Sequence 470 AA;
xx
xx Query Match 99.2%; Score 2498; DB 19; Length 470;
xx Best Local Similarity 98.9%; Pred. No. 2.3e-143;
xx Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
xx
Qy 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 mgwscililflvatatgvhsqvlvqsgaevkkpgasvkvsckasgytftsywmqwrqap 60
Qy 61 GQGLEWMEIDPDSYTNYNQKFKGRVITRDTSTSTAYMELSLRSEDATVYICARNRD 120
Db 61 ggglewmgeidpsdysytnynqkfgkatltvdtststaymelslrse dtavyyicarnrd 120
Qy 121 YSNWNYFDWGEGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 180
Db 121 ysnwnyfdwgeglvtvssastkgpsvfplapsksts ggtaalgc lvykdyfpepvtvs 180
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
Db 181 wnsгалtsgvhtfpav lqssg lylsslsvtvtpssslgtqt yicnvn hnkpsntkvdkrv 240
Qy 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkhtccpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
Qy 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnatkpreeqynstyrvsvsltlv l hqdwlngkeykckvsnkalpapiektis 360
Qy 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 361 kakgqprepqvytlppsreemtknqvsltclvkgyfypsdiavewesngqpennykttppv 420
Qy 421 LDSGSEFFLYSKLTVDKSRWQQGNVFCSVNHEALHNHYTOKSLSLSPGK 470
Db 421 lds gsefflyskltvdksrwqqgnvfscsvnmhealhnhytokslslspgk 470
xx
RESULT 3
ID AAB14779
xx AAB14779 standard; Protein; 470 AA.
xx
xx AAB14779;
xx
```

```
DT 24-NOV-2000 (first entry)
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:117.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pannyelophthisis;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
JP2000169393-A.
20-JUN-2000.
XX
30-SEP-1999; 99JP-0278301.
XX
30-SEP-1998; 98JP-0276883.
XX
(SANY ) SANKYO CO LTD.
XX
WPI; 2000-485645/43.
DR N-PSDB; AAA72184.
XX
Preventive or treating agent for the diseases caused by an abnormality
in the Fas/Fas ligand system e.g. autoimmune diseases, contains
anti-Fas antibody -
XX
Claim 21; Page 108-109; 139pp; Japanese.
XX
The invention relates to compositions for the prevention or treatment
or diseases caused by an abnormality in the Fas/Fas ligand system
containing an anti-Fas antibody as the active component. The anti-Fas
antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
or a humanised version of HFE7A containing identical CDRs
(complementarity determining regions) to antibody HFE7A. Via its
interaction with Fas, the antibody of the invention may therefore be used in
of apoptosis. The compositions of the invention may therefore be used in
the treatment or prevention of conditions such as autoimmune diseases,
allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
represent the heavy chains (or fragments thereof) of various humanised
HFE7A-derived anti-Fas antibodies.
XX
Sequence 470 AA;
XX
Query Match 99.2%; Score 2498; DB 21; Length 470;
Best Local Similarity 98.9%; Pred. No. 2.3e-143;
Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 mgwscililflvatatgvhsqvlvqsgaevkkpgasvkvsckasgytftsywmqwrqap 60
Qy 61 GQGLEWMEIDPDSYTNYNQKFKGRVITRDTSTSTAYMELSLRSEDATVYICARNRD 120
Db 61 ggglewmgeidpsdysytnynqkfgkatltvdtststaymelslrse dtavyyicarnrd 120
Qy 121 YSNWNYFDWGEGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 180
Db 121 ysnwnyfdwgeglvtvssastkgpsvfplapsksts ggtaalgc lvykdyfpepvtvs 180
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
Db 181 wnsгалtsgvhtfpav lqssg lylsslsvtvtpssslgtqt yicnvn hnkpsntkvdkrv 240
Qy 241 KSCDKHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkhtccpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
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Db 241 kscdkthtccpccpapellggpsvflfpkpkdltmsrtpevtcvvvdvshedpevkfnw 300
 QY 301 YVDGVEVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIS 360
 CC |||||||
 Db 301 yvdgvevhnaktprceeqnystyrsvltvlhqdwlngkeyckvsnkalpapiektis 360
 CC |||||||
 QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPV 420
 CC |||||||
 Db 361 kagqpreqvyltppsreemtknqvsltclvkgyfypsdiavewesngqpennnyktppv 420
 CC |||||||
 QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFSCVSMHEALHNHYTQKSLSLSPGK 470
 CC |||||||
 Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispgk 470
 CC |||||||

RESULT 4
 AAW90929 standard; Protein; 470 AA.
 AC AAW90929;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised HFE7A designed heavy chain protein #2.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 XX
 OS Synthetic.
 XX
 PN EP990663-A2.
 XX
 PD 05-APR-2000.
 XX
 PF 29-SEP-1999; 99EP-0307711.
 XX
 PR 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI: 2000-258930/23.
 XX N-PSDB: AA11622.
 DR
 DR
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Example reference 22; Page 150-152; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic

CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 470 AA;

Query Match 99.2%; Score 2498; DB 21; Length 470;
 Best Local Similarity 98.9%; Pred. No. 2.3e-143;
 Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSQVQLVQSGAEVKKPCASVKVSKASGTYFTSYWQWVRQAP 60
 Db 1 mgwscililflvatatgvhsqqlvqsgaevkpkpgasvkvsckasgytfsywmqwkqap 60
 QY 61 GQGLEWNGEIDPSDSTNNQKFKGRVITRDTSTAYMELSSLSRSEDFAVYTCARNRD 120
 Db 61 gqglewngeidpsdstnynqkfkgtatitvdtstststststststststststststst 120
 QY 121 YSNWYFDVWNGEGLTVTVSSASTKGPSVPLAPSKSTSGGTAAALGCLVKDYDPEPVTVS 180
 Db 121 ysnwyfdvwgegltlvtvsastkgpsvplapskstsgtgaalgclvkdypetvts 180
 QY 181 WNSGALTSGVHFFPAVLQSSGLYSLSSVTVTPSSSLGCTQTYICNVNHNKPSNTKVDKRV 240
 Db 181 wnsгалtsгvhtfpavlqssglyslssvstvtpssslgtqtyicnvnhkpsntkvdkrv 240
 QY 241 KSCDKHTPCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
 Db 241 kscdkhtcpcpccpapellggpsvflfpkpkdltmsrtpevtcvvvdvshedpevkfnw 300
 QY 301 YVDGVEVHNAKTPREEQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIS 360
 Db 301 yvdgvevhnaktprceeqnystyrsvsvltvlhqdwlngkeyckvsnkalpapiektis 360
 QY 361 KAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPV 420
 Db 361 kagqpreqvyltppsreemtknqvsltclvkgyfypsdiavewesngqpennnyktppv 420
 QY 421 LQSDGSFFLYSKLTVDKSRWQGNVFSCVSMHEALHNHYTQKSLSLSPGK 470
 Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhealhnhytqkslsispgk 470

RESULT 5
 AAW90935
 ID AAW90935 standard; Protein; 470 AA.
 XX
 AC AAW90935;
 XX
 DT 08-AUG-2000 (first entry)
 XX
 DE Humanised anti-Fas designed heavy chain Heu 3 protein.
 XX
 KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;

CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 2
 CC which is described in the method of the invention.

XX
 SQ Sequence 470 AA:

Query Match 99.2%; Score 2497; DB 21; Length 470;
 Best Local Similarity 98.9%; Pred. No. 2.6e-143;
 Matches 465; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIILFLVATATGVHQSQVQLVQSGAEVKKPGASVKYSCASGTYFTSYWQWVROAP 60
 DB 1 mgwscilflvatatgvhqsqvlvqsgaevkkpgasvkyscasgyftfsywmqwkqap 60
 QY 61 GQGLEWMEIDPSDSTYNQKFGKRVTTITRTSTSTAYMELSSRSEDVAVYYCARNRD 120
 DB 61 gqglewmgeidpsdsytnynqkfgkatitvdtststaymelslrsedtavyycaarnrd 120
 QY 121 YSNWYFDVWGEGTLVTVSASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYS 180
 DB 121 ysnwyfdvwwggtlvtvsastkgsvpflapsskstsggtaalgclvdyfpeptvys 180
 QY 181 WNSGALTSVGHVFPVQLQSGSLYSLSSVYVTPVSSSLGTQTYICNVNHKPSNTKVDKRVP 240
 DB 181 wnsгалtsvghvfpavlqsgslgylsylvtpvssslgtqtyicnvnhkpsntkvdkrvp 240
 QY 241 KSCDKHTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNM 300
 DB 241 kscdkthtccpcapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
 QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVTLHQDLNGKEVKCKVSKNALPAPIETK 360
 DB 301 yvdgvevhnaaktpreeqynstyrvvsvltvltlhdqdlngkevckvsknkalpapietk 360
 QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPV 420
 DB 361 kagqprepqvylppsreemtknqvsltcclvkgyfypsdiavewesngqpennnyktppv 420
 QY 421 LDSGDSFFLYSKLTVDKSRWQQGNFVSCSVMEALHNHYTQKSLSLSPGK 470
 DB 421 ldsdgsfflyskltdksrwqqgnvfscsvmhealhnhytqkslsispok 470

RESULT 7

AAW90933
 ID AAW90933 standard; Protein; 470 AA.

XX AAW90933;

XX DT 08-AUG-2000 (first entry)

XX

DE Humanised anti-Fas designed heavy chain Heu 1 protein.
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
 OS Synthetic.
 XX EP990663-A2.
 PN 05-APR-2000.
 XX 29-SEP-1999; 99EP-0307711.
 PF 30-SEP-1998; 98JP-0276881.
 PR 30-SEP-1998; 98JP-0276882.
 XX (SANY) SANKYO CO LTD.
 PA Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI WPI; 2000-258930/23.
 XX N-PSDB; AAA11644.
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX Claim 2; Page 169-170; 263pp; English.

CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody heavy chain construct designated Heu 1
 CC which is described in the method of the invention.

SQ Sequence 470 AA:

Query Match 99.1%; Score 2495; DB 21; Length 470;
 Best Local Similarity 98.7%; Pred. No. 3.5e-143;
 Matches 464; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYSFTSTWMMQVROAP 60
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkvpasvkvsckasgytftsymbqwkqap 60
QY 61 GQGLEWMEIDPDSYNYNQKFGRYVITTRDTSTSTAYMELSSLSRSEDTAIVYVCARNRD 120
Db 61 gqglewmgeidpsdsynynqkfkgkatltvdtststaymelslrsedtaviycarnrd 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVTS 180
Db 121 ysnwfyfdvwgegltlvtvssastkgpsvfplapssksts ggtaalglclvkdypfpvptvs 180
QY 181 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQRTYICNVNHNKPSNTKVDKRVPE 240
Db 181 wnsгалtsqvhtfpavilqssglsylssvvtvpssslgtqtyicnvnhkpsntkvdkrvpe 240
QY 241 KSCDKTHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpcapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNNAKTPREEQYNSTYRVWSVLTVLHODWLNKREYCKVSNKALPAPIETIS 360
Db 301 yvdgvevhnaktprreeqynstyrvwsvltvlhqdwlngkeyckvsnkalpapiektis 360
QY 361 KAKQCPREPQVYIPLPREEETKKNQVSLTCLVKGFGYFSDIAVESNGQPNNTKTPPV 420
Db 361 kakqgprepqvtyiplpreetknqvsltcclvkgfypsdiaveshgqpennytktppv 420
QY 421 LDSGSEFLYSLKLVNDRSRWQGVNFCVSMHEALHNHYTOKLSLSPGK 470
Db 421 ldsgefflyskltvdksrwqgvnfcsvmhealhnhytqkslspsgk 470
RESULT 8
ID AAW83036
XX AAW83036 standard; Protein; 470 AA.
AC AAW83036;
XX
DT 15-MAR-1999 (first entry)
XX
DE Anti-Fas humanised antibody HFE7A heavy chain.
XX
KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody;
KW apotosis; HFE7A; autoimmune disease; Hashimoto's disease;
KW systemic lupus erythematosus; graft versus host disease;
KW Sjogren syndrome; pernicious anaemia; Addison's disease;
KW scleroderma; Goodpasture syndrome; Crohn's disease; sterility;
KW rheumatoid arthritis; autoimmune haemolytic anaemia;
KW myasthenia gravis; multiple sclerosis; Basedow's disease;
KW thrombopenia purpura; insulin-dependent diabetes; allergy;
KW atopy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
KW transplant rejection; therapy.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /label= Sig_peptide
FT /label= Mat_protein
FT Region 20..470
FT /label= Variable
FT Region 141..464
FT /label= Constant
FT Region 50..54
FT /label= CDR_H1
FT /note= "claim 9"
FT Region 69..84
FT /label= CDR_H2
FT /note= "claim 9"

Region 118..129
/label= CDR_H3
/note= "claim 9"
AU9859701-A.
08-OCT-1998.
30-MAR-1998; 98AU-0059701.
08-OCT-1997; 97JP-0276064.
01-APR-1997; 97JP-0082953.
25-JUN-1997; 97JP-0169088.
(SANY) SANKYO CO LTD.
Akio S, Hideyuki H, Hiroko Y, Jun O, Kimihisa I;
Masahiko O, Nobufusa S, Shin Y, Tohru T;
WPI; 1998-543440/47.
N-PSDB; AAV70079.
New antibodies and proteins bind conserved epitope of Fas antigen -
used to evaluate drugs in animal models and to treat Fas-associated
diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
myocarditis, hepatitis and AIDS
Claim 22; Page 212-213; 292pp; English.
This is the amino acid sequence of the VD type humanised heavy
chain of murine anti-human Fas monoclonal antibody HFE7A. E. coli
pghSL7A62 SANK 7397 harbors plasmid pghSL7A62 carrying a fusion
fragment of the humanised VD type HFE7A heavy chain and DNA
encoding human IgG1 constant region (see AAV70079), and is deposited
as FERM BP-6074 (claimed). The invention provides methods for
producing humanised antibodies by culturing host cells. Humanised
versions of HFE7A (see AAW83031-37), like native HFE7A, are capable
of inducing apoptosis in abnormal cells expressing Fas, and of
inhibiting Fas-induced apoptosis in normal cells. The humanised
antibodies are used to evaluate, in animal models, treatments of
diseases that involve Fas/Fas ligand interactions, and also to
treat such diseases, including autoimmune disease (e.g. systemic
lupus erythematosus, Hashimoto's disease, graft versus host disease,
Sjogren syndrome, pernicious anaemia, Addison's disease, scleroderma,
Goodpasture syndrome, Crohn's disease, rheumatoid arthritis,
autoimmune haemolytic anaemia, sterility, myasthenia gravis,
multiple sclerosis, Basedow's disease, thrombopenia purpura and
insulin-dependent diabetes), allergies, atopy, arteriosclerosis,
myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic
anaemia, hepatitis, AIDS and transplant rejection (all claimed).
Sequence 470 AA;
Query Match 98.7%; Score 2485; DB 19; Length 470;
Best Local Similarity 98.5%; Pred. No. 1.4e-142;
Matches 463; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MGWSCIIILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYSFTSTWMMQVROAP 60
Db 1 mgwsciiilflvatatgvsqvlvqsgaevkvpasvkvsckasgytftsymbqwkqap 60
QY 61 GQGLEWMEIDPDSYNYNQKFGRYVITTRDTSTSTAYMELSSLSRSEDTAIVYVCARNRD 120
Db 61 gqglewmgeidpsdsynynqkfkgkatltvdtststaymelslrsedtaviycarnrd 120
QY 121 YSNWYFDVWGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPTVTS 180
Db 121 ysnwfyfdvwgegltlvtvssastkgpsvfplapssksts ggtaalglclvkdypfpvptvs 180
QY 181 WNSGALTSQVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQRTYICNVNHNKPSNTKVDKRVPE 240
Db 181 wnsгалtsqvhtfpavilqssglsylssvvtvpssslgtqtyicnvnhkpsntkvdkrvpe 240

QY 241 KSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpapelggpsvflfpkpdkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db 361 kagqgprepqvyltppsrreemtknqvsltcclvkgyfypsdiavwesngqpennnykttpv 420
QY 421 LDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhytqkslsispgk 470

RESULT 9
AAB14776
ID AAB14776 standard; Protein; 470 AA.
XX
AC AAB14776;
XX
DT 24-NOV-2000 (first entry)
XX
DE Humanised anti-Fas antibody heavy chain, SEQ ID NO:89.
XX
KW Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
KW murine; humanised antibody; complementarity determining region; CDR;
KW human Fas; Fas ligand; apoptosis modulator; programmed cell death;
KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
KW hepatitis; AIDS; graft rejection; heavy chain.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN JP2000169393-A.
XX
PD 20-JUN-2000.
XX
PF 30-SEP-1999; 99JP-0278301.
XX
PR 30-SEP-1998; 98JP-0276883.
XX
PA (SANY) SANKYO CO LTD.
XX
DR WPI; 2000-485645/43.
DR N-PSDB; AAA72159.
XX
PT Preventive or treating agent for the diseases caused by an abnormality
PT in the Fas/Fas ligand system e.g. autoimmune diseases, contains
PT anti-Fas antibody -
XX
PS Claim 21; Page 95-96; 139pp; Japanese.
XX
CC The invention relates to compositions for the prevention or treatment
CC of diseases caused by an abnormality in the Fas/Fas ligand system
CC containing an anti-Fas antibody as the active component. The anti-Fas
CC antibody is either the murine anti-human Fas monoclonal antibody HFE7A,
CC or a humanised version of HFE7A containing identical CDRs
CC (complementarity determining regions) to antibody HFE7A. Via its
CC interaction with Fas, the antibody of the invention acts as a modulator
CC of apoptosis. The compositions of the invention may therefore be used in
CC the treatment or prevention of conditions such as autoimmune diseases,
CC allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS
CC and organ graft rejection. Sequences AAB14775-B14776 and AAB14779
CC represent the heavy chains (or fragments thereof) of various humanised
CC HFE7A-derived anti-Fas antibodies.
XX
SQ Sequence 470 AA;

Query Match 98.7%; Score 2485; DB 21; Length 470;
Best Local Similarity 98.5%; Pred. No. 1.4e-142;
Matches 463; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MGWSCIILFLVATATGVHISOVLQSGAEVKKPGASVKVSCKASGVTFTSYWQWVRQAP 60
Db 1 mgwscililflvatatgvhsqqlvqgaevkpgasvkvsckasgytftsywmqwkqap 60
QY 61 GQGLEWMEIDSDSTNNQKFKGRVTITRDTSTSTAYMELSLRSEDATVYICARNRD 120
Db 61 gqrlewmgeidpsdsytnynqkfkgtatltdtsastaymelslrsedatvyyicarnrd 120
QY 121 YSNWYFDVWGEGLTVTSASATKGPSVFPLAPSSKSTSGTAALGCLVKDYPEPEPTVS 180
Db 121 ysnwyfdvwwgegltlvtssastkgpsvfplapsskstsgttaalgclvkdyppeptvs 180
QY 181 WNSGALTSGVHTFPAVLQSGSLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKYDKRVEP 240
Db 181 wnsгалtsgvhtfpavllqsgslyslssvvtvpssslgtqtyicnvnhkpsntkydkrvrep 240
QY 241 KSCDKTHTCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 241 kscdkthtccpapelggpsvflfpkpdkdtlmisrtpevtcvvvdvshedpevkfnw 300
QY 301 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 360
QY 361 KAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPV 420
Db 361 kagqgprepqvyltppsrreemtknqvsltcclvkgyfypsdiavwesngqpennnykttpv 420
QY 421 LDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 421 ldsdgsfflyskltvdksrwqgnvfscsvmhéalhnhytqkslsispgk 470

RESULT 10
AAW90926
ID AAW90926 standard; Protein; 470 AA.
XX
AC AAW90926;
XX
DT 08-AUG-2000 (first entry)
XX
DE Humanised HFE7A designed heavy chain protein.
XX
KW Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
XX
OS Synthetic.
XX
PN EP990663-A2.
XX
PD 05-APR-2000.
XX
PF 29-SEP-1999; 99EP-0307711.
XX
PR 30-SEP-1998; 98JP-0276881.
XX
PR 30-SEP-1998; 98JP-0276882.
XX
PA (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 XX WPI; 2000-258930/23.
 DR N-PSDB; AAA11597.
 XX
 PT New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems -
 XX
 XX Example reference 15; Page 134-136; 263pp; English.
 XX
 CC This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thyromimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive
 CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC a humanised anti-Fas antibody HFE7A designed heavy chain which is used in
 CC the method described in the invention.
 XX
 SQ Sequence 470 AA;

Query Match 98.7%; Score 2485; DB 21; Length 470;
 Best Local Similarity 98.5%; Pred. No. 1.4e-142;
 Matches 463; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MGWSCILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWRQAP 60
 DB 1 mgwscilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftsyymmqrkqap 60
 QY 61 GQGLEWMGEIDPDSYNYNOKFKGRVTITRTDTSTAYMELSLRSEDATVYYCARNRD 120
 DB 61 gqglewmgeidpsdyntynokfgrvttitrtdstaymelslrsedatvyyccarnrd 120
 QY 121 YSNWNYFDVWGEGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 DB 121 ysnwnyfdvwegtltvtvssastkgpsvfplapsskstsaggtaalgclvkdypfepvtvs 180
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
 DB 181 wnsгалtsgvhtfpavllqssglyslssvwtvppssslgtqtyicnvnhnkpsntkvdkrv 240
 QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKFNN 300
 DB 241 kscdkthtccpcpapelggpsvflfppkpkdtlmisrtpevtcvvyvshedpevkfnw 300
 QY 301 YVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHDWLNKGKEYCKVSNKALPAPIETIS 360
 DB 301 yvdgvevhnaktkpreeqynstyrvvsvltvlhdwlngkeyckvsnkalpapietis 360
 QY 361 KAGQPREPQVYTLPPSREEMTKNQVSLTCLVLKGFPYSDIAVEWESNGQPENNYKTTPPV 420
 DB 361 kagqprepqvylppspreemtknqvsltclvlkgfpydsiavewesngqpennyktppv 420

DB 361 kagqprepqvylppspreemtknqvsltclvlkgfpydsiavewesngqpennyktppv 420
 QY 421 LDSGSEFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTQKSLSPGK 470
 DB 421 ldsdgsfllyskltvdksrwqgnvfscsvmhealhnhytqkslspgk 470
 RESULT 11
 AAM52156
 ID AAM52156 standard; Protein; 731 AA.
 XX
 AC AAM52156;
 XX
 DT 05-FEB-2002 (first entry)
 XX
 DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.
 XX
 KW Humanised monoclonal antibody; polymorphic epithelial mucin; PBML;
 KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200174905-A1.
 XX
 PD 11-OCT-2001.
 XX
 XX 26-MAR-2001; 2001WO-GB01324.
 PF
 PR 03-APR-2000; 2000GB-0008049.
 PR 02-OCT-2000; 2000US-237159P.
 XX
 XX (ANTI-) ANTISOMA RES LTD.
 XX
 PI Young RJ;
 XX
 DR WPI; 2001-662969/76.
 XX
 PT Novel compound used to treat cancer has target cell-specific portion
 PT comprising humanised monoclonal antibody having specificity for
 PT polymorphic epithelial mucin, and cytotoxic portion having
 PT endonucleolytic activity -
 XX
 PS Claim 20; Figure 7; 176pp; English.
 CC
 CC The invention relates to a compound which comprises a target
 CC cell-specific portion, comprising an humanised monoclonal antibody,
 CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
 CC binding fragment and a cytotoxic portion having endonucleolytic activity,
 CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
 CC compound has cytostatic activity useful for treating cancer and acting as
 CC a potential inducer of apoptosis.
 XX
 SQ Sequence 731 AA;

Query Match 93.9%; Score 2363.5; DB 22; Length 731;
 Best Local Similarity 93.6%; Pred. No. 5.1e-135;
 Matches 440; Conservative 19; Mismatches 8; Indels 3; Gaps 1;
 QY 1 MGWSCILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCKASGYFTSYMMQWRQAP 60
 DB 1 mgwscilflvatatgvhsqvlvqsgaevkpgasvkvsckasgyftsyymmqrkqap 60
 QY 61 GQGLEWMGEIDPDSYNYNOKFKGRVTITRTDTSTAYMELSLRSEDATVYYCARNRD 120
 DB 61 gqglewmgeidpsdyntynokfgrvttitrtdstaymelslrsedatvyyccarnrd 120
 QY 121 YSNWNYFDVWGEGTLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
 DB 121 ysnwnyfdvwegtltvtvssastkgpsvfplapsskstsaggtaalgclvkdypfepvtvs 177
 QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVWTVPPSSSLGTQTYICNVNHNKPSNTKVDKRV 240

CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 729 AA;

Query Match 93.7%; Score 2358.5; DB 22; Length 729;
Best Local Similarity 93.6%; Pred. No. 1e-134;
Matches 439; Conservative 19; Mismatches 8; Indels 3; Gaps 1;
QY 1 MGWSCIIILFLVATATGVHSQVQLVOSGAEVKKPGASVKVCKASGYTFTSYMMQWVRQAP 60
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvcasgytftsyawiewvrqap 60
QY 61 GQGLEWGEIDPSDYTNYNOKFKGRVTITRDTSTSTAYMELSSLRSEDATVYYCARNRD 120
DB 61 gqglewgeidpsdytnynokfgrvtitrdtststaymelslrsedatvyycarsyd 120
QY 121 YSNWNYFDVWEGTGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepptvs 177
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240
DB 178 wnsгалтsgvhtfpavlgssglyslssvtpssslgtqtyicnvnhnkpstkvdkkvep 237
QY 241 KSCDKHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 238 kscdkhtccpcapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297
QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
DB 298 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
DB 358 kakgqprepqvtytlppsreemtqnqvsitclvkgfypsdiavewesngqpennykttppv 417
QY 421 LDSGSEFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 469
DB 418 ldsdgsfflyskltvdksrwggnvfscsvmhealhnhytdqkslsisp 466

RESULT 14

AAM52161
ID AAM52161 standard; Protein; 739 AA.

XX AC AAM52161;

XX DT 05-FEB-2002 (first entry)

XX DE Humanised HMFg-1 heavy chain/DNase I fusion protein 6.

XX XX Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO200174905-A1.

XX PD 11-OCT-2001.

XX XX 26-MAR-2001; 2001WO-GB01324.

XX XX 03-APR-2000; 2000GB-0008049.

XX PR 02-OCT-2000; 2000US-237159P.

XX XX (ANTI-) ANTISOMA RES LTD.

XX

PI Young RJ;

XX DR WPI; 2001-662969/76.

XX XX Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -

XX PS Claim 20; Figure 12; 176pp; English.

XX CC The invention relates to a compound which comprises a target
CC cell-specific portion, comprising an humanised monoclonal antibody,
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen
CC binding fragment and a cytotoxic portion having endonucleolytic activity,
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.

XX SQ Sequence 739 AA;

Query Match 93.7%; Score 2358.5; DB 22; Length 739;
Best Local Similarity 93.6%; Pred. No. 1e-134;
Matches 439; Conservative 19; Mismatches 8; Indels 3; Gaps 1;
QY 1 MGWSCIIILFLVATATGVHSQVQLVOSGAEVKKPGASVKVCKASGYTFTSYMMQWVRQAP 60
DB 1 mgwsciiilflvatatgvhsqvlvqsgaevkpgasvkvcasgytftsyawiewvrqap 60
QY 61 GQGLEWGEIDPSDYTNYNOKFKGRVTITRDTSTSTAYMELSSLRSEDATVYYCARNRD 120
DB 61 gqglewgeidpsdytnynokfgrvtitrdtststaymelslrsedatvyycarsyd 120
QY 121 YSNWNYFDVWEGTGLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTS 180
DB 121 fa---wfaywgggtlvtvssastkgpsvfplapsskstsggtaalgclvkdypfepptvs 177
QY 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVEP 240
DB 178 wnsгалтsgvhtfpavlgssglyslssvtpssslgtqtyicnvnhnkpstkvdkkvep 237
QY 241 KSCDKHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
DB 238 kscdkhtccpcapellggpsvflfppkpkdtlmisrtpevtcvvvdshedpevkfnw 297
QY 301 YVDGVEVHNATKPREQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 360
DB 298 yvdgvevhnatkpreeqynstyrvvsvltvlhqdwlngkeyckvsnkalpapiektis 357
QY 361 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
DB 358 kakgqprepqvtytlppsreemtqnqvsitclvkgfypsdiavewesngqpennykttppv 417
QY 421 LDSGSEFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 469
DB 418 ldsdgsfflyskltvdksrwggnvfscsvmhealhnhytdqkslsisp 466

RESULT 15

AAM52157
ID AAM52157 standard; Protein; 730 AA.

XX AC AAM52157;

XX DT 05-FEB-2002 (first entry)

XX XX Humanised HMFg-1 heavy chain/DNase I fusion protein 2.

XX DE Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.

XX OS Homo sapiens.

Search completed: August 14, 2002, 15:15:41
Job time: 839 sec

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OS Synthetic.
XX WO200174905-A1.
XX PD 11-OCT-2001.
XX PF 26-MAR-2001; 2001WO-GB01324.
XX PR 03-APR-2000; 2000GB-0008049.
XX PR 02-OCT-2000; 2000US-237159P.
XX PA (ANTI-) ANTISOMA RES LTD.
XX PI Young RJ;
XX WPI; 2001-662969/76.
XX PT Novel compound used to treat cancer has target cell-specific portion
PT comprising humanised monoclonal antibody having specificity for
PT polymorphic epithelial mucin, and cytotoxic portion having
PT endonucleolytic activity -
XX
XX Claim 20; Figure 8; 176pp; English.
XX
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity,
XX exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
XX compound has cytostatic activity useful for treating cancer and acting as
XX a potential inducer of apoptosis.
XX
XX Sequence 730 AA;
SQ
Query Match 93.4%; Score 2352.5; DB 22; Length 730;
Best Local Similarity 93.6%; Pred. No. 2.3e-134;
Matches 438; Conservative 19; Mismatches 8; Indels 3; Gaps 1;
QY 1 MGWSCILFLVATATGVHSGVQLVQSGAEVKKPGASVKVSCRASGYTFTSYNMQWVRQAP 60
Db 1 mgwscilflvatatgvhsqqlvqsgaevkpgasvkvsckasgytfsaywiewvrqap 60
QY 61 GCGLEWMEIDPDSVTNTNQKFKRVTTTRDTSTSTAYMELSSLRSEDTAVYYCARNRD 120
Db 61 gkglewmeidpdsvtntnqkfkrvtttrdtststaymelsslrseDTVYYCARSYD 120
QY 121 YSNNNWYFDVWGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS 180
Db 121 fa---wfywgggtlvvssastkgpsvfplapsskstsggtaalgclvkdyfpepvts 177
QY 181 WNSGALTSVHTFPVAVLQSSGLYSLSVVTVPSSSLGTQYICNVNHNKPSNTKVKRVERP 240
Db 178 wnsгалtsvhtfpavlgsgglysissvvtvpssslgtqyicnvnhkpsntkvdkkvep 237
QY 241 KSCDKTHTCCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 300
Db 238 kscdkthtccpcpapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnw 297
QY 301 YVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 360
Db 298 yvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektis 357
QY 361 KAKGQPREPQVYTLPPSRDEQNKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPV 420
Db 358 kakgqprepqvylppsrdeitknqvsitclvkfgypsdiavewesngqpennyktctppv 417
QY 421 LPSDGSFFLYSKLTVDKSRWQQGNVPCSMHEALHNNHYTKQSLSLSP 468
Db 418 lsdsgsfflyskltvdksrwqqgnvfscsmhealhnhytkqslslslsp 465
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Db 1 MDWTWRFVFAAATGVQSQMVQVQSGAEVKKPGSSVTVVSCSKASGCTFNSYALISWVRQAP 60
QY 61 GQLEWNGEIDPSDSTNTNQKFKGRVTITRTSTSTAYMELSSLRSEDATVYICARNR- 119
Db 61 GQLEWNGGIPLFGTPTTSQNFQGRVTITADKSTSTAHMELTSLRSEDATVYICATDRY 120
QY 120 ----DYSNNVYDVWNGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 174
Db 121 RQANFDRARVGFDPWGQGTFLTVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFP 180
QY 175 EPTVSWNSGALTSVGHVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKV 234
Db 181 EPTVSWNSGALTSVGHVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKV 240
QY 235 DKRVEPKCDKTHCPCPCAPPELLGSPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDP 294
Db 241 DKRVEPKCDKTHCPCPCAPPELLGSPSVFLPPKPKDTLMISRTPEVTVVVDVSHEDP 300
QY 295 EVKFNMYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 354
Db 301 EVKFNMYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
QY 355 IEKTSKAGQPREPOVYITLPSREMTKNQVSLICLVKGFPSDIAVWESNGQPENNY 414
Db 361 IEKTSKAGQPREPOVYITLPSREMTKNQVSLICLVKGFPSDIAVWESNGQPENNY 420
QY 415 KTTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSQVWHEALHNHYTQKSLSLSPGK 470
Db 421 KTTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSQVWHEALHNHYTQKSLSLSPGK 476

RESULT 2

US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085

; GENERAL INFORMATION:
; APPLICANT: CO. Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIb/IIIa
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/458,516

; PRIORITY INFORMATION:
; CLASSIFICATION: 424
; APPLICATION NUMBER: US 08/059,159

; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-458-516-13

Query Match 88.6%; Score 2230; DB 1; Length 449;

Best Local Similarity 93.1%; Pred. No. 2.2e-162;

Matches 420; Conservative 14; Mismatches 15; Indels 2; Gaps 2;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASQYTFSTYMMQVROAPGQLEWMGIDPSDSVNY 79

Db 1 QVQLVQSGAEVKKPGSSVKVSCKASQYATNLYIEWRQAPGQGLEWIGVYIPGSGGTNY 60

QY 80 NQKFKGRVITITDSTSTAYMELSSLRSEDATVYICARNRDYNNYFDVWEGTLTVTS 139

Db 61 NEKFKGRVITLTVDEINTAYMELSSLRSEDATVYFCAR-RDGNYGW-FAYWGQGLTVTS 118

QY 140 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPTVSWNSGALTSVGHVTFPAVLQS 199

Db 119 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPPEPTVSWNSGALTSVGHVTFPAVLQS 178

QY 200 SGLYSLSVSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDTHTCPCPCAPPELLG 259

Db 179 SGLYSLSVSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKRVKPKSCDTHTCPCPCAPPELLG 238

QY 260 GPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 319

Db 239 GPSVFLFPPKPKDTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQY 298

QY 320 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPOVYITLPPSRE 379

Db 299 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTSKAGQPREPOVYITLPPSRE 358

QY 380 EMTKQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVYDKSR 439

Db 359 ELTKNQVSLTCLVKGFPSDIAVWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVYDKSR 418

QY 440 WQGNVFSQVWHEALHNHYTQKSLSLSPGK 470

Db 419 WQGNVFSQVWHEALHNHYTQKSLSLSPGK 449

RESULT 3

US-09-027-449-71

; Sequence 71, Application US/09027449
; Patent No. 6025158

; GENERAL INFORMATION:

; APPLICANT: Gonzalez, Tania R.

; APPLICANT: Leong, Steven R.

; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and

; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/027,449

; FILING DATE: 20-Feb-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/074,330

; FILING DATE: 22-Jan-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/038,664

FILING DATE: 21-Feb-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Love, Richard B.
 REGISTRATION NUMBER: 34,
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-5530
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 452 amino acids
 TYPE: Amino acid
 TOPOLOGY: Linear
 US-09-027-449-71

Query Match 87.8%; Score 2210.5; DB 3; Length 452;
Best Local Similarity 90.3%; Pred. NO. 6.9e-161;
Matches 408; Conservative 27; Mismatches 16; Indels 1; Gaps 1;

Qy	20	QVQLVQSAGAEVKKPGASVKSCAKSGYTTSTSYMQWVRQAPGGLEWMGEIDPSDSYTN	79
Dd	1	EVLVQSGGGLVQPGLSRSLRSCAASGYSSFSHHMHVRQAPGKLGLEWGVYIDPSNGETTY	60
Qy	80	NQKFKGRTITRTDSTSTAYMELSSLRSDEDTAVYYCAR-NRDYSNNNYFDVWGEGFLTV	138
Dd	61	NQRFKGFTILSRDNKNNTAYLQNLSRAEDTAVYYCARGDYRYNGDWFFDVWGQGTLVTV	120
Qy	139	SSASTKGPSVFPLAPSSKTSSTGTGAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAAVLQ	198
Dd	121	SSASTKGPSVFPLAPSSKTSSTGTGAALGCLVKDYFPEPTVSNNSGALTSGVHTFPAAVLQ	180
Qy	199	SSGLYSLSVVTVPPSSSLGQTITICNVNHNKPSNTKYDKVEPKSCDKTHTCPCPAPELL	258
Dd	181	SSGLYSLSVVTVPPSSSLGQTITICNVNHNKPSNTKYDKVEPKSCDKTHTCPCPAPELL	240
Qy	259	GGPSVFLPFPKPDLMIISRTPEVTCTVVDVSHDEDPVKFNMYDVGVEVHNAKTCPREEQ	318
Dd	241	GGPSVFLPFPKPDLMIISRTPEWTCTVVDVSHDEDPVKFNMYDVGVEVHNAKTCPREEQ	300
Qy	319	YNSTRYRVSVLTIVLHDWLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVITYLPSPR	378
Dd	301	YNSTRYRVSVLTIVLHDWLNGKEYCKVSNKALPAPIEKTISKAKQPREPQVITYLPSPR	360
Qy	379	EEMTKNOVSLTCLVKGFYPSDIAVENESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKS	438
Dd	361	EEMTKNOVSLTCLVKGFYPSDIAVENESNGQPNNTKTPPVLDSDGSFFLYSKLTVDKS	420
Qy	439	RWOQGNVFCFSVMHEALHNHYTOKSLSLSPGK	470
Dd	421	RWOQGNVFCFSVMHEALHNHYTOKSLSLSPGK	452

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RESULT      4
US-09-026-985-71
; Sequence 71, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fra
; TITLE OF INVENTION: Humanized An
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB
;

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genetech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-026-985-71

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Query Match	87.8%;	Score	2210.5;	DB	4;	Length	452;
Best Local Similarity	90.3%;	Pred.	No. 6.9e-161;				
Matches	408;	Conservative	27;	Mismatches	16;	Indels	1;
Gaps							
Qy	20	QVQLVQSGAEVKKPGASVKYSCKASGVTFTSYNQWQVRQAPGGGLEWNGEIDPDSDSYTN	79				
Db	1	EVQLVQSGGGLVPGGSLRLISLCAASGYFSFSHHYHWVRQAPGKGLWGVYIDPSNGETTY	60				
Qy	80	NQKFKGRTVITRTDSTSYAMELSSLSRSEDATVYYCAR-NRDYSNNWYFDVMGEGTLVTY	138				
Db	61	NQKFKGRTILSRDNRKNTAYLQNSLRAEDATVYYCARGDYRYNGDWFFDVMGQGLTVTY	120				
Qy	139	SSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTSNNSGALTSGVHTFPAVLQ	198				
Db	121	SSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPTVTSNNSGALTSGVHTFPAVLQ	180				
Qy	199	SSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKRVPEKSCDKTHTCPPCPAPELL	258				
Db	181	SSGLYSLSSVTVTPSSSLGQTQYICNVNHPKSTKVDKRVPEKSCDKTHTCPPCPAPELL	240				
Qy	259	GGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAAKTGPREEQ	318				
Db	241	GGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAAKTGPREEQ	300				
Qy	319	YNSTYRVVSVLTVTHQDWLNGKEYCKVSNKALPAPIETKISAKGQPREPQVYITLPPSR	378				
Db	301	YNSTYRVVSVLTVTHQDWLNGKEYCKVSNKALPAPIETKISAKGQPREPQVYITLPPSR	360				
Qy	379	EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS	438				
Db	361	EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKS	420				
Qy	439	RWQGNVFSCSVMEALHNHYTQKSLSLSPGK	470				
Db	421	RWQGNVFSCSVMEALHNHYTQKSLSLSPGK	452				

```

RESULT      5
US-09-049-672A-8
; Sequence 8, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

```


Patent No. 6350860
GENERAL INFORMATION:
APPLICANT: Buysse, Marie-Ange
ATTORNEY: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS-015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: 711
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90

Query Match 86.3%; Score 2172; DB 4; Length 711;
Best Local Similarity 88.0%; Pred. No. 1.1e-157;
Matches 409; Conservative 20; Mismatches 32; Indels 4; Gaps 1;
Qy 6 IILFLVATGTVHVSQVLQSGAEVKKPGASVKVSKRAGSYTFTSYNMQWVRQAPGQGLE 65
Db 7 IFSELLISASVILQVQLVQSGSELKPKGASVKISCRASGYTFTDYGNNWVKQAPGQGLK 66
Qy 66 WMGEIDPSDSTYNTNQKFKGRVTTTRDTSTSTAYMELSLRSEDYAVYICARNRDSNNW 125
Db 67 WMGWINYTGESTVDDFKGRFVSLDSVSAALQLISLKAEDTATYFCARRGFYA--- 123
Qy 126 YFDVMGEGTLTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 185
Db 124 -MDYWGQGTITVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGA 182
Qy 186 LTSVHTFPVAVLQSSGLYSLSVTVPSSSLGQTQYICNVNHNKPSNTKVKRVEPKSCDK 245
Db 183 LTSVHTFPVAVLQSSGLYSLSVTVPSSSLGQTQYICNVNHNKPSNTKVKRVEPKSCDK 242
Qy 246 THTCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKENYVDGV 305
Db 243 THTCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGV 302
Qy 306 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ 365
Db 303 EVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQ 362
Qy 366 PREQVYTLPPSREMTKNQVSLTCLVKGYFSPDSIAVWESNGQPENNYKTTPPVLDSDG 425
Db 363 PREQVYTLPPSREMTKNQVSLTCLVKGYFSPDSIAVWESNGQPENNYKTTPPVLDSDG 422
Qy 426 SFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 423 SFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 467

RESULT 8
US-08-793-450-8
Sequence 8, Application US/08793450
Patent No. 6312690
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: MARGARITTE, CHRISTEL
APPLICANT: KACZOREK, MICHEL
APPLICANT: CHARABIH, HASSAN
TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION:
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8

Query Match 85.2%; Score 2146; DB 4; Length 472;
Best Local Similarity 85.3%; Pred. No. 6e-156;
Matches 405; Conservative 25; Mismatches 37; Indels 8; Gaps 3;

Qy 1 MGWSCIILFLVATGTVHVSQVLQSGAEVKKPGASVKVSKRAGSYTFTSYNMQWVRQAP 60
Db 1 MGWSCIILFLVATGTVHVSQVLQSGAEVKKPGASVKVSKRAGSYTFTSYNMQWVRQAP 60
Qy 61 GQGLEWMEIDPSDSTYNTNQKFKGRVTTTRDTSTSTAYMELSLRSEDYAVYICARNR 120
Db 61 GQGLEWMEIDPSDSTYNTNQKFKGRVTTTRDTSTSTAYMELSLRSEDYAVYICARNR 119
Qy 121 YSNW----YFDVMGEGTLTVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPE 175
Db 120 Y--KWKYHGDWFDPMGQGTITVSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPE 177
Qy 176 PVTYSWNSGALTSGVHTFPVAVLQSSGLYSLSVTVPSSSLGQTQYICNVNHNKPSNTKVD 235
Db 178 PVTYSWNSGALTSGVHTFPVAVLQSSGLYSLSVTVPSSSLGQTQYICNVNHNKPSNTKVD 237
Qy 236 KRVEPKSCDKTHTCPAPPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPE 295
Db 238 KKAEPKSCDKTQTCPCPAPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPE 297
Qy 296 VKFNMYVDGVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 355
Db 298 VKFNMYVDGVEVHNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 357
Qy 356 EKTISKAKGQPREQVYTLPPSREMTKNQVSLTCLVKGYFSPDSIAVWESNGQPENNYK 415
Db 358 EKTISKAKGQPREQVYTLPPSREMTKNQVSLTCLVKGYFSPDSIAVWESNGQPENNYK 417
Qy 416 TTPPVLDSDGSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 418 TTPPVLDSDGSFFLYSKLTVDKSRWQOQNVFSCSVNHEALHNHYTQKSLSLSPGK 472

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          9
RESULT
US-07-934-373C-22
; Sequence 22, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-JUN-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-9881
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-22

Query Match      85.1%; Score 2142.5; DB 2; Length 454;
Best Local Similarity 88.3%; Pred. No. 1.le-155;
Matches 401; Conservative 20; Mismatches 30; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGGLEWMGGEIDPDSYTN 79
Db 1 QVQLQSGPELVKPGASVKISCKTSGYTFETMTMHWKSHGKSLWIGGFPNKGSSH 60
QY 80 NQKFKGRVITITRDITSTAYMELSLRSDEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
Db 61 NQREWDKATLAVDKSTSTAYMELSLTSDESGIYYCARNRGLNYGFDVYFDVWGAGTIV 120
QY 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSVNSGALTSGVHTFPAV 196
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSVNSGALTSGVHTFPAV 180
QY 197 LOSGGLYSLSSVTVTPSSSLGQTICNVNHRKPSNTKVDKRVKPSCKDTHTCPCPAPPE 256
Db 181 LOSGGLYSLSSVTVTPSSSLGQTICNVNHRKPSNTKVDKRVKPSCKDTHTCPCPAPPE 240
QY 257 LLGGSPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 316
Db 241 LLGGSPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 300
QY 317 EQYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
          9
RESULT
US-08-437-642B-22
; Sequence 22, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-22

Query Match      85.1%; Score 2142.5; DB 3; Length 454;
Best Local Similarity 88.3%; Pred. No. 1.le-155;
Matches 401; Conservative 20; Mismatches 30; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGGLEWMGGEIDPDSYTN 79
Db 1 QVQLQSGPELVKPGASVKISCKTSGYTFETMTMHWKSHGKSLWIGGFPNKGSSH 60
QY 80 NQKFKGRVITITRDITSTAYMELSLRSDEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
          9
RESULT
US-08-437-642B-22
; Sequence 22, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-22

Query Match      85.1%; Score 2142.5; DB 3; Length 454;
Best Local Similarity 88.3%; Pred. No. 1.le-155;
Matches 401; Conservative 20; Mismatches 30; Indels 3; Gaps 1;

QY 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWVRQAPGGLEWMGGEIDPDSYTN 79
Db 1 QVQLQSGPELVKPGASVKISCKTSGYTFETMTMHWKSHGKSLWIGGFPNKGSSH 60
QY 80 NQKFKGRVITITRDITSTAYMELSLRSDEDTAVYYCARNRDYSNNW---YFDVWGEGTLV 136
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Db 61 NORFMDKATLAVDKSTSTAYMELSLRSDSGIYYICARWRLNYGFDVRYFDVWGAGTTV 120
Qy 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 196
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 180
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCCPCPAPE 256
Db 181 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCCPCPAPE 240
Qy 257 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNAKTKPRE 316
Db 241 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNAKTKPRE 300
Qy 317 EOYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
Db 301 EOYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
Qy 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 420
Qy 437 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 454

RESULT 11

PCT-US93-07832-22
; Sequence 22, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

PCT-US93-07832-22

Query Match 85.1%; Score 2142.5; DB 5; Length 454;
Best Local Similarity 88.3%; Pred. No. 1.1e-155;
Matches 401; Conservative 20; Mismatches 30; Indels 3; Gaps 1;
Qy 20 QVQLVQSGAEVKKPQASVKVKSCASGYFTSYVMQWVROAPQOGLWEIGEIDPSDYNYK 79
Db 1 QVQLVQSGPELVKPGASVKISKSTGYFTTEYTHMWMKQSHGKSLIEWIGGFNPKNGGSSH 60
Qy 80 NQKFKGRVTITRDSTSTAYMELSLRSDSGIYYICARWRGLNYGFDVRYFDVWGAGTTV 136
Db 61 NORFMDKATLAVDKSTSTAYMELSLRSDSGIYYICARWRGLNYGFDVRYFDVWGAGTTV 120
Qy 137 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 196
Db 121 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTFPAV 180
Qy 197 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCCPCPAPE 256
Db 181 LQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKTHTCCPCPAPE 240
Qy 257 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNAKTKPRE 316
Db 241 LLGSPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVEVHNAKTKPRE 300
Qy 317 EOYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 376
Db 301 EOYNSTYRVSVSLTVLHQDLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 360
Qy 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 436
Db 361 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 420
Qy 437 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 470
Db 421 KSRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 454

RESULT 12

US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P1123
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 14:

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,151
FILING DATE:
CLASSIFICATION:

; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-466-151-65

Query Match 85.08; Score 2141; DB 3; Length 451;
Best Local Similarity 88.3%; Pred. No. 1.4e-155;
Matches 399; Conservative 23; Mismatches 28; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQWVVRQAPGQGLEWMGEIDPDSYSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASI-TYDGSN 59
Qy 79 YNQKFKGRVTITRTDSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQTLTV 119
Qy 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRVPEKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRVPEKSCDKTHTCPCPAPELL 239
Qy 259 GGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419
Qy 439 RWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 15
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 6172213
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide

; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109.207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
; US-09-109-207C-14

Query Match 85.08; Score 2141; DB 4; Length 451;
Best Local Similarity 88.3%; Pred. No. 1.4e-155;
Matches 399; Conservative 23; Mismatches 28; Indels 2; Gaps 2;

Qy 20 QVQLVQSGAEVKKPGASVKVSCKASGYTFTS-YMQWVVRQAPGQGLEWMGEIDPDSYSTN 78
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASI-TYDGSN 59
Qy 79 YNQKFKGRVTITRTDSTSTAYMELSSLRSEDTAVYYCARNRDYSNNWYFDVWGEGTLTV 138
Db 60 YNPSVKGRITISRDDSKNTFYLMNSLRAEDTAVYYCARGSHYFGHWHFAVWGQTLTV 119
Qy 139 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 198
Db 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 179
Qy 199 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRVPEKSCDKTHTCPCPAPELL 258
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTRKVDKRVPEKSCDKTHTCPCPAPELL 239
Qy 259 GGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 318
Db 240 GGPSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATKPREEQ 299
Qy 319 YNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 378
Db 300 YNSTYRVVSVLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSR 359
Qy 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 438
Db 360 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKS 419
Qy 439 RWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 470
Db 420 RWQOGNVEFSCVMHEALHNHYTQKSLSLSPGK 451

Search completed: August 14, 2002, 15:17:09
Job time: 692 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:19:02 ; Search time 108.64 Seconds
(without alignments)
415.703 Million cell updates/sec

Title: US-09-499-662-157
Perfect score: 2518
Sequence: 1 MGWSCIIILVATATGVHQS.....MHEALHNYTOKSLSPGK 470
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1758	69.8	330	1 GHU	Ig gamma-1 chain C
2	1639.5	65.1	377	2 A23511	Ig gamma-3 chain C
3	1637.5	65.0	377	2 A60764	Ig gamma-3 chain C
4	1610	63.9	326	1 G2HU	Ig gamma-2 chain C
5	1599.5	63.5	327	1 G4HU	Ig gamma-4 chain C
6	1591.5	63.2	459	2 S37483	Ig gamma-2a chain
7	1535	61.0	474	1 G2MS11	Ig gamma-2b chain
8	1525	60.6	446	2 S40295	Ig gamma-2a chain
9	1485	59.0	470	2 S22080	Ig heavy chain pre
10	1482.5	58.9	475	2 S01321	Ig gamma-2b chain
11	1481	58.8	472	2 S31459	Ig gamma-1 chain -
12	1443	57.3	374	2 S69339	Ig heavy chain v r
13	1440.5	57.2	444	2 PC4436	monoclonal antibod
14	1267	50.3	328	2 I47159	Ig gamma 2a chain
15	1261	50.1	328	2 I47160	Ig gamma 2b chain
16	1253	49.8	255	4 S31866	Ig gamma-1 chain C
17	1245	49.4	234	2 PT0207	Ig gamma chain C r
18	1235	49.0	328	2 I47158	Ig gamma 1 chain C
19	1231.5	48.9	323	1 GHRB	Ig gamma chain C r
20	1231	48.9	328	2 I47161	Ig gamma 3 chain C
21	1210.5	48.1	329	1 G2GP	Ig gamma-2 chain C
22	1165.5	46.3	308	2 C30554	Ig heavy chain C r
23	1157	45.9	289	1 G3HUW1	Ig gamma-3 heavy c
24	1155	45.9	326	2 PS0017	Ig gamma-1 chain C
25	1150	45.7	329	1 G3MSC	Ig gamma-1 chain C
26	1145	45.5	324	1 GLMS	Ig gamma-1 chain C
27	1144.5	45.5	333	2 PS0018	Ig gamma-2b chain
28	1140	45.3	393	1 GLMSM	Ig gamma-1 chain C
29	1139	45.2	398	1 G3MSM	Ig gamma-3 chain C

RESULT 1
GHU

Ig gamma-1 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S3887; B90563; A90564; B91668; A91723; A02146

R;Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A;Reference number: A93433; MUID:82274238

A;Accession: A93433

A;Molecule type: DNA

A;Residues: 1-330 <ELL>

A;Cross-references: EMBL:Z17370

A;Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) marker

A;Note: Lys-330 is removed after translation

R;Harris, L.J.

submitted to the EMBL Data Library, October 1992

A;Reference number: S33904

A;Accession: S36861

A;Molecule type: DNA

A;Residues: 2-330 <HAR>

A;Cross-references: EMBL:Z17370

R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A;Title: Structure of human immunoglobulin gamma genes: Implications for evolution of

A;Reference number: S33887; MUID:83001943

A;Accession: S33887

A;Molecule type: DNA

A;Residues: 88-113;235-330 <TAK>

A;Cross-references: EMBL:Z17370

R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A;Reference number: A90563; MUID:71064024

A;Contents: myeloma protein Eu

A;Accession: B90563

A;Molecule type: protein

A;Residues: 1-96,'R',98-135 <CUN>

A;Note: this sequence has the Gln(3) marker, 97-Arg

R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A;Reference number: A90564; MUID:71064025

A;Contents: Eu

A;Accession: A90564

A;Molecule type: protein

A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',;

A;Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met

R;Fonstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

igen Primaerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', '36-96', 'K', '98-115', 'Q', '117-197', 'D', '199-238', 'D', '240', 'L', '242-268', 'E', '27
A:Note: this sequence has the Gm(17) and Gm(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-197', 'D', '199-238', 'E', '240', 'M', '242-266', 'D', '268-271', 'D', '273-330' <SCH
A:Note: this sequence has the Gm(3) and Gm(non-1) markers
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMTM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

RESULT 2
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene:
A:Reference number: A23511; MUID:86148507
A:Accession: A23511
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMTM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>
Query Match 65.1%; Score 1639.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 9.9e-87;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;
QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPCSRSTSGTAAAGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSVVTVPSLSIGTQTYICNVNHPKNTKVDKRV----- 238
Db 61 GLYSLSVVTVPSLSIGTQTYICNVNHPKNTKVDKRVELKPTLGDTHTCPRCPKSC 120
QY 239 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKPDT 273
Db 121 DTPPCPCPCPCPCDTPPPCPCPCPCDTPPPCPCPCPCDTPPPCPCPCPCDTPPPCPCPCDTP 180
QY 274 LMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSLTVLH 333
Db 181 LMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREEQYNSTYRVVSLTVLH 240
QY 334 QDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVK 393
Db 241 QDLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNOVSLTCLVK 300
QY 394 GYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHE 453
Db 301 GYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRWQQGNVSCVMHE 360
QY 454 ALHNHYTQKSLSLSPCK 470
Db 361 ALHNHYTQKSLSLSPCK 377
RESULT 3
A06764
Ig gamma-3 chain C region, form LAT - human
C:Species: Homo sapiens (man)
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
C:Accession: A06764
R:Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A:Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conv
A:Reference number: A06764; MUID:90007613
A:Accession: A06764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 65.0%; Score 1637.5; DB 2; Length 377;
Best Local Similarity 82.8%; Pred. No. 1.3e-86;
Matches 312; Conservative 7; Mismatches 11; Indels 47; Gaps 1;

Qy 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Qy 201 GLYSLSVVTVPSSSLGTQTVCNVNHNKPSNTKVDKRV----- 238
Db 61 GLYSLSVVTVPSSSLGTQTYTCNVNHNKPSNTKVDKRVELKTPGLDTHTCPCRPPEKSC 120
Qy 239 -----EPKSCDKTHTCPCPAPPELLGGPSVFLFPPPKKDT 273
Db 121 DTPPCPCRPCKSDTPPCPCRPPEKSCDTPPCPCRPAPPELLGGPSVFLFPPPKKDT 180
Qy 274 LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYNSTYRVWSVLTVLH 333
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEVHNNAKTKPREEQYNSTYRVWSVLTVLH 240
Qy 334 ODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITPPSREEMTKNQVSLTCLVK 393
Db 241 ODWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITPPSREEMTKNQVSLTCLVK 300
Qy 394 GFYPSTDAVENESGPENNYKTTTPPVLDSDGSFFLYSLKLVNDRKQWQGNVFCSCVMHE 453
Db 301 GFYPSTDAVENESGPENNTTPPVLDSDGSFFLYSLRSLVDRKQWQGNVFCSCVMHE 360
Qy 454 ALHNHYTQKSLSLSPGK 470
Db 361 ALHNRYTQKSLSLSPGK 377

RESULT 4

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con-
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A:Note: This sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g

A:Reference number: A93132; MUID:80114419
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation: Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the ami
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation: myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation: Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light i
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.9%; Score 1610; DB 1; Length 326;
Best Local Similarity 91.8%; Pred. No. 4.1e-85;
Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
Qy 141 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
Qy 201 GLYSLSVVTVPSSSLGTQTYTCNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPPELLGG 260
Db 61 GLYSLSVVTVPSSSLGTQTYTCNVNHNKPSNTKVDKRVKPKSCDKTHTCPCPAPPELLGG 116
Qy 261 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 320
Db 117 PSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 176
Qy 321 STYRVVSVLTVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITPPSREE 380
Db 177 STFRVSVLTVHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITPPSREE 236
Qy 381 MTKNQVSLTCLVKGPYPSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSLKLVNDRKSW 440
Db 237 MTKNQVSLTCLVKGPYPSDIAVWESNGOPENNYKTTTPVLDSDGSFFLYSLKLVNDRKSW 296
Qy 441 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
Db 297 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326

RESULT 5

G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150

R:Ellison, J.: Buxbaum, J.: Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Note: the sequence was determined from the germline gene
E:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclasses. Partial amino acid sequencing of the heavy chain.
A:Reference number: A90249; MUID:70207560
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two i chain disulfide bonds. In some cases, such as IgA and IgM, the subunit chain disulfide bonds. In immunoglobulin C region; immunoglobulin homology
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 1.6e-84;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

Qy	141	ASTKGPVFLPAPSSKSTSGGTAAAGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS	200
Db	1	ASTKGPVFLPAPSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS	60
Qy	201	GLYSLSSVWTVPPSSSLGTQYICNVNHHKPSNTKVDKRVPEKSCDKTHTCTPCPAPELLGG	260
Db	61	GLYSLSSVWTVPPSSSLGTQYICNVNHHKPSNTKVDKRVPEKSGTHTCTPCPAPELLGG	117
Qy	261	PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYDGVGVNNAKTKPREQYN	320
Db	118	PSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYDGVGVNNAKTKPREQEN	177
Qy	321	STYRVSVLTVLHQDWLNGKEYCKYKSNKALPAIEKTSKAGQPREQVYTLPPSREE	380
Db	178	STYRVSVLTVLHQDWLNGKEYCKYKSNKGLPSSIEKTSKAGQPREQVYTLPPSQEE	237
Qy	381	MTKNQVSLTCLVKGFPYSDIAWEVMSGQPPENNYKTTPTPVLSDSGSFFLYSLITVDKSRW	440
Db	238	MTKNQVSLTCLVKGFPYSDIAWEVMSGQPPENNYKTTPTPVLSDSGSFFLYSLITVDKSRW	297
Qy	441	QQGNVFCSYVMEALHNHYTQKSLSLSPGK	470
Db	298	QEGNVFCSYVMEALHNHYTQKSLSLGLK	327

RESULT 6
S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483

A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-469 <DUC>
A: Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C: Superfamily: immunoglobulin C region; immunoglobulin homology
C: Keywords: immunoglobulin
F: 276-345/Domain: immunoglobulin homology <IMM>

Query Match	63.2%;	Score 1591.5;	DB 2;	Length 469;
Best Local Similarity	63.3%;	Pred. No. 7e-84;		
Matches 299; Conservative	63;	Mismatches 105;	Indels 5;	Gaps 4;

Qy	1	MGWSCIILFLVATATG	VHSHQVOLVQSGAEVKKPGASVKVSKCASGYTFYSYWNQWVRQAP	60
Db	1	MGWSEIFLLSLGSPAGV	HCIOIQOQSGPELVKPGASVKISKASGYTFDYYINWVQKP	60
Qy	61	GQGLWGEIDPDS	SYNYNQKFKGRVYITRDSTSTAYMELSSLRASEDTAVFYCARNRD	120
Db	61	GQGLKWIGWIYPAS	GNTKYENFKGKATLVITDSSSTAYMQLSSLTSEDTAVFYECARAMG	120
Qy	121	YSNNWYEDVWGE	GLVTVSSASTKGSPVFPLAPASPKSTSGGTAAALGCLVKDYDPEPVTVVS	180
Db	121	-ATATLLDYWGQ	GYTLTVSSAKTTAPSVYPLAPYCGDGTGSSVTLGCLVKGYEPPEVTLT	179
Qy	181	WNSGALTSGVHT	FPFVPLQSSGLTSSLVWVPSSSLGTQYICNVNHPKSTNVDKRRVEP	240
Db	180	WNSGSLSGVHT	FPFVPLQSD-LYTLSSSVTVTSTWPSQISITCNVAHPASSTKVDKKIEP	238
Qy	241	KSCDKTTKCP	-CPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVYVDVSHEDPEVKF	298
Db	239	RG-PTIKPCPC	KCAPNLLGGPSVFIFPPKIDVLMISLSPITCVYVDVSDSDPDVQI	297
Qy	299	NWYVDGVEVHN	AKTKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVYSNKALPAPIEKT	358
Db	298	SWFYNNVEVHT	QAQTQTHREDYNSTLRVYSALPIQHQQDMWSGKEFKCKVNNKDLPAPIEKT	357
Qy	359	ISKAKGPREPOV	YTLPLPSREEMTKNOVSLTCLLVKGYPSDIAVESNGSGPENNYKTPP	418
Db	358	ISKPKGSVRAP	QVTVLPLPPEEMTKKQVTLTCWVTDPMPEDIYVEWTVNGKTELTNAYNTE	417
Qy	419	PVLSDSGSFFLY	SKLTVDKSRWQQQGNVFCSSVMHEALHNNHYTKQSLSPGK	470
Db	418	PVLSDSGYPMY	SKLRFVEKKNWYERNYSYCSVYHEGLHNNHTTKSFSRTGPK	469

7	RESULT	G2MS11
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G245311
 Ig gamma-2b chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
 C:Accession: S25057; A02157; A26235; A26232; A26233; A53598
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
 submitted to the EMBL Data Library, July 1992
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific
 A:Reference number: S25057
 A:Accession: S25057
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-474 <FIS>
 A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fr
 A:Reference number: A02157; MUID:80120716
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
 A:Cross-references: GB:J00461
 A:Note: the sequence was determined from the germline gene
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979

A::title: Structure of the constant and 3' untranslated regions of the murine gamma2b heavy chain disulfide bonds

A::reference number: A26235; MUID:80081501

A::contents: MPC 11

A::accession: A26235

A::molecule type: mRNA

A::residues: 138-172,'P','174-189,'FP','193-376','T','378-474 <TUI>

A::note: Lys-474 is probably removed posttranslationally

R:tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979

A::title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglobulin heavy chain disulfide bonds

A::reference number: A26232; MUID:80081502

A::accession: A26232

A::molecule type: DNA

A::residues: 138-172,'P','174-189,'FP','193-376','T','378-474 <TU2>

R:ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982

A::title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma2b heavy chain disulfide bonds

A::reference number: A26233; MUID:82173203

A::contents: b allele

A::accession: A26233

A::molecule type: DNA

A::residues: 138-161,'L','163-189,'FP','193-300,'R','302-331,'A','333-437','DI','440-474 <OLL>

A::cross-references: GB:J00461

R:kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi, J.; Biol. Chem. 269, 12345-12350, 1994

A::title: O-glycosylation in hinge region of mouse immunoglobulin G2b.

A::reference number: A53598; MUID:94216359

A::accession: A53598

A::status: preliminary

A::molecule type: protein

A::residues: 234-251 <KIM>

C::comment: The a allele sequence is shown.

C::genetics:

A::introns: 138/1: 236/1: 258/1: 368/1

C::complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes: immunoglobulin C region; immunoglobulin homology

C::superfamily: Immunoglobulin C region; immunoglobulin homology

F::keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin heavy chain disulfide bonds; interchain (to heavy chain) #status predicted

F::247,250,253,256/disulfide bonds: interchain (covalent) #status predicted

F::324/binding site: carbohydrate (Asn)

Query Match 61.0%; Score 1535; DB 1; Length 474;
Best Local Similarity 60.4%; Pred. No. 1.2e-80;
Matches 288; Conservative 70; Mismatches 109; Indels 10; Gaps 3;

QY 1 MGWSCIILFLVATGTVHSGVOLVQSAGAEVKKPGASVKVSCKASGYFTSYMMWRQAP 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MEWSWIFLFLLSTAGVHSEVQQSGPELVNPGASVKMSCKASGYFTITVMHWKQKP 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 GGLEWMGEIDPSDSITYNOKTKGRVTITRDPTSTAYMELSSRLSRSDTAVYYCARND 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GGLEWIGLYINPKDGTKFNEFKGNALTSKSSNTAYMELSSLTSEDNAVYYCARDYD 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 YSNWYFDVWGEGTLTYVSSASTGSPVPFPLAPSSKSTGGTGAAAGCLVKIRDFEPVTVS 180
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 YD---WFAYWGQGLTVTVAAKTPPPSVYPLAPCGCGDTTGTSSVTSGLVKYGFPESVTVT 177
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 WNSGALTSGVHTPAVLLOSGLYSLSVVIVPSSSLGTQYICNVNHKPSNTKVDKRVEP 240
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 178 WNSGSLSYVHTLSQAALLQSLGLTMSSSVYPVSPSTWP SQTVTCTGAHPASSTTVDKKLPE 237
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 241 KSCDKT-HTCP-----CPAPELGGPSVFLEPPKPDLTMLISRTPEVTCVVVDVSHED 293
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 SGPISTINPCPCKECHKCAPNLGEGSPVFIFFPNITKDVLMISLTLPKVTCCVVVDVSEDD 297
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 294 PEVKFNWYDGVCHNAKTKEPEQNSTVRYSVLTVLTHODWLNGKEYCKYSNKALPA 353
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db	298	PVQISFVNVEYHTAQTOFHREDYNSTIRWSTLPIQHODWMSGKEFKCKVNNKDLP	357
Qy	354	PIETISKAKGQPREPOVYTLPPREEMTKNOVSLTCLVKGFYPSDIAVENEWGOPENN	413
Db	358	PIERTISKIKGLVRAPQVYILPPAEQLSRKDVSLTCLVGFNPGDISVETWSNGHTTEN	417
Qy	414	YKTTTPVLDSDGSFPLYSKLTVDKSRMQQGNVFCSCVMHEALHNHYTQKSLSLSPGK	470
Db	418	YKDTAPVLDSDGSYFIYSKLNKMTSKWEKTSFSCNVRHEGLKNLYLKKTTISRSPGK	474
RESULT 8			
S40295			
Ig gamma-2a chain (mAb735) - mouse			
C:Species: Mus musculus (house mouse)			
C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999			
C:Accession: S40295			
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.			
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against			
A:Reference number: S40295			
A:Accession: S40295			
A:Molecule type: protein			
A:Residues: 1-446 <KLE>			
C:Genetics:			
A:Map position: 12			
C:Superfamily: immunoglobulin C region; immunoglobulin homology			
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid			
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>			
F:1-117/Domain: V-D-J region <VDJ>			
F:118-446/Domain: C region <CHR>			
F:118-214/Domain: C1 region <CH1>			
F:215-230/Region: hinge			
F:231-340/Domain: C2 region <CH2>			
F:341-446/Domain: C3 region <CH3>			
F:360-427/Domain: immunoglobulin homology <IMM>			
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted			
F:132/Disulfide bonds: interchain (to light chain) #status predicted			
F:224,227,229/Disulfide bonds: interchain #status predicted			
F:237/Binding site: carbohydrate (Asn) (covalent) #status experimental			
Query Match 60.6%; Score 1525; DB 2; Length 446;			
Best Local Similarity 63.3%; Pred. No. 4.2e-80;			
Matches 286; Conservative 62; Mismatches 96; Indels 8; Gaps 4;			
Qy	20	QVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYNQMWVRQAPQGLGWMGEIDPSDSYNY	79
Db	1	QIQLOQSGPELVPGASVKISKASGYFTDYTHVVKORPGEGLWIGWIPGSGNTKY	60
Qy	80	NQKPKGRVITRDYSTAYNELSLSESDYVYICARNRDYSNWYFDVWGEGLTVTS	139
Db	61	NEKPKGATLEVDTSSTAYNQLSLSESDSAVYFCARGGKEA----MDYWGQGFSTVTS	116
Qy	140	SASTKGPSVFPPLAPSSKTSGGTAALGLVKDYFPEPVTVSWNSGALTSGYHTTFAVLQS	199
Db	117	SAKTTATSVYPLAPVCGDFTGSSVTLGCLVKGYFPEPVTLTWSGSLSSGYHTTFAVLQS	176
Qy	200	SGLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKRVPEKSCDKTHTCPP--CPAPEL	257
Db	177	D-LVTLSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNL	234
Qy	258	LGGPSVFLFPPKPKDTLMISRTPEVTVVQDVSHEDPEVKENWYVDGVEVINAKTKPREE	317
Db	235	LGGPSVTFPPKIKDVLMLISLSPWTCVVDVSDSDPDQVQISWFVNVEVLTAQTQTHRE	294
Qy	318	QYNSTYRVVSVLTVYLHODWLNKQYKCKVSNKALPAPLEKTIISKAKGQPREPOVYTLPPS	377
Db	295	DYNSTLRVVSALPFIQHODWMSGKEFKCKVNNKDLPAPLERTISKPGSVRAPQVTVLPP	354
Qy	378	REEMTKNOVSLTCLVKGFYPSDIAVENEWGOPENNYKTTTPVLDSDGSFFLYSKLTVDK	437

Db 355 EEMTKKQVLTCTMVTDFMPEDIVETWNTNGKTELNYKTEPVLDSDGSYFMYSKLRVEK 414
Qy 438 SRWQGNVFCSCVMHEALHNHYTKQSLSPG 469
Db 415 KNWVERNSYSCSVVHEGLHNHHTKSFSPRTGP 446

RESULT 9
S22080
Ig heavy chain precursor (B/MT 4A.17 H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 1
A:Reference number: S06610; MUID:90097956
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYN>
A:Cross-references: EMBL:X16701
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: Ig CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.0%; Score 1485; DB 2; Length 470;
Best Local Similarity 60.6%; Pred. No. 8.5e-78;
Matches 286; Conservative 63; Mismatches 113; Indels 10; Gaps 7;

Qy 3 WSCIILFLVATATGVSQVLQSGAEVKKPGASVKVCKASGYTFTSYMMQVROAPGQ 62
Db 5 WT--LFLVLSAPIGVLSQVLREGSLVKPSQTLSTCTVSGFSLSYALTWVRQAPGK 62
Qy 63 GLEWMGEIDPDSYTNYNQKFKGRVTITRDTSTSTAYMELSLRSRSEDATVYYCARNR--D 120
Db 63 ALEWVGGI--TSGGTYTYPALKSRSLTITKENSQSQVLSVSSVTPEDTATYYCARSTYGE 121
Qy 121 YSNWTFDVMGEGTLTVSSASTKGPSVFLPAPSSKSTSGTGAALGCLVKVDYPPPEVTVS 180
Db 122 VGDGAIADAMGQGLLTVSSASTAPKVPYPLSSCCGDKSSSTVTLGCLVSSYMPPEVTVT 181
Qy 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVPSLSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 182 WNSGALKSGVHTFPVAVLQSSGLYSLSSVTVPSLGTSG-QFTCNVAHPASSTKVDKRAVDP 240
Qy 241 KSCDKTHTCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 300
Db 241 -TC-KPSPCDCCPPPELPGGPSVFIFPPKPKDTLTISGTEPVCVVVDVGHDDPEVKFSW 298
Qy 301 YVDGVEVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKVNAKALPAPIEKTIS 360
Db 299 FVDDVEVNTATTKPREQNFNSTYRVVSVLTVLHQDWLNGKEYCKVSKVNAKALPAPIVRTIS 358
Qy 361 KAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTTP 418
Db 359 RTKGPAREQVYVLAAPQELSASTVSLICWVTSFYFDYIAVEWQRNGQPESEDKYGTTP 418

Qy 419 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 419 PQLDADSSYFLYSKLVRDRNSWQEGDYYTCVVMHEALHNHYTKQSTKSACK 470

RESULT 10
S01321
Ig gamma-2b chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: S01321
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Pliers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A:Reference number: S01320; MUID:88329081
A:Accession: S01321
A:Molecule type: mRNA
A:Residues: 1-475
A:Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F:159-223/Domain: immunoglobulin homology <IMM>

Query Match 58.9%; Score 1482.5; DB 2; Length 475;
Best Local Similarity 59.5%; Pred. No. 1.2e-77;
Matches 284; Conservative 69; Mismatches 115; Indels 9; Gaps 4;

Qy 1 MGWSCIILFLVATATGVSQVLQSGAEVKKPGASVKVCKASGYTFTSYMMQVROAP 60
Db 1 MEWIFLFLITAGTGVQSVQVLQSGAELAPGASVKLSCASGYTLTSYGISVWVQRT 60
Qy 61 GQGLEWGEIDPDSYTNYNQKFKGRVTITRDTSTSTAYMELSLRSRSEDATVYYCARNRD 120
Db 61 GQGLEWIGEITPGSGNSYFNKFKGKATLVDRKSSSTAYLHLSSLTSEDSAVYFCAGPRQ 120
Qy 121 YSNWTFDVMGEGTLTVSSASTKGPSVFLPAPSSKSTSGTGAALGCLVKVDYPPPEVTVS 180
Db 121 V-GLLPFGYWGQGLTVLTASAATTPPSVYPLAPCGGDTGSSVTGLGCLVKGYFPESVTVT 179
Qy 181 WNSGALTSGVHTFPVAVLQSSGLYSLSSVTVPSLSLGTQTYICNVNHPKNTKVDKRVPE 240
Db 180 WNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQVTVCSVAHPASSTTVDDKLEP 238
Qy 241 KSCDKT-HTCPP-----CPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHED 293
Db 239 SGPTSTINPCPCCKECHKCPAPNLEGGPSVFIFPPNPKDVLMLSLTPKTVCVVDVSEDD 298
Qy 294 PEVKFNKYVDGVHNAKTPREEQNSTYRVVSVLTVLHQDWLNGKEYCKVSKVNAKALPA 353
Db 299 PDVOISMFVNNEVLTQAQTQTHREDYNSTIRVVSALDIQHDWMSGKEFKCKVNNKDLPA 358
Qy 354 PIEKTSKAKGQPREQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGOPENN 413
Db 359 PIERTSKINGIVRAQVYTLSPPEQLSRKDVSLTCLAVGFSPEDISVWTSNGHTEEN 418
Qy 414 YKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKQSLSPGK 470
Db 419 YKDTAPVLDSDGSYFYIYSLNMTKWEKTDSPSCNVRHEGLKNYLLKTKTISRSPGK 475

RESULT 11
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459

RESULT
I47160

Search completed: August 14, 2002, 15:19:03
Job time: 691 sec

RESULT
I47160

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:23:16 ; Search time 53.64 Seconds
(without alignments)
339.265 Million cell updates/sec

Title: US-09-499-662-157

Perfect score: 2518

Sequence: 1 MGWSCILFLVATATGVHSQ.....MHEALHNHYTQKSLSPGK 470

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	1758	69.8	330	1	GCL_HUMAN
2	1610	63.9	326	1	GCL_HUMAN
3	1599.5	63.5	327	1	GCL_HUMAN
4	1231.5	48.9	323	1	GC_RABIT
5	1210.5	48.1	329	1	GC2_CAVPO
6	1162	46.1	290	1	GC3_HUMAN
7	1155	45.9	326	1	GCL_RAT
8	1150	45.7	329	1	GC3_MOUSE
9	1145	45.5	324	1	GCL_MOUSE
10	1144.5	45.5	333	1	GCB_RAT
11	1140	45.3	393	1	GC1M_MOUSE
12	1139	45.2	398	1	GC3M_MOUSE
13	1129	44.8	330	1	GCAA_MOUSE
14	1127.5	44.8	329	1	GCC_RAT
15	1126.5	44.7	335	1	GCAB_MOUSE
16	1124	44.6	399	1	GCAM_MOUSE
17	1115	44.3	322	1	GCA_RAT
18	1085	43.1	336	1	GCB_MOUSE
19	1080	42.9	405	1	GCB_MOUSE
20	540.5	21.5	139	1	HV07_MOUSE
21	509	20.2	117	1	HV06_MOUSE
22	506.5	20.1	137	1	HV11_MOUSE
23	502	19.9	138	1	HV48_MOUSE
24	497	19.7	117	1	HV05_MOUSE
25	495	19.7	117	1	HV16_MOUSE
26	492	19.5	140	1	HV02_MOUSE
27	486.5	19.3	429	1	EPC_RAT
28	486	19.3	428	1	EPC_HUMAN
29	485	19.3	117	1	HV09_MOUSE
30	484	19.2	117	1	HV18_MOUSE
31	480	19.1	117	1	HV04_MOUSE
32	471	18.7	421	1	EPC_MOUSE
33	469	18.6	117	1	HV49_MOUSE

34	463.5	18.4	147	1	HV1C_HUMAN	P01744	homo sapien
35	463	18.4	117	1	HV10_MOUSE	P01754	mus musculus
36	461	18.3	136	1	HV15_MOUSE	P01759	mus musculus
37	445	17.7	454	1	MUC_HUMAN	P01871	homo sapien
38	445	17.7	455	1	MUC_MOUSE	P01872	mus musculus
39	441.5	17.5	120	1	HV50_MOUSE	P06329	mus musculus
40	441	17.5	117	1	HV12_MOUSE	P01756	mus musculus
41	440	17.5	117	1	HV13_MOUSE	P01757	mus musculus
42	439	17.4	458	1	MUC_RABIT	P03988	oryctolagus
43	435	17.3	476	1	MUCM_MOUSE	P01873	mus musculus
44	433	17.2	120	1	HV03_MOUSE	P01747	mus musculus
45	429	17.0	479	1	MUCM_RABIT	P04221	oryctolagus

ALIGNMENTS

RESULT 1

GCL_HUMAN

ID GCL_HUMAN STANDARD; PRT; 330 AA.

AC P01857;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 16 gamma-1 chain C region.

DE 19 gamma-1 chain C region.

GN IGHG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RA [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82274238; PubMed=6287432;

RA Ellison J.W., Berson B.J., Hood L.E.;

RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";

RL Nucleic Acids Res. 10:4071-4079(1982).

RN [2]

RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).

RX MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

RA Wexdal M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";

RL Biochemistry 9:3161-3170(1970).

RN [3]

RP SEQUENCE OF 136-329 (EU).

RX MEDLINE=71064025; PubMed=5530842;

RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,

RA Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";

RL Biochemistry 9:3171-3181(1970).

RN [4]

RP SEQUENCE (MYELOMA PROTEIN NIE).

RX MEDLINE=77070269; PubMed=826475;

RA Ponstingl H., Hilschmann N.;

RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

RN [5]

RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.

RX MEDLINE=83289131; PubMed=6884994;

RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";

RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

RN [6]

RP DISULFIDE BONDS.

RX MEDLINE=71064027; PubMed=4923144;

RA Gall W.E., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
CC -1- MISCELLANEOUS: NIE HAS THE G1M(17) ALLOTYPIC MARKER, 97-K, & THE
CC G1M(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE G1M(3)
CC MARKER & THE G1M (NON-1) MARKERS.
CC -1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
CC 35.116,198,269 & 272.
CC -1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
CC 268-272.
CC -1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
CC RESIDUES 198,267&272.
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CC -----
DR EMBL; J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 223 CH2.
FT DOMAIN 224 330 CH3.
FT DISULFID 27 83
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT MOD_RES 330 330
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT STRAND 123 126
FT HELIX 130 134

FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
FT STRAND 165 166
FT STRAND 175 178
FT STRAND 183 190
FT HELIX 193 197
FT TURN 198 199
FT STRAND 202 206
FT STRAND 215 219
FT STRAND 227 227
FT STRAND 230 234
FT HELIX 238 240
FT TURN 241 242
FT STRAND 245 256
FT STRAND 260 266
FT TURN 267 268
FT STRAND 269 270
FT STRAND 274 276
FT STRAND 280 281
FT TURN 283 284
FT STRAND 287 296
FT HELIX 297 301
FT TURN 302 303
FT STRAND 306 312
FT TURN 313 314
FT TURN 316 317
FT STRAND 320 324
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match 69.8%; Score 1758; DB 1; Length 330;
Best Local Similarity 99.1%; Pred. No. 1.1e-114;
Matches 327; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 141 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
DB 1 ASTKGSVPFLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
QY 201 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKRVKPKCDKHTCCPCPAPELLGG 260
DB 61 GLYSLSVVTVPSSSLGTQYICNVNHPKSTKVDKRVKPKCDKHTCCPCPAPELLGG 120
QY 261 PSVFLEPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 320
DB 121 PSVFLEPPPKDFTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNKATKPREQYN 180
QY 321 STYRVSVLTFLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSREE 380
DB 181 STYRVSVLTFLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYITLPPSRDE 240
QY 381 MTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 440
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300
QY 441 QGQNVFSCSVMHREALHNYTQKSLSPGK 470
DB 301 QGQNVFSCSVMHREALHNYTQKSLSPGK 330

RESULT 2
GC2_HUMAN
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE OF 2-326 FROM N.A.
 RA MEDLINE=82197621; PubMed=6804948;
 RX Ellison J.W., Hood L.E.;
 RT "Linkage and sequence homology of two human immunoglobulin gamma
 RL heavy chain constant region genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
 RN [2]
 RP SEQUENCE OF 88-115 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=83001943; PubMed=6811139;
 RA Takahashi N., Ueda S., Obata M., Nikaido T., Nakai S., Honjo T.;
 RT "Structure of human immunoglobulin gamma genes: Implications for
 RL evolution of a gene family.";
 RL Cell 29:671-679(1982).
 RN [3]
 RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=84235992; PubMed=6329676;
 RA Krawinkel U., Rabbitts T.H.;
 RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
 RL heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
 RL genes.";
 RL EMBO J. 1:403-407(1982).
 RN [4]
 RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
 RX MEDLINE=81007873; PubMed=6774012;
 RA Wang A.-C., Tung E., Fudenberg H.H.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RL evolutionary, and functional implications.";
 RL J. Immunol. 125:1048-1054(1980).
 RN [5]
 RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
 RX MEDLINE=80001357; PubMed=113060;
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RL domains of a human IgG2 myeloma protein.";
 RL Can. J. Biochem. 57:758-767(1979).
 RN [6]
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE=80114419; PubMed=118920;
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RL immunoglobulins gamma chains.";
 RL Mol. Immunol. 16:923-925(1979).
 RN [7]
 RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.;
 RL Submitted (MAR-1980) to the PIR data bank.
 RN [8]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE=9525298; PubMed=7737190;
 RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RL immunoglobulins.";
 RL Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RX MEDLINE=72033500; PubMed=4940472;
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RL Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE=69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RL Nature 221:145-148(1969).
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 CC -----
 DR EMBL; J00230; AAB59393.1; -.
 DR PIR; A02148; G2HU.
 DR HSSP; P01857; 1FC1.
 DR MIN; 147110; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003600; Ig_Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; Ig_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 83
 FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 103 103 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT SITE 156 156
 FT MOD_RES 326 326
 FT VARIANT 60 60
 FT CONFLICT 109 109 AT OR NEAR THE COMPLEMENT-BINDING SITE.
 FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 SQ
 Query Match 63.9%; Score 1610; DB 1; Length 326;
 Best Local Similarity 91.8%; Pred. No. 1.9e-104;
 Matches 303; Conservative 10; Mismatches 13; Indels 4; Gaps 2;
 Qy 141 ASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 200
 Db 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
 Qy 201 GLYSLSSVTVPSSSLGTQTYICNVNHRKPSNTKYDKVEPKSCDKTHTCPCPAPPELLGG 260
 Db 61 GLYSLSSVTVPSNFGTQTYICNVDRHPSNITKYDKTVERKCCVE--CPPCAPP-VAG 116
 Qy 261 PSVFLFPPPKRDTLMISRTPEVTCVYVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 320
 Db 117 PSVFLFPPPKRDTLMISRTPEVTCVYVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN 176
 Qy 321 STYRVVSVLTVHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPQVYTLPPSREE 380
 Db 177 STFRVYSVLTVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREE 236
 Qy 381 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
 Db 237 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296
 Qy 441 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
 Db 297 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 326
 RESULT 3
 GC4_HUMAN
 ID GC4_HUMAN STANDARD; PRT; 327 AA.
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DR 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; G4HU.
DR HSSP; P01842; 7FAB.
DR MIM; 147130; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003600; Ig_Like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig_Like; 1.
DR SMART; SM00407; IgC1; 2.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
FT SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 63.5%; Score 1599.5; DB 1; Length 327;
Best Local Similarity 91.8%; Pred. No. 1e-103;
Matches 303; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

QY 141 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 200
DB 1 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQSS 60
QY GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRRPEPKSCDKTHTCPPCPAPPELLGG 260
DB 61 GLYSSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKRRPEPKSCDKTHTCPPCPAPPELLGG 117
QY PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQYN 320
DB 118 PSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPREEQFN 177
QY 321 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380
DB 1 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 380

Db 178 STYRVSVLTVLHODWLNKGKEYCKVSNKALPAPIETKISKAKGQPREPQVYTLPPSREE 237
QY 381 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 440
Db 238 MTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 297
QY 441 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 470
Db 298 QGNVFSCSVMHEALHNHYTQKSLSLSPGK 327

RESULT 4
GC_RABIT ID GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
F-I haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.H., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
MARKERS AND REF.5 THE E15 MARKER.
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CC -----
DR EMBL; M16426; AAA31289.1; -.
DR PIR; A02161; GHRB.
DR HSSP; P01857; 1FCL.
DR InterPro; IPR003006; Ig_MHC.

```
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AAl18D579A8B CRC64;

Query Match 48.9%; Score 1231.5; DB 1; Length 323;
Best Local Similarity 70.0%; Pred. No. 2.8e-78;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 144 KGPSVEPLAPSSKSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSGLY 203
DB 4 KAPSVFPLAPCGDPPSSFTVTLGCLVKGLPPEPTVWNSGTLNGVTFPSVQSSGLY 63
QY 204 SLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPEKSCDKTHPCPCAPELILGGPSV 263
DB 64 SLSSVSVTSSS---QPTCNVAHPATNTKYDKTVAPSTCSK----PTCPPPELLGGPSV 116
QY 264 FLFPKPKDTHLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPREOYNSTY 323
DB 117 FLFPKPKDTHLMISRTPEVTCVVDVSDQDPEVQFTWYINNEQVTRAPPLREQQFNSTI 176
QY 324 RVSVTLVTHDNLGKGVCKVSKNKPALPAIEKTIKAKGPQREPOVYTLPPSPREMTK 383
DB 177 RVSVTLVTHDNLGKGVCKVSKNKPALPAIEKTIKAKGPQREPOVYTLPPSPREMTK 236
QY 384 NOVSLTCLVKGYFSDIAVESNGSQPNNTKTPPVLDSDGSSEFFLYSKLTVKDSRMQQG 443
DB 237 RVSVLTCHMGFYPSDISVEWENKKAEDNYKTPPAVLDSGSEFFLYNKLVSPTSEWQRG 296
QY 444 NVFSCSVNHEALHNHYTQKSLSLSPGK 470
DB 297 DVFTCSVNHEALHNHYTQKSISRSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
ID 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
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RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cystine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2EB4.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003600; IG_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_like; 1.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 N-LINKED (GLCNAC. . .).
FT CARBOHYD 178 178
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 48.1%; Score 1210.5; DB 1; Length 329;
Best Local Similarity 69.8%; Pred. No. 8.1e-77;
Matches 233; Conservative 30; Mismatches 62; Indels 9; Gaps 4;

QY 140 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 199
DB 1 SARTTAPSVFPLAASCVDTSGMTLGLVKGYFPEPTVKVNSGALTSGVHTFPAVLQ- 59
QY 200 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRVKPEKSCDKTH--TCPPCAPDEL 257
DB 60 SGLYSLTSMVTPSSQKAT---CNVAHPASSTKVDKTVETIRTPZBPCTCKCPPPEN 115
QY 258 LGGPSVFLFPKPKDTHLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPREE 317
DB 116 LGGPSVFLFPKPKDTHLMISLTPRTVTCVVDVSDQDPEVQFTWFDNKPVGNAETKPRVE 175
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Db 179 ISKTGQPREQVYTLPPSREMTKNQVSLTCLVKGFPSPDIADVWESSGQPPENNYNTTP 238
Qy 419 PVLDSGDSFFLYSLKLTVDKSRWQGNVFCVSMHEALHNHYTOKSLSLSPCK 470
Db 239 PMLDSGDSFFLYSLKLTVDKSRWQGNIFSCVSMHEALHNHYTOKSLSLSPCK 290

RESULT 7
GCI_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 36, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Rueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;

Query Match 45.9%; Score 1155; DB 1; Length 326;
Best Local Similarity 63.4%; Pred. No. 5.5e-73;
Matches 211; Conservative 52; Mismatches 60; Indels 10; Gaps 4;

Qy 141 ASTKGPSVEPLAPSKSTSGTALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
Db 1 AETAPSVIPLAPGALKSNMTLGLGVGFPEPTVTWNSGALSSGVHTFPAVLQ-S 59

Qy 201 GLYSLSSVTVPSSSLGQTGYICNVNHNKPSNTKVDKRVKPSCKDTHTCPCPAPELIG 260
Db 60 GLYTLTSSVTVPSSTWPSQVTCNVHPASTKVDKKIVPRNCG-GDCKPC---ICTG 113

Qy 261 ---PSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATPKPRE 317
Db 114 SEVSVFIFPPKPKDMLTITLTPKATCVVVDISQDDPEVHFSWFVDDVEVHTAQTTRPEE 173

Qy 318 QYNSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPS 377
Db 174 QFNSTFRSVSELPILTVLHDWLNKGRFRCKVTSAAPFSPSEIETISKPEGRQTQVPHVYTSPT 233

Qy 378 REEMTKNQVSLTCLVKGFYPSDIAVEESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDK 437
Db 234 KEEMTQNEVSLTCWKVGFPDPIIWEQMONGQPENYKNTPTPTMDTDSGYFLYSLKNYK 293
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Qy 438 SRWQGNVFCVSMHEALHNHYTOKSLSLSPCK 470
Db 294 EKWQGNFTFTCSVLHGLNHNHTEKSLSHSPCK 326

RESULT 8
GCI_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A.; Word C.J.; Rimm D.; Der-Balan G.P.; Martinez H.M.;
RA Tucker P.W.; Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
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CC or send an email to license@sib-sib.ch).
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR: B02156; G3MSC.
DR HSP; P01857; 1FC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 45.7%; Score 1150; DB 1; Length 329;
Best Local Similarity 65.0%; Pred. No. 1.2e-72;
Matches 215; Conservative 44; Mismatches 68; Indels 4; Gaps 3;

Qy 142 STKGPSVEPLAPSKSTSGTALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 201
Db 1 TTTAPSVIPLVPGCSDTSGSSVTGLCLVKGFPEPTVKNYGNALSSGVRTVSSVLQ-SG 59

Qy 202 LYSLSVVTVPSSSLGQTGYICNVNHNKPSNTKVDKRVKPSCKDTHTCP---PCPAPELLG 259
Db 60 FYSLSLVTVPSSTWPSQVTCNVHPASTKVDKKIVPRNCG-GDCKPC---ICTG 118

Qy 260 GPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATPKPREQY 319
Db 119 GPSVFLFPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKATPKPREQY 178

Qy 320 NSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRE 379
Db 179 NSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIETISKAKGQPREPQVYTLPPSRE 238
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QY 380 EMTKNVSLTCLVKGYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSR 439
Db 239 QMSKKVSLTCLVTNFSEISVWERNGLQDYKNTPTPLDSDGTYFLYSLKLTVDTD 298
QY 440 WQOGNVFSCSVMEALHNYHTQKSLSPCK 470
Db 299 WLQGEFTCSVMEALHNYHTQKSLSPCK 329

RESULT 9
GCL_MOUSE STANDARD; PRT; 324 AA.
ID GCL_MOUSE 97
AC P01868; 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE=80202559; PubMed=6769752;
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid.";
RL Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=80012837; PubMed=113776;
RA Rogers J., Clarke P., Salser W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain.";
RL Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
RX MEDLINE=78242288; PubMed=98524;
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma1 chain.";
RL J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE=73008889; PubMed=5073237;
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";
RL Biochem. J. 126:837-850(1972).
RN [6]
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or send an email to license@isb-sib.ch).
RN [7]
DR EMBL; V00793; CAA24172.1; -
DR EMBL; V00793; CAA24173.1; -
DR EMBL; V00793; CAA24174.1; -
DR EMBL; V00793; CAA24175.1; -
DR EMBL; V00795; CAA24176.1; -
DR PIR; A02159; G1MS.
DR HSSP; P01842; 7FAB.

DR GlycosuiteDB; P01868; -
DR MGD; MGI:96446; Igh-4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
FT FTID=CAR_000055.
FT DISULFID 244 302 REMOVED POST-TRANSLATIONALLY.
FT MOD_RES 324 324 N -> D (IN REF. 3).
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match 45.5%; Score 1145; DB 1; Length 324;
Best Local Similarity 62.3%; Pred. No. 2.7e-72;
Matches 207; Conservative 55; Mismatches 60; Indels 10; Gaps 4;
QY 141 ASTKGPSPVPLAPSSKTSSTGTAALGCLVKDYPEPTVYSWNSGALTSVHTFPVQLSS 200
Db 1 AKTTPSVIPLAPCSAAQNSWVTLGCLVKGYPEPTVYSWNSGALTSVHTFPVQLSS 60
QY 201 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKRVKPKSCDKHTHTCPP--CPAPELL 258
Db 61 -LYTLSSSVTVFPSSPRPSETVTCNVAHPASSTKVDKKIVPRDCG---CKPCICTVPEV- 114
QY 259 GGPVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPREEQ 318
Db 115 --SSVEIFPPKPKDVLITLTTPKVTCTVVDVSKDDPEVQVSWFVDDVEVHTAQTQPREQ 172
QY 319 YNSTYRWSVLTVLHODWLNGLNGKEYCKVSNKALPAPKEKTIKAKGQRPQVPTLPPSR 378
Db 173 FNSTFSVSELPIHQDWLNGLNGKEYCKRVNSAAPPAPKEKTIKAKGQRPQVPTLPPPK 232
QY 379 EMTKNQVSLTCLVKGYPSDIAVWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKS 438
Db 233 EQMAKDKVSLTCLMITDFFPEDITVEWQNGQPAENYKNTQPIINTNGSVFVSKLVNQS 292
QY 439 RWOQGNVFCVSMHEALHNYHTQKSLSPCK 470
Db 293 NWEAGNTFTCSVLHLEGLHNHTKSLSPCK 324
RESULT 10
GCL_MOUSE STANDARD; PRT; 333 AA.
ID GCL_MOUSE 97
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;

RA Brueggemann M.;
 RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
 RL Gene 74:473-482(1988).
 DR PIR; PS0018.
 DR HSP; P01842; 7FAB.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_cl.
 DR InterPro: IPR003600; Ig_like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; IG_like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 80
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 147 207
 FT DISULFID 253 311
 SQ SEQUENCE 333 AA; 3649 MW; 55F8B64D48D460A6 CRC64;
 Query Match 45.5%; Score 1144.5; DB 1; Length 333;
 Best Local Similarity 63.7%; Pred. No. 3e-72;
 Matches 214; Conservative 45; Mismatches 68; Indels 9; Gaps 3;
 QY 141 ASYKGPSVFFPLAPSKSTSGTAALGCLVKDYPPPEVTVSWNSGALTSVHTFPVAVLQSS 200
 Db 1 AQTAPSVPLAPCGDTTSTVLGCLVKGYPPEVTVTWSGALSSDVHTFPVAVLQ-S 59
 QY 201 GLXSLSWVTPSSSLGTQYICNVNHPKPSNTKVDKKEPKS-----CDKTHTCPCPA 254
 Db 60 GLYLTSSVT--STWFSQVITCVNHPASTKVDKVERRNGIGHKCTCPTCHKCPV 117
 QY 255 PELLGSGVFLFPKPKDLMISRTPEVTVVVDVSHEDPEVKFNMVVDGVEVHNATKTP 314
 Db 118 PELLGSGVFLFPKPKDILLISONAKVTCVVDVSEEDPVQSFVNVEVHTAQTP 177
 QY 315 REQYNSTYRVSVLTVHDLNGKYEKCKVSNKALPAPIETIISKAKQPREPQVYTL 374
 Db 178 REQYNSTFRVWSALPIQHODMWSGKEFKCKVNNKALPSPIETIISKPKGLVRKPQVYV 237
 QY 375 PPSREMTKNQVSLTCLVKGYFSDIAVESNGQPENNYKTPPVLDSDGSFFLYSKLT 434
 Db 238 GPTEQLTEQTVSLTCLTSGFLNDIGVETSNGHIEKNYKNTPEVWDSGDSFFMYSKLN 297
 QY 435 VDKSRWQGNVFCSSVMHEALHNHYTKSLSPGK 470
 Db 298 VERSRWDSRAPVCGSVVHGLNHHHVEKSISSRPCK 333
 RESULT 11
 GCIN_MOUSE STANDARD; PRT; 393 AA.
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ig gamma-1 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";

RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 conserved transmembrane sequence and a 28-residue intracellular
 domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 immunoglobulin gamma chains.";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 immunoglobulin gamma chains"; 9:2623-2627(1982).
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 SEGMENT OF MU CHAINS.
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 CC EMBL; V00793; CAA24172.1; -;
 CC EMBL; V00793; CAA24173.1; -;
 CC EMBL; V00793; CAA24174.1; -;
 DR PIR; B02159; GIMSAB.
 DR HSP; P01842; 7FAB.
 DR MGD; MGI:96446; IgH-4.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_cl.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing; Transmembrane.
 FT NON_TER 1
 FT DOMAIN 1 97 CHI.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
 FT DISULFID 244 302
 FT TRANSEM 340 357 POTENTIAL.
 FT DOMAIN 358 393 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7AICE27 CRC64;
 Query Match 45.3%; Score 1140; DB 1; Length 393;
 Best Local Similarity 62.2%; Pred. No. 7.6e-72;
 Matches 206; Conservative 55; Mismatches 60; Indels 10; Gaps 4;

RX MEDLINE=81223894; PubMed=6787604;
 RA Olio R., Aufiray C., Morchamps C., Rougeon F.;
 RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RA MEDLINE=74175517; PubMed=4831970;
 RX Bourgois A., Fougereau M., Rocca-Serra J.;
 RT "Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RL Eur. J. Biochem. 43:423-435(1974).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE=73056887; PubMed=4565406;
 RA De Preval C., Fougereau M.;
 RT "Determination of the primary structure of a mouse gamma G2a
 RT immunoglobulin. Identification of the disulfide bridges";
 RL Eur. J. Biochem. 30:452-462(1972).
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; V00798; CAA24178.1; -;
 DR PIR; A02152; G2MSA.
 DR HSSP; P01842; 7FAB.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003600; Ig-like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 KW NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
 SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;
 Query Match 44.8%; Score 1129; DB 1; Length 330;
 Best Local Similarity 63.9%; Pred. No. 3.5e-71;
 Matches 212; Conservative 43; Mismatches 73; Indels 4; Gaps 3;
 QY 141 ASTKGPSVFLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
 DB 1 AKTTAPSVYPLAPVCGDTGSSVTLGCLVKGYFPEPTVLTWNSGSLSGVHTFPAVLQSD 60
 QY 201 GLYLSVVTPVSSSLGTQTYICNVNHNKPSNTKVDKRVKPKCDKTHTCPP--CPAPEL 258
 DB 61 -LYTLSSSVTVTSSTWSPQSITCNVAHPASSTKVDKIEPRG-PTIKPCPPCKCPANLL 118
 QY 259 GGPVLEFPKPKDPLMLSRPTVTCVVDVSHEDPEKFNWYDGVVEVHNKAKTPREQ 318
 DB 119 GGPVFIFFPKIKDVLMLSLPIVTCVVDVSEDDPDQVQISFNVFNVEVHTAQQTTHRED 178
 QY 319 YNSTVRVSVLTVLHODMLNGKEYCKVSKNALPAPIEKTISKAKGQPREPOVYTLPPSR 378
 DB 179 YNSTLRVVSALPIQHODMWSGKEFKCKVKNKDLPAPIERTISKPKGSVRAFOVYVLPPE 238

QY 379 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 438
 DB 239 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDK 298
 QY 439 RWOQGNVSCSVNHEALHNHYTQKSLSLSPGK 470
 DB 299 NWVERNSYSCSVNHEALHNHYTQKSLSLSPGK 330
 RESULT 14
 GCC_RAT
 ID GCC_RAT STANDARD: PRT; 329 AA.
 AC P20762;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig gamma-2c chain C region.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88166903; PubMed=3127222;
 RA Brueggemann M., Delmastro-Galile P., Waldmann H., Calabi F.;
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
 RT region cDNA: extensive homology to mouse gamma 3.";
 RL Eur. J. Immunol. 18:317-319(1988).
 CC -----
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 CC -----
 DR EMBL; X07189; CAA30169.1; -;
 DR PIR; S00847; S00847.
 DR HSSP; P01857; 1FC1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003600; Ig-Like.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00410; IG_Like; 1.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 222 CH2.
 FT DOMAIN 223 329 CH3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 143 203
 FT DISULFID 249 307
 SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;
 Query Match 44.8%; Score 1127.5; DB 1; Length 329;
 Best Local Similarity 62.8%; Pred. No. 4.5e-71;
 Matches 209; Conservative 51; Mismatches 66; Indels 7; Gaps 3;
 QY 141 ASTKGPSVFLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 200
 DB 1 AKTTAPSVYPLVPGCGTSGSLVTLGCLVKGYFPEPTVTKWNSGALSSGVHTFPAVLQ-S 59
 QY 201 GLYLSVVTPVSSSLGTQTYICNVNHNKPSNTKVDKRVKPKCDKTHTCPP--CPAPEL 257
 DB 60 GLYTLSSSVTVPSSTWSSQTVTCVAHPATKSNLIKRIEPR---RPKPRPTDICSDDN 116

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QY 258 LGSPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 317
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Db 117 LGRPSVFEIPEPKDILMITLTPKVCVVVDVSEEPDQVQSFVDMVRVFTAQTPHEE 176
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 318 QYNSTRVVSVLVLVHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 377
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 OLNGTRFVSVTLHIQHDWMSGKEFKCKVNNKDLPSPIEKTISKAKGKARTPQVYTIPT 236
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 378 REEMTKNOVSLTCLVKGFPDIAVWESNGQPNENYKTPPPVLDSDGSPFLYSLKTVDK 437
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 REOMSKNKVSLTCWVTSFYPASISVWERNGELEQDKNTLPVLDSDSEYFLYSLKVS 296
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 438 SRMQQGNVFCSCYMHREALHNNHYTKQSLSLSPGK 470
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Db 297 DSNMRGDIYTCVVVHEALHNNHTQKNLSRSPGK 329
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 15
GCAB_MOUSE STANDARD; PRT; 335 AA.
AC P01864;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT IgG2a and IgG2b alleles of the mouse."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain FC regions of Ig1a and Ig1b allotypic forms."
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC 1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
-----
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DR EMBL; J00479; -; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; 1FCL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBBI3C6 CRC64;
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Query Match 44.7%; Score 1126.5; DB 1; Length 335;
Best Local Similarity 61.6%; Pred. No. 5.3e-71;

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Matches 207; Conservative 52; Mismatches 70; Indels 7; Gaps 2;
QY 141 ASTKGPSVFLPLAPSSSKSTSGTAAALGCLVXDYFPEPTVTVSNWNSGALTSGVHTFFPAVLQSS 200
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Db 1 AKTAPSVYPLVPVCGGTGSSVTLCGLVKGYFPEPTVLTWNSGSLSSGVHTFFALLQ-S 59
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 201 GLYSLSVWTVPSSSSLGTQTYICNVNHPKNTKVDKRVKPK-----SCDKTHTCPCPCPA 254
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 GLVTLSSSVTISNTWPSQTITCNVAHPASSTKVDDKIEPRVPIITQNCPPPHQVRVPCAA 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 255 PELLGGPSVFLPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPK 314
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PDLGGPSVFEIPEPKIKDVLMSLSPMVTVCVVVDVSEDDPDVQISWFNWVNHVHTAQTT 179
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QY 315 REEOYNSTRVVSVLTVLHODWLNGLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTL 374
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 HREDYNSTLRVVSALPIQHODWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 375 PPSREEMTKNOVSLTCLVKGFPDIAVWESNGQPNENYKTPPPVLDSDGSPFLYSLKLT 434
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 PPAEEMTKKEFSLTCTMTGFLPAETAVDWTSGRTQNYKNTATVLDSDGSPYPMYSKLR 299
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 435 VDKSRMQQGNVFCSCYMHREALHNNHYTKQSLSLSPGK 470
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Db 300 VQKSTWERSLFAFACSVVHEVLHNNHLTKTISRSLGK 335
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Search completed: August 14, 2002, 15:23:17
Job time: 690 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 14, 2002, 15:22:19 ; Search time 187.61 Seconds
(without alignments)
433.386 Million cell updates/sec

Title: US-09-499-662-157
Perfect score: 2518
Sequence: 1 MWSCHILFLVATATGVHSQ.....MHEALHHYTKLSLSLSPGK 470

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL19.*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1623.5	64.5	473	11 Q9D8L4	Q9d8l4 mus musculus
2	1612.5	64.0	463	11 Q99LC4	Q99lc4 mus musculus
3	1572.5	62.5	473	11 Q99L25	Q99l25 mus musculus
4	1350	61.6	468	11 Q99L31	Q99l31 mus musculus
5	1446.5	57.4	437	11 Q99L31	Q99l31 mus musculus
6	1434.5	57.0	473	11 Q91205	Q91205 mus musculus
7	1263.5	50.2	337	6 Q95M34	Q95m34 equus caball
8	1257	49.9	701	4 Q96P08	Q96pq8 mus sapien
9	967	38.4	278	11 Q92L1K	Q92l1k mus musculus
10	944.5	37.5	614	4 Q96GA6	Q96ga6 homo sapien
11	875.5	34.8	481	11 Q91WT3	Q91wt3 mus musculus
12	866	34.4	500	4 Q9BRV0	Q9brv0 homo sapien
13	826.5	32.8	597	4 Q96BB9	Q96bb9 mus sapien
14	824.5	32.7	481	11 Q91WT1	Q91wt1 mus musculus
15	812	32.2	496	4 Q96DK0	Q96dk0 homo sapien
16	798	31.7	488	11 Q91WR1	Q91wr1 mus musculus

17	764.5	30.4	597	4 Q9BU10	Q9bu10 homo sapien
18	760.5	30.2	597	4 Q9BOB8	Q9bob8 homo sapien
19	754.5	30.0	618	4 Q96AA6	Q96aa6 homo sapien
20	753	29.9	484	11 Q99LA6	Q99la6 mus musculus
21	748	29.7	494	4 Q96K68	Q96k68 homo sapien
22	738.5	29.3	487	11 Q99KA4	Q99ka4 mus musculus
23	735.5	29.2	479	11 Q91WP5	Q91wp5 mus musculus
24	731	29.0	613	4 Q96EY0	Q96ey0 homo sapien
25	714	28.4	486	11 Q91X07	Q91x07 mus musculus
26	706.5	28.1	480	11 Q91XE1	Q91xe1 mus musculus
27	669	26.6	479	11 Q99M22	Q99m22 mus musculus
28	667	26.5	482	11 Q91X92	Q91x92 mus musculus
29	643	25.5	496	4 Q96KX8	Q96kx8 homo sapien
30	591.5	23.5	416	4 Q9NPP6	Q9npp6 homo sapien
31	586	23.3	426	11 Q9DCD9	Q9dcd9 mus musculus
32	523.5	20.8	143	11 Q91V67	Q91v67 mus musculus
33	523	20.8	150	4 Q9Y298	Q9y298 homo sapien
34	520	20.7	157	4 Q95978	Q95978 homo sapien
35	508.5	20.2	143	11 Q924P9	Q924p9 mus musculus
36	508.5	20.2	159	4 Q96OS0	Q96os0 homo sapien
37	495	19.7	142	11 Q924Q2	Q924q2 mus musculus
38	494.5	19.6	145	11 Q924R3	Q924r3 mus musculus
39	482.5	19.2	124	4 Q9UL92	Q9ul92 homo sapien
40	480.5	19.1	384	4 Q9UP60	Q9up60 homo sapien
41	479.5	19.0	143	11 Q924Q5	Q924q5 mus musculus
42	477	18.9	144	11 Q924P5	Q924p5 mus musculus
43	475	18.9	146	11 Q924R8	Q924r8 mus musculus
44	473.5	18.8	145	11 Q924Q7	Q924q7 mus musculus
45	473	18.8	119	4 Q9UL94	Q9ul94 homo sapien

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	473 AA.
Q9D8L4	AC Q9D8L4;			
DT	01-JUN-2001 (TREMBLrel. 17, Created)			
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	181006009RIK PROTEIN.			
GN	IGH-1 OR 18100600009RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=PANCREAS;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Famanaka I.,			
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto S.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,			
RT	*Functional annotation of a full-length mouse cDNA collection.*;			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK007918; BAB25349.1; -			
DR	HSSP; P01842; 7FAB.			

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DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR003597; Ig.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match      64.5%; Score 1623.5; DB 11; Length 473;
Best Local Similarity 62.8%; Pred. No. 1e-128;
Matches 299; Conservative 73; Mismatches 95; Indels 9; Gaps 4;

QY 1 MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYMMQWVRQAP 60
DB 1 MENSWFELFLSVTAGVHCQVQLKQSGAEELVKPGASVKISKASGYFTFTDYINWVKRP 60

QY 61 GQGLEWMEIDPSDSYNNYKQKGRVITITRDTSTSTAYMELSLRSEDYAVYICARNRD 120
DB 61 GQGLEWIGIKPGSGSYNNYNEKFKGKATLTADKSSSTAYMQLSLSLSEDSAVYFCARS-G 119

QY 121 YSNWYFDWEGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVS 180
DB 120 YDWDW-FAYWGQGLTVTVSSAAKTATPSVPLAPVCGGTGSSVTLGCLVKGYFPEPTLT 178

QY 181 WNSGALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
DB 179 WNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQITTCNVAHPASSTKVDKKIEP 237

QY 241 K-----SCDKTHTCCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 294
DB 238 RVPTQNCPPLKECPCCAAPDLLGGPSVFIFPPKIKDVLMSLSPMTCVVVDVSEDDP 297

QY 295 EVKFNKYVDGVEVHNNAKTPREEQYNSYRYVSVLTVLHODWLNKGYCKVSNKALPAP 354
DB 298 DVOISFVNVEVHTAQTHREDYNSTLRVVSALPIHODWMSGKEFKCKVNNALPSP 357

QY 355 IEKTSKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNY 414
DB 358 IEKTSKPRGPVPAPQVYLVLPAAEEMTKKEFSLTCTMITGFLPAEIAVDWTSNGRTEQNY 417

QY 415 KTTPPVLDSGDFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 418 KNTATVLDSGDFMYSKLRVQKSTWERSLFACSVVHEGLHNHLTKTISRSLGK 473

RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AA03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Igc1; 2.
DR SMART; SM00407; Igc1; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match      64.0%; Score 1612.5; DB 11; Length 463;
Best Local Similarity 62.7%; Pred. No. 8.2e-128;
Matches 296; Conservative 75; Mismatches 90; Indels 11; Gaps 5;

QY 1 MGWSCILFLVATATGVHSQVQLVQSGAEVKKPGASVKVSCKASGYFTFTSYMMQWVRQAP 60
DB 1 MENTWIFLFLISGTAGVHSQVQLQSGAELARPASVRLSCKASGYFTTGYGVSNNKQRT 60

QY 61 GQGLEWMEIDPSDSYNNYKQKGRVITITRDTSTSTAYMELSLRSEDYAVYICARNRD 120
DB 61 GQGLEWVGEIYPGSGTYNNYSEKFKGKATLTDDKSSSTAYMHLSSLTSEDSAYIFCARSSY 120

QY 121 YSNWYFDWEGEGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYRPEPTVS 180
DB 121 YSYD-LFAYWGQGLTVTVSSAAKTTPPSVYPLAPGAAQTNSMVTLGCLVKGYFPEPTVT 179

QY 181 WNSGALTSVGHVTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKRV 240
DB 180 WNSGSLSSGVHTFPAYLQSD-LYTLSSSVTVTPSSVTPSETVTCNVAHPASSTKVDKKIYP 238

QY 241 KSCDKTHTCCP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 298
DB 239 RDCG----CKPCICTVPEV---SSVFIFPPKPKDVLTTITLPKVTCTVVVDISKDDPEVQ 291

QY 299 NWYVDGVEVHNNAKTPREEQYNSYRYVSVLTVLHODWLNKGYCKVSNKALPAPIEKT 358
DB 292 SWFVDDDEVHFAQTPREEQFNSTFRSVSELPIMHQDWLNKGEKFCRVNSAFAFPAPIEKT 351

QY 359 ISKAKGQPREPVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 418
DB 352 ISKTKGRPKAPQVYTIPTPPKEQMAKDKVSLTCTMITDFPEDITVEMQWNGQPAENYKNTQ 411

QY 419 PVLDSGDFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 470
DB 412 PIMTDGDFYIYSKLVNOKSNWEAGNTFTCSVLHEGLHNHHTKSLSHSPGK 463

RESULT 3
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AA03888.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Igc1; 2.
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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 62.5%; Score 1572.5; DB 11; Length 473;
Best Local Similarity 62.5%; Pred. No. 2e-124;
Matches 297; Conservative 64; Mismatches 107; Indels 7; Gaps 5;

Qy 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 MEWSWVLFELVATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Qy 61 GQLEWMEIGIDPSDYSYNNQKFKGRVITRTDTSTSTAYMELSSLSRSEDYVYICARNR 120
Db 61 EGQLEWIGWIDEDGETKYPKFKGRVITRTDTSSNTAYLQSLSTSEDTAYIYCARNLL 120
Qy 121 YSNNNYEDVWVGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 180
Db 61 EGQLEWIGWIDEDGETKYPKFKGRVITRTDTSSNTAYLQSLSTSEDTAYIYCARNLL 120
Qy 121 YGG--YIDWVGOGTTITVSSAKTAPSVPLAPVCGDTTGGSSVTLGCLVKGYFPEPV 178
Db 121 YGG--YIDWVGOGTTITVSSAKTAPSVPLAPVCGDTTGGSSVTLGCLVKGYFPEPV 178
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVKR 240
Db 179 WNSGSLSSGVHTFPAVLQSD--LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVK 237
Qy 241 KSCDTHTCPP--CPAPELGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVK 298
Db 238 RG-PTIKPCPCPCAPNLLGGPSVFIFPKIKDVLMISSLPMVTCVVDVSEDDPDV 296
Qy 299 NNYVDGVEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNGLKYEKCKVSNKALPAP 358
Db 297 SFVNVNVEVLTAQTQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAP 356
Qy 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNY 418
Db 357 ISKPGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIVVEWNTNGKTELNY 416
Qy 419 PVLDSGDSGFFLYSKLTVDKSRQOGNVFSCSVHHEALHNHYTQKSLSLSPGK 470
Db 417 PVLDSGDSGYFMYSKLRVEKKNVYERNYSYSCSVVHGLHNHHTTKFSRTPGK 468

RESULT 5
Q99L31 ID Q99L31 PRELIMINARY; PRT; 437 AA.
AC Q99L31;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 62.5%; Score 1572.5; DB 11; Length 473;
Best Local Similarity 62.5%; Pred. No. 2e-124;
Matches 297; Conservative 64; Mismatches 107; Indels 7; Gaps 5;

Qy 1 MGWSCIILFLVATATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Db 1 MEWSWVLFELVATGVSQVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMMQWRQAP 60
Qy 61 GQLEWMEIGIDPSDYSYNNQKFKGRVITRTDTSTSTAYMELSSLSRSEDYVYICARNR 120
Db 61 EGQLEWIGWIDEDGETKYPKFKGRVITRTDTSSNTAYLQSLSTSEDTAYIYCARNLL 120
Qy 121 YSNNNYEDVWVGEGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV 180
Db 121 YGG--YIDWVGOGTTITVSSAKTAPSVPLAPVCGDTTGGSSVTLGCLVKGYFPEPV 178
Qy 181 WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVKR 240
Db 179 WNSGSLSSGVHTFPAVLQSD--LYTLSSSVTVTSSTWPSQSIITCNVAHPASSTKVK 237
Qy 241 KSCDTHTCPP--CPAPELGGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVK 298
Db 238 RG-PTIKPCPCPCAPNLLGGPSVFIFPKIKDVLMISSLPMVTCVVDVSEDDPDV 296
Qy 299 NNYVDGVEVHNNAKTPREEQYNSTYRVSVLTVLHODWLNGLKYEKCKVSNKALPAP 358
Db 297 SFVNVNVEVLTAQTQTHREDYNSTLRVVSALPIQHDWMSGKEFKCKVNNKALPAP 356
Qy 359 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNY 418
Db 357 ISKPGSVRAPQVYVLPPEEEMTKKQVTLTCMVTDFMPEDIVVEWNTNGKTELNY 416
Qy 419 PVLDSGDSGFFLYSKLTVDKSRQOGNVFSCSVHHEALHNHYTQKSLSLSPGK 470
Db 417 PVLDSGDSGYFMYSKLRVEKKNVYERNYSYSCSVVHGLHNHHTTKFSRTPGK 468

RESULT 4
Q99L31 ID Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003878; AAH03878.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003600; IG_like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
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Query Match          57.4%; Score 1446.5; DB 11; Length 437;
Best Local Similarity 59.7%; Pred. No. 7.9e-114;
Matches 270; Conservative 70; Mismatches 95; Indels 17; Gaps 7;

QY 21 VOLVQSGAEVKKPGASVKVSCKASGYFTSYWMQWRQAPQGGLWGEIDPSDYNNYN 80
DB 1 VOLQESGGGLVKPGSLKLSCAASGFTSSYAMSWVRQTPKRLWNASFS-SGIIYYT 59
QY 81 QKFGKRVITRDITSTAYMELSLRSEDYAVYICARNRDNYSNNWYFDVWGEGLTVTSS 140
DB 60 DSVKGRFTIYKDKRNTLSQMSSLRSEDYAMYYCARG-DYS-----AYWPGGLTVTVA 113
QY 141 ASTKGPSEVFLAPSSKSTSGTAAALGCLVVDYFPEPTVSNWNSGALTSVHTFFAVLQSS 200
DB 114 AKTPPSSVFLAPGSAATQSMVTLGCLVKGYPFVTVTNWNSGSLSSGVTFFAVLQSD 173
QY 201 GLYSLSWVTVPSSTLGTQYICNVNHPKNTKVKRVEPKSCDKTHTCPP--CPAPPELL 258
DB 174 -LVTLSSTVTPSSWTPSEIVTCNVHPASTKVDKLIIVPRDCG---CKPCICTVPEV- 227
QY 259 GGSVFLFPKPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQ 318
DB 228 --SSVFIFPKPKDVLITLTPKVTCCVVVDISKDDPEVQFSWFVDVDEVHTAQTPREEQ 285
QY 319 YNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR 378
DB 286 FNSTFRSVSELPINHQDLWLNKGEYKCKVNSAAPPAPTEKTSITKGRKPAQVYTIPTPK 345
QY 379 EEMTKNOVSLTCLVKGYPSPDIKLVKGYPSDIKLVKGYPSDIKLVKGYPSDIKLVKGYPS 438
DB 346 EQMAKDKVSLTCLTDFPEPDIIVEMQWNGQPAENYKNTQPIMDTDSGYFVSKLVNQKS 405
QY 439 RWQGNVFSVSMVHEALHNYTKQSLSPGK 470
DB 406 NWEAGNTFTCSVLHLEGLHNHTKNIHSPGK 437

RESULT 6
Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DE 01-DEC-2001 (TREMREL. 19, Last annotation update)
OS HYPOTHETICAL 51.9 KDA PROTEIN.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match          57.0%; Score 1434.5; DB 11; Length 473;
Best Local Similarity 57.5%; Pred. No. 9.1e-113;
Matches 272; Conservative 73; Mismatches 113; Indels 15; Gaps 5;

QY 7 ILFLVATATGVHSQVLQVSGAEVKKPGASVKVSCKASGYFTSYWMQWRQAPQGGLW 66
DB 7 LVFLVLILKGVCEVLQVSGGLVKPGSKRLSCAASGFTSDYGMHWVRQAPKGLW 66
QY 67 MGEIDPSDSYNNYKQKGRVITRDITSTAYMELSLRSEDYAVYICARNRDNYSNNY 126
DB 67 VAYINSGSTIYVADTVKGRFTISRDNNAKNTLFLQMTLSRSEDYAVYICAREL-----WL 121
QY 127 --FDVWGEGLTVTSSASVTKGSEVFLAPSSKSTSGTAAALGCLVVDYFPEPTVSNWNSG 184
DB 122 RRDITWQGTITIVSSAKTTPPSVYPLAPGCGDTTGGSVTLGCLVKGYPFESVTVTNWSG 181
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QY 185 ALTSGVHTFPVQLQSSGLYSLSVVTVFSSSLGTQYICNVNHPKNTKVKRVEPKSCD 244
DB 182 SLSSSVHTFPALLO-SGLYTWSSSVTVFSSSLGTQYICNVNHPKNTKVKRVEPKSGPI 240
QY 245 KT-HTCPP-----CPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 297
DB 241 STINPCPPCKECHKCPAPNLEGGPSVFIFFPNIKDVLISLTPKVTCTVVDVSEDDPDVQ 300
QY 298 FNWYVDGVEVHNNAKTKPREEQYINSTRYVSVLTVLHODWLNKGEYKCKVSNKALPAPIEK 357
DB 301 ISWFNVNVEVHTAQITQTHREDYINSTRVVSALPIHQDMSCKEYKCKVNNKDLSPIER 360
QY 358 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYKTT 417
DB 361 TISKIKGLVRAQVYVILPPPAEQLSRKDVSLTCLVVGNGPGDISVEWTSNGHTENYKDT 420
QY 418 PPVLDSGSGFLYSLKTLVDKSRWQGNVFSVSMVHEALHNYTKQSLSPGK 470
DB 421 APVLDSGSGYFIYSKLDIKTSWEKTDSCNVRHEGLKNYLYKKTISRSPGK 473

RESULT 7
Q95M34 PRELIMINARY; PRT; 337 AA.
AC Q95M34;
DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DE 01-DEC-2001 (TREMREL. 19, Last annotation update)
DE IMMUNOGLOBULIN GAMMA 1 HEAVY CHAIN CONSTANT REGION
DE (FRAGMENT).
GN IGHC1.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner B.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98383416; PubMed=9717671;
RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C.,
RA Leibold W., Radbruch A.;
RT "Organization of the equine immunoglobulin heavy chain constant region
RT genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes.";
RL Immunobiology 199;105-119(1998).
DR EMBL; AJ300675; CAC44624.1; -.
FT NON_TER 1
SQ SEQUENCE 337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;

Query Match          50.2%; Score 1263.5; DB 6; Length 337;
Best Local Similarity 68.9%; Pred. No. 1.5e-98;
Matches 233; Conservative 44; Mismatches 52; Indels 9; Gaps 3;

QY 141 ASTKGPSEVFLAPSSKSTSGTAAALGCLVVDYFPEPTVSNWNSGALTSVHTFFAVLQSS 200
DB 1 ASTAPKRVFALAPCGGTTSDTVALGCLVSGYFPEYKVPKVSNNWNSGSLTSGVHTFFSVLQSS 60
QY 201 GLYSLSWVTVPSSTLGTQYICNVNHPKNTKVKRVEP-----KSCDKTHTCPPCPA 254
DB 61 GFYSLSWVTVPASTWTSEYICNVVHAASNFVKDKRIEIPIDNHQKVCDSM-KCPKCPA 119
QY 255 PELLGSPSVFLFPKPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKP 314
DB 120 PELLGSPSVFIPPNPKDTLMITRTPEVTCVVDVSDQENPDVKNWMDGVEVETATRP 179
QY 315 REQYINSTRYVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL 374
DB 180 KEQFNSTRYVSVLRIHQDLWLNKGEYKCKVNNQALPQPIERTITTKTKGRSQEPQVYL 239
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QY 375 PPSREMTKNQVSLTCLVKGFPSPDIAYEWESNGQP--ENNYKTTTPPVLDSDGSEFLYSK 432
Db 240 APHPELSKSKSVSYTKLVKDFYPPINIEWQNGQPELETETSTTQAQDSDGSEFLYSK 299

QY 433 LTVDKSRWQOQNVFSCSYMHAEALHNYHTQKLSLSPGK 470
Db 300 LSVDRNRWQOQNTTFCGYMHAEALHNYHTQKNSKNPGK 337

RESULT 8
Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "targeting tissue factor on tumor vascular endothelial cells and tumor
RL cells for immunotherapy in mouse models of prostatic cancer.";
DR EMBL; AF272774; AAK58686.1; -.
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 49.9%; Score 1257; DB 4; Length 701;
Best Local Similarity 99.1%; Pred. No. 1.6e-97;
Matches 230; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 239 EPKSCDKTHTPCPPAPPELLGGPSVFLFPPPKDITMISRTEPTVCVVVDVSHEDPEVKF 298
Db 470 EPKSCDKTHTPCPPAPPELLGGPSVFLFPPPKDITMISRTEPTVCVVVDVSHEDPEVKF 529

QY 299 NWYDGVGVHNAKTPREQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 358
Db 530 NWYDGVGVHNAKTPREQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 589

QY 359 ISKAGQPREQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTPP 418
Db 590 ISKAGQPREQVYTLPPSREEMTKNQVSLTCLVKGFPSPDIAYEWESNGQPENNYKTPP 649

QY 419 PVLDSDGSEFLYSKLTVDKSRWQOQNVFSCSYMHAEALHNYHTQKLSLSPGK 470
Db 650 PVLDSDGSEFLYSKLTVDKSRWQOQNVFSCSYMHAEALHNYHTQKLSLSPGK 701

RESULT 9
Q92IK1 PRELIMINARY; PRT; 278 AA.
AC Q92IK1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:18977).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC012207; AAH12207.1; -.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

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Query Match 38.4%; Score 967; DB 11; Length 278;
Best Local Similarity 65.7%; Pred. No. 1.3e-73;
Matches 182; Conservative 35; Mismatches 52; Indels 8; Gaps 3;

QY 1 MGWSCILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYWMQWVRQAP 60
Db 1 MGWNCILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYWMQWVRQAP 60

QY 61 GQGLEWMGEIDPSDSTYNNQKFKGRVTITRDTSTSTAYMELSLRSEDYAVYICARNRD 120
Db 61 GQGLEWIGNINPNSGGTNNYNEKFKKATLAVDKSSSTVYMQLSLTSSEDSAVYICRGY 120

QY 121 YSNWTFDVMGEGTLVTVSASTKGPSVFPLAPSSKSTSGTAAALGLVLDYFPEPPTVS 180
Db 121 Y-DDVYFDMGAGTTVTVSAAKTPAPSVPLAPVCGGTGGTSTGLVGLVGYFPEPPTLT 179

QY 181 WNSGALTSGVHTPAPVQLQSSGLYSLSVTVPSLSLGTQYICNVNHPKNTKYDKRVEP 240
Db 180 WNSGSLSSGVHTPAPVQLQ- SGLVTLSSSVIVTNTWFSQITCNVAHPASSTKYDKKIEP 238

QY 241 K-----SCDKTHTCPPCPAPPELLGGPSVFLFPPPKP 271
Db 239 RVETITQNPCCPLKECPKCAAPDLGGPSVFIEFPPRSR 275

RESULT 10
Q96GA6 PRELIMINARY; PRT; 614 AA.
AC Q96GA6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE UNKNOWN (PROTEIN FOR MGC:15420).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC009851; AAH09851.1; -.
SQ SEQUENCE 614 AA; 67921 MW; 55EF536E77AA9BBB CRC64;

Query Match 37.5%; Score 944.5; DB 4; Length 614;
Best Local Similarity 37.3%; Pred. No. 3.1e-71;
Matches 215; Conservative 83; Mismatches 164; Indels 115; Gaps 17;

QY 1 MGWSCILFLVATATGVSQVQLVQSGAEVKKPKGASVKVSKASGYTFTSYWMQWVRQAP 60
Db 1 MDWTRILFLVAAATDAYSQMLVQSGAEVKKPKGSSVKVSKASGYTFTSYRLHWRQAP 60

QY 61 GQGLEWMGEIDPSDSTYNNQKFKGRVTITRDTSTSTAYMELSLRSEDYAVYICARNRD 120
Db 61 GQALEWMGMITPFGNTNTAQAQFQDRVTITRDRSMNTAYMELSLRSEDYAVYICARG-- 118

QY 121 YSNW--YFDVMGEGTLVTVSASTKGPSVFPLAPSSKSTG-GTAALGLVLDYFPEPV 177
Db 119 YSSWDADFIMQGGTMTVTVSSGASAPTLFPLVSCNSPDSSTSSVAVGCLAQFLPDSI 178

QY 178 TVSW--NSGALTSGVHTPAPVQLQSSGLYSLSVTVPSLSL--GTQTY-ICNVNHPKSN- 231
Db 179 TFSWKYKNSDISSTRGFPSVLR-GGKYAATSQVLLPSKDVMOGTDEHVVKVQHPNGNK 237

QY 232 -----TKVDKRVPEKS-----CDKTHTCP----- 250
Db 238 EKNVPLPIAELPPKVSFVFPFPRDGFNGPRKSKLIQATGFSRQIQVSWLREGKQVGS 297

QY 251 -----PCPAPPELLGGPS----- 262
Db 298 GVTTDQVQAEAKESGPTTKYKVTSTLTIKESDWLSQSMTCKVDHRLGTLFOQNASSMVCYPD 357

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Qy	395	FYPSDIAVESNQ--PENNYKTPPVLID-SDG--SFFLYSKLTVDKSRWQGQGVNFSCS	4449
Dd	402	FSPKDVLVRWGSOELPREKYLTWASROBPSQGTTFATVTSILRVAAEDKKGDFTSCM	461
Qy	450	VMHEALHNHYTKQSLSLSPCK	470
Dd	462	VGHEALPLAFTQETIDLAKG	482
RESULT 13			
Q96BB9	ID	Q96BB9 PRELIMINARY;	PRT; 597 AA.
AC	Q96BB9;		
DT	01-DEC-2001	(TEMBRel. 19, Created)	
DT	01-DEC-2001	(TEMBRel. 19, Last sequence update)	
DT	01-DEC-2001	(TEMBRel. 19, Last annotation update)	
DE	HYPOTHETICAL 65,0 KDA PROTEIN.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=PRIMARY B-CELLS FROM TONSILLS;		
RA	Strausberg R.;		
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.		
DR	EMBL; BC015760; AH15760.1; -.		
KW	Hypothetical protein.		
SQ	SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRG64;		

Query Match.	32.8%;	Score 826.5;	DB 4;	Length 597;
Best local Similarity	33.0%;	Pred. No. 2.8e-61;		
Matches 192;	Conservative 93;	Mismatches 178;	Indels 119;	Gaps 18;
Qy	1	MGWSCIIILFVATATGVHSQVQLVQSQAEGVKKPGCASVKVSKASGYFTSYVMQWRQAP	60	
Db		: : : : : : : : :		
Qy	5	LSW-----LFLVAILKVOCEVOLLSEGGVLVOPGSGURLSCAASGFSSSTAMNWRQAP	60	
Db		: : : : : : : : :		
Qy	61	GGLEWMEIGDIPDSYTYNQKFKGRYITRTDSTSTAYMELSSLRSEDSTAVYYCARN-R	119	
Db		: : : : : : : :		
Qy	61	GKGLEWYSATSGSGSYADSVKGRFTISRDNSRDTLYLQMNLSRAEDTAVYYCAKDP	120	
Db		: : : : : : : : :		
Qy	120	DYSNNWTF--DWWGEGTLVTVSSASTKGPSVFPLPSSKSTSG-GTAAAGCLVKDYPPE	175	
Db		: : : : : : : : :		
Qy	121	GYSASGNYTRDYWGOGTFLTVSSGSASAPLFLPLVSCENSPDSTSSVAVGAQAQDEL	180	
Db		: : : : : : : : :		
Qy	176	PVTYSW--NSGALTSGVHTTTPAVLOSGLYSLSSVTVTPSSSL-GTQTY-ICNVNHIKPS	230	
Db		: : : : : : : : : :		
Qy	181	SITFSWKYKNSDISSTIRGFPFSLR-GGKYAANTSOVLLPSKDVMOGQDEHVVKVQHPNG	239	
Db		: : : : : : : : : :		
Qy	231	N-----TKVDKRVPEKS-----CDKTHTCP-----	250	
Db		: : : : : : : : : : : : :		
Qy	240	NKEKNVPLPVLAEPPKVSFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV	299	
Db		: : : : : : : : : : : : :		
Qy	251	-----PCPAPELLGGS-----	262	
Db		: : : : : : : : : : : : :		
Qy	300	GSVTTDQVQAEKESGPTTKVKTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMCV	359	
Db		: : : : : : : : : : : : :		
Qy	263	-----VFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP	314	
Db		: : : : : : : : : : : : :		
Qy	360	PQDQTAIRVFAIPPS-PASIFLTKSTKLTCLVTLDTLTHYD-SVTSWTRQNGEAVKTHINI	417	
Db		: : : : : : : : : : : : :		
Qy	315	REQDYNTSYRVVSVLTVLHQDLWNGEYKCKVSKNAKLPAPIEKTISKAKGQP-REPQVYT	373	
Db		: : : : : : : : : : : : :		
Qy	418	SESHPNATFSAVGEASICEDDWNSEGERFTCTVTTDLPSPKQITSRPKGVALLHRPDPVL	477	
Db		: : : : : : : : : : : : :		
Qy	374	LPPSREMT-KNOYSLKLVKGYFPSDIADVWESNGQP--ENNYKTTTPPVLDD--SDGSFF	428	
Db		: : : : : : : : : :		
Qy	478	LPPAREQLNRESATITCLVTFGSPALVFVOMQORGQPSPEKVTYTSAPMPEQPAPGRFY	537	
Db		: : : : : : : : : :		
Qy	429	LYSKLTVDKSRWQOGNVFCSGVMHEALHNHYTKRSLSLSPGK	470	

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Db 538 ASHSLTVSEENWTGTYTCVVAHEALPNRVTERTVDKSTCK 579
      : | | | | : | | : : | | | | | | | : : : : | | |
RESULT 14
Q91WT1 PRELIMINARY; PRT; 481 AA.
AC Q91WT1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 52.1 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu;
RX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases
DR EMBL; BC013490; AAH13490.1; -
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 32.7%; Score 824.5; DB 11; Leng
Best Local Similarity 39.6%; Pred. No. 3e-61;
Matches 191; Conservative 76; Mismatches 184; Indel:

Qy 1 MGWSCIIILFLVATATGVHSQVLVQSGAEVKKPGASVKVSKASGYTTFS
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 1 MGWRWIFLELLSGTAGVQCQVQLQSGPELVKPGASVKISCKASGYTFTS
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 61 GGLWEMGIDPSDSTVNTYKQFKGRVITITDSTSTAYMELLSLSRSDST
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 61 GGLVWVGWIYDGDNKTKYKEKFKTKTLTADKSSSTAYMELLSLTSDDSS
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 121 YSNWYFVWVGEGTLVTVSASTKGPSVFPPLAPSKSTSGTGAALGLVKV
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 118 -GGWAFDYWGQGTTLTVSSEPAEPTIYPLT-PPQALSDPVIIGLIH
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 180 SNWSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGT-QTYICNVNHH
   : ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 176 TWGKSGKDITTVNFPPALASGGRYTMSSQLTLPAVECPGESVKCSVQH-I
   ||| ||| : || ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 239 EPKSCDKHTCPCPAPELGGPSVFLFPPKPKDTLMTSRPEVTCVVDV
   : ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 235 NCGICSPPTTPPPSCQ----PSLSLORPALED-LLLGSDASITCTLNG
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 298 FNNYVDGVVHNAKTRPEQYNST---YRVSVLTVLHQDWLNGKEYKCC
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 288 FTW-----EPSTGKDAVKKAVQNSCCGYSSVSLPGCAERNWSGAFKFC
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 355 IEKTIKAKGQPREPOVYITLPPGREEMTKNQ-VSLTCLVKLGYPSPDIAVEF
   : ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 342 LTGTIAKVTVNTFPPQVHLLPPSEELANLVELSLTCLVRAFNPKPELVRI
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 411 ENNYKTTTPVLSDG--SFELYSKLTVDKSRWQGNVFCSCVMHEALNHH
   : ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 402 ESYLVFEPLKEFGEGATTTLTVSLRVSAETIKWQGDQYSCMVGHEALPMN
   ||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Qy 469 GK 470
Db 462 GK 463

RESULT 15
Q96DK0 PRELIMINARY; PRT; 496 AA.
ID Q96DK0
AC Q96DK0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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RESULT	15
Q96DK0	
ID	Q96DK
AC	Q96DK
DT	01-DEC
DT	01-DEC

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CDNA FLJ25298 FIS, CLONE STM07683, HIGHLY SIMILAR TO PROTEIN TRO
DE ALPHA1 H, MYELOMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GASTRIC MUCOSA;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hatanaka T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujinori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058027; BAB71633.1; -.
SQ SEQUENCE 496 AA; 53532 MW; C72EE1E247C86FED CRC64;

Query Match      32.2%; Score 812; DB 4; Length 496;
Best Local Similarity 39.6%; Pred. No. 3.6e-60;
Matches 197; Conservative 65; Mismatches 189; Indels 46; Gaps 16;

QY 1 MGWSCILFLVATATGVSQVQVQSGAEVVKPGASVKVSKASGYFTFTSYMMQWVRQAP 60
DB 1 MDKTRFLFVAAVTGVSQVHLVQSGAELKMPGSSVKVSKASANNFRSYAFTWVRQAP 60
QY 61 GQGLEWGEIDPSDSTYNQKFKGRVTTTRDTSTSTAYMELSSLRSEDFAVYVCARNRD 120
DB 61 GQGLWMGGIIPNFGAPNAQNFQDRVTISADDSSTTVYVYVYVYVYVYVYVYVYVYVYV 120
QY 121 Y---SNNWYEDVWGEGLTVTVSSASTKGPSVFPPLAPSSKSTSGTALGCLVKDYFP-EP 176
DB 121 YGSGSYIYLQHWGGQGLTVTVSSASTSPKVPFLSLCS-TQPDGNVVIACLVQGFPPQEP 179
QY 177 VIVSMNSGALTSGVHTFPAVLQSSG-LYSLSSVTVTPSSS-LGTQTVICNVNHPKSNTKV 234
DB 180 LSVTWSESQGVTAARFPSPQSDASGDLTYTSSQLTLPATCLAGKSVTCHKHY-TNPSQ 238
QY 235 DKRVEPKCDKTHTCPPCPAPELLGGPSVFLFPPKPK-----DTLMISRT 279
DB 239 DVTV-----PCVPVSTPTPTSPST-PPTPSPSCCHPRLSLHRALEDLLLGSE 285
QY 280 PEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYRVYVSLTFLHODWNLG 339
DB 286 ANLTCTLTGL-RDASGVTTWTPSSSK--SAVGGPPDRDLCCGYSVSSVLPGCAEPWNHG 342
QY 340 KEYCKVSNKALPAIEKTSKAGQPREPQVYTLPPPSREEMTKNQ-VSLTCLVKGFYPS 398
DB 343 KFTFTCAAYPESKPTLTATLSKS-GNTRFEVHLLPPPSSEALNELVTLTCLARGFSFK 401
QY 399 DTAVERESNGQ--PENNYKTPPVLD-SDG--SFFLYSKLTVDKSRWQQGNVFCSCVMHE 453
DB 402 DVLVRLVQSQELPREKYLTVASRQPSQGTTFVAVTSILRVAEDWKKGDTFSCVMVGE 461
QY 454 ALHNHYVTKSLSLSPCK 470
DB 462 ALPLAFTQTIDRLAGK 478
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Search completed: August 14, 2002, 15:22:21
Job time: 689 sec